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Original article

Combining Ability and Heterosis for Yield and Yield Components in Field Pea (*Pisum sativum* L.)

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Abstract

The objective of this research was to select parents and hybrids that would constitute a suitable initial population to develop new forage pea varieties with high herbage and seed yields suitable for the Thrace Region in Edirne province. Furthermore, the aim was to develop a forage pea breeding program suitable for the region by investigating the genetic structure of the divergence generation of hybrid compatibility. Three-line (Drujba, Gölyazı, M65) and six tester (Kurtbey, Taşkent, Mir, Kirazlı, Naota, Pleven10) parents were used as the hybrids and rootstocks as material using the Line x Tester analysis method. The study was conducted under field conditions at the Thrace Agricultural Research Institute using a randomized complete block design with three replications. In the study, measurements, counting, weighing, and analysis were conducted for plant height, biological yield, number of pods per plant, number of seeds per pod, number of seeds per plant, seed yield, and 1000-seed weight. Statistical analysis was conducted using R. For the traits studied, general and specific compatibility abilities, heterosis and heterobeltiosis values, and broad and narrow-sense heritability were determined for the parents and F1 generations using line x tester analysis. In conclusion, there is sufficient genetic variation in the studied population for the yield components. Non-additive gene effects were detected for all traits studied in the F1 generation.

Keywords: Forage Peas, General Combinig Ability, Specific Combinig Ability, Heritability.

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INTRODUCTION

One of the main problems encountered in livestock nutrition management is the uneven distribution of feed quantity and feed quality throughout the year depending on the seasons (Evers, 2008). This imbalance can be mitigated to some extent by including legume forage crops, which have high protein content and digestibility, in production systems (Collins et al., 2017; Peccetti et al., 2009; Girgin et al., 2020).

Forage pea, an annual legume forage crop, has significant potential for Türkiye as both a main and intermediate crop in forage cultivation (İleri et al., 2020). Forage pea (Pisum sativum L.) is an annual legume plant belonging to the Fabaceae family with 2n=14 chromosomes and self-pollinating (Praça-Fontes et al., 2014).

Although Turkey is among the genetic centers of peas, it is difficult to say that the existing pea genetic resources are adequately and effectively utilized in breeding programs conducted in our country. The low number of registered pea varieties and production quantities in our country are among the most prominent indicators of this situation. Therefore, it is of great importance to reveal the existing richness in pea genetic resources through scientific studies and to utilize these materials in new variety development processes.

One of the main problems encountered in breeding programs is the limited source of variation. This significantly limits the probability of success in the studies conducted. However, by selecting suitable parental materials, it is possible to create a wide source of genetic variation and develop new lines aimed at the target. Knowing the characteristics of parental material and the genetic structure of the characters targeted for development in the plants is of great importance in determining the breeding method to be followed (Ceyhan, 2003, Dar et al., 2017).

In variety development programs, genetic information is a fundamental prerequisite, especially for yield (Dar et al., 2017). The limited number of varieties and the use of the same parent plants lead to the formation of a narrow gene pool, resulting in low genetic diversity among pea varieties (Esposito et al., 2007).

Genetic variation is generally accepted as a crucial factor, a fundamental prerequisite for obtaining high-yielding offspring and conducting variety development programs (Tiwari and Lavanya, 2012). To assess genetic variation, it is important to know the sources of genes responsible for specific traits within the existing genotype pool (Bhardwaj and Kohli, 1999; Chakraborty and Haque, 2000). There is no universal criterion for genotype selection for specific purposes among plant materials. For this reason, the goal in pea breeding is not total biological yield, but rather the development of varieties with high and stable seed yield (Abdou et al., 1999; Gritton, 1986; Tiwari et al., 2001). Genetic variation is crucial for identifying suitable genotypes from different populations to achieve this breeding objective. Observed variability should be separated into heritable and non-heritable components using genetic parameters such as the coefficient of genotypic variation (GCV), heritability estimates, and genetic progress (Hanson et al., 1956, Johnson et al., 1955). At the same time, comparative examination and evaluation of several characters to identify and select desired traits among different genotypes will increase selection success.

Yield and production are shaped by the effect of one or several major genes and the influence of multiple gene interactions. Separating these effects and understanding the genetic variation at the phenotypic level as a result of hybridization in the field is of great importance in breeding studies (Jiang et al., 1994).

Combining ability is an important parameter in plant breeding as it allows for the identification of promising parents to be used in creating genetic variation for final use in the development of suitable varieties; it also helps to characterize the nature and magnitude of genetic effects that govern yield and yield component traits (Başbağ et al., 2007).

Combining ability analyses improve the selection and evaluation of self-pollinated parent lines, thus increasing the opportunity to select superior hybrids. Therefore, information on combining ability is essential for selecting suitable parents with different genetic structures to produce transgressive lines with high adaptability and to produce higher-yielding hybrids from lines with low combining ability (Dar et al., 2017). Estimating the additive and non-additive gene effects on combining ability can be advantageous for good hybrids (Gündüz, 2008). Some findings exist regarding additive and non-additive effects associated with yield and yield-affecting traits in peas (Dar et al., 2017; Kumari et al., 2015; Singh et al., 2013). However, it should be considered that this information and genetic materials were obtained under limited environmental conditions within a specific ecological region and country.

The study aim is to establish a suitable starting population for the development of new forage pea varieties with high forage and seed yield, suitable for the ecological conditions of the Thrace Region in Türkiye. In accordance with this purpose, the study focuses on selecting appropriate parent and hybrid combinations; examining the genetic structures of hybrids in the F1 generation; and, developing a forage pea breeding program adapted to the region's conditions based on the findings.

MATERIAL and METHOD

The material consisted of 18 hybrids and 9 parental plants resulting from the hybridization of 3 lines and 6 testers forage pea genotypes according to a line x tester mating design. All genotypes used as lines had white flowers. Of the genotypes used as testers, Kurtbey had pink flowers, while Taşkent, Mir, Kirazlı, Naota, and Pleven10 had purple flowers. The experimental field has a loamy structure, is slightly alkaline, has a very low salt content, and a low organic matter content. The experimental field, which is low in lime, contains sufficient levels of phosphorus. Edirne province, located in the Thrace part of the Marmara Region, generally exhibits cold semi-continental climate characteristics.

The trials, conducted to determine the agricultural performance and combining ability of forage pea (Pisum sativum L.) hybrids, were established in the experimental fields of the Thrace Agricultural Research Institute during the 2022-2023 growing season according to a randomized block design with 3 replications. In the experiment, 10 seeds were used per plot and 30 seeds in 3 replications, with 2 rows of 1 m length and 5 seeds per row. 20 kg of CAN fertilizer per decare was applied at sowing time during the experimental year. Weed control was carried out mechanically with hoe. Plants were harvested separately in May-June when they reached maturity. Insecticide (Cypra plus, active ingredient cypermethrin) was applied to all experimental plots three times at 10-day intervals starting from the beginning of flowering to control Bruchus spp. pest. Since the experiment was a winter planting, no irrigation was performed. No significant disease problems were encountered in Edirne during the experiment.

Measurements and counts of the characteristics examined in the study were performed on all plants obtained in each plot from F1 hybrids. The characteristics focused on in the study were plant height (cm), biological yield (g/plant), number of pods per plant, number of seeds per pod, number of seeds per plant, seed yield (g/plant), and 1000-seed weight (g).

Statistical analyses were performed using R Studio 4.3.3 software, via the “agricoloe” library, line x tester package, and AGD-R software.

RESULTS and DISCUSSION

Plant Height (cm)

Plant height is an important morphological characteristic in forage peas because it affects lodging resistance and yield components (Ceyhan, 2003). Plant height is a key characteristic of forage peas influencing forage yield and harvest suitability.

According to Table 1, it was determined that the parental plant height values in the F_1 generation ranged from 85.00-146.00 cm, while in the hybrids they varied between 32.75-126.50 cm. The highest mean was recorded in the Pleven 10 tester with (146.00 cm), and the lowest mean was recorded in the Drujba x Taşkent hybrid (32.75 cm). In various studies conducted on peas, plant height values have been observed to vary between 31.83 and 180.00 cm (Avcı and Ceyhan, 2013; Ceyhan et al., 2005; Karayel and Bozoğlu, 2008; Ömeroğlu 2016; Tan et al., 2013). This indicates a wide variation in plant height among genotypes.

When general combining ability (GCA) values were examined in the F_1 generation, Kurtbey (18.00) and Drujba (5.79) genotypes stood out with high positive GCA values at the 1% and 5% probability levels, respectively. This suggests that these genotypes possess superior alleles in terms of plant height and that additive gene effects are significant in increasing plant height (Falconer and Mackay, 1996). Taşkent (-12.50) and M65 (-7.67), which have negative GCA values, showed a significant negative effect at the 1% probability level. Based on these results, it can be said that lines and testers showing a positive effect contribute to plant height increase, while those showing a negative effect contribute to plant height reduction. Genotypes with positive and significant GCA effect values can be easily used to increase plant height, while genotypes with negative and significant values can be used to develop shorter pea varieties.

The specific combining ability (SCA) values of F_1 for plant height ranged from 25.45 (Gölyazı x Taşkent) to -45.95 (Drujba x Taşkent). When the SCA effects of the hybrids were examined, it was observed that, except for 8 hybrids, none of the hybrids showed a statistically significant SCA effect. The Gölyazı x Taşkent (25.45), M65 x Taşkent (20.50), and Drujba x Kurtbey (17.29) hybrids showed statistically significant positive and negative effects at a 1% probability level. Excessively tall plants are undesirable in forage peas as it can lead to lodging. Medium-sized genotypes are therefore important. It was determined that parents with negative and significant GCA values can be easily used to shorten plant height, while parents with positive and significant GCA values can be easily used to lengthen plant height. Hybrids with positive and significant SCA effects can be used for tall plants, while hybrids showing negative and significant SCA effects can be used to obtain short or medium-sized plants. Studies on plant height have been conducted by Borah (2009); Dar et al., (2017); Joshi et al., (2016); and Kosev (2013); Kumar et al. (2017) and Zaman and Hazarika (2005) found statistically significant effects of GCA and SCA on numerous parents and hybrids. It is expected that hybrid showing significant specific combining ability in terms of plant height in either a positive or negative direction will have a wider variability in their segragation generations.

As can be seen from the examination of Table 1, when the heterosis and heterobeltiosis values of hybrids in the F_1 generation are examined, the mean heterosis value is -29.43%; and the heterobeltiosis value is -34.95%. In most hybrids, heterosis and heterobeltiosis values were found to be statistically significant in a negative direction at the 1% probability level; this indicates that plant height in hybrids is generally shorter than in parents. However, the Drujba x Kurtbey hybrid (27.14% Hs; 10.96% Hb) stood out with positive heterosis values at the 1% probability level, indicating that hybrid has superior hybrid performance. When hybrids showing positive heterosis and heterobeltiosis effects are evaluated for tall forage pea, it can be said that they are promising hybrids for developing varieties suitable for silage production. Abdou et al. (1999); Ateş and Ceyhan (2016); Ceyhan (2003); Ceyhan et al. (2008); Sarawat et al. (1994b); Sarawat et al. (1994c) and Singh et al. (1994), who examined heterosis and heterobeltiosis values for plant height, reported that they detected high or low heterosis and heterobeltiosis values for this trait.

The broad sense heritability in the F_1 generation is 0.93, which is quite high. However, the narrow sense heritability is -0.02, which is quite low. This shows that the effects of dominant genes and environmental factors are dominant (Allard, 1999). The high degree of heritability in a broad sense indicates that, in addition to genetic factors, the environment also has a significant influence on the emergence of this trait. These results suggest that selection in terms of plant height should be considered together with seed yield, and therefore, it may be more appropriate to start selection after the F_3 generation (Hallauer et al., 2010).

Drujba x Kurtbey and Gölyazı x Taşkent hybrids stood out with both high heterosis and positive SCA values, and were identified as superior hybrids that can be evaluated in breeding programs in terms of plant height.

Table 1. Means of plant height, specific combining ability (SCA), general combining ability (GCA), heterosis (Hs), heterobeltiosis (Hb), and heritability in the F_1 generation of parents and hybrids

F_1 Genotypes	Means (cm)	GCA	SCA	Hs (%)	Hb (%)
Kirazlı	117,50	1,67			
Kurtbey	85,00	18,00**			
Mir	127,25	-5,67			
Naota	120,00	2,75			
Pleven 10	146,00	-4,25			
Taşkent	109,75	-12,50**			
Drujba	114,00	5,79*			
Gölyazı	143,00	1,88			
M65	127,50	-7,67**			
Drujba x Kirazlı	92,00		-0,87	-20.52**	-21.70**
Gölyazı x Kirazlı	83,75		-5,21	-35.70**	-41.43**
M65 x Kirazlı	85,50		6,08	-30.20**	-32.94**
Drujba x Kurtbey	126,50		17,29**	27.14**	10.96**
Gölyazı x Kurtbey	91,25		-14,04*	-19.96**	-36.19**
M65 x Kurtbey	92,50		-3,25	-12.94**	-27.45**
Drujba x Mir	97,00		11,45	-19.59**	-23.77**
Gölyazı x Mir	89,75		8,12	-33.58**	-37.24**
M65 x Mir	52,50		-19,58**	-58.78**	-58.82**
Drujba x Naota	103,50		9,54	-11.54**	-13.75**
Gölyazı x Naota	70,00		-20,04**	-46.77**	-51.05**
M65 x Naota	91,00		10,50	-26.46**	-28.63**
Drujba x Pleven10	95,50		8,54	-26.54**	-34.59**
Gölyazı x Pleven10	88,75		5,71	-38.58**	-39.21**
M65 x Pleven10	59,25		-14,25*	-56.67**	-59.42**
Drujba x Taşkent	32,75		-45,95**	-70.73**	-71.27**
Gölyazı x Taşkent	100,25		25,45**	-20.67**	-29.90**
M65 x Taşkent	85,75		20,50**	-27.71**	-32.75**
LSD %1 : 15,53	Mean Hs % : -29,434		H^2 : 0,934	SE (Lineler) : 1,697	
LSD %5 : 11,71	Mean Hb % : -34,952		h^2 :-0,029	SE (Testerler) : 2,401	
				SE (SCA) : 4,159	

Note: *: p<0.05 level, **: p<0.01 level, specific combining ability (SCA), general combining ability (GCA), heterosis (Hs), heterobeltiosis (Hb), least significant difference (LSD), broad sense heritability (H^2), narrow sense heritability (h^2) and standard error (SE)

Biological Yield (g/plant)

Biological yield is an indicator of total vegetative-generative production and is generally positively correlated with seed yield (Greveniotis et al., 2021; Uhlarik et al., 2022). Hybrids with specific combining ability can offer significant increases in biological yield if they also exhibit heterosis.

Based on single plant biological yields in F_1 generations, parent values ranged from 52.00 g/plant (Kurtbey) to 151.00 g/plant (Drujba), while hybrid yields ranged from 18.00 g/plant (M65 x Mir) to 162.00 g/plant (Gölyazı x Kurtbey). It was shown that the Gölyazı x Kurtbey hybrid has high potential and can exhibit superior performance in terms of yield. These results indicate that genetic variation persists among hybrids. The findings of this study are consistent with those of Ceyhan (2003). Furthermore, Halil and Uzun (2019) reported biological yield values between 95.32 and 339.59 g/plant in their research with peas.

When the general combining ability (GCA) values were examined in the F_1 generation, Kurtbey (42.41) showed a positive and significant effect at the 1% probability level, and Kirazlı (16.32) showed a positive and significant effect at the 5% probability level. This indicates that the genetic effects of these parents contributing to biological yield are predominantly additive. Mir (-31.59) and Taşkent (-49.93) parents, on the other hand, had a negative effect on yield with negative and significant GCA values at the 1% probability level. These results demonstrate the diversity of the genetic base in terms of biological yield and the presence of significant variations among genotypes.

When the SCA effects of the F_1 generation hybrids on biological yield traits were examined in Table 2, Drujba x Mir (39.22) was found to be positively significant at the 1% probability level and Drujba x Kirazlı (32.06) at the 5% probability level. These hybrids are noteworthy in terms of their specific combining abilities and show that dominant gene effects play an important role. Gölyazı x Kirazlı (-47.32), M65 x Mir (-35.82) and Drujba x Taşkent (-37.44) showed negative effects at the 1% probability level; while M65 x Kurtbey (-27.32) and Drujba x Pleven 10 (-30.78) showed negatively significant effects at the 5% probability level.

As can be seen in Table 2, when the heterosis and heterobeltiosis values of the hybrids in the F_1 generation were examined, the average heterosis value was -3.17%; and the heterobeltiosis value was -20.19%. Heterosis was found to be positively significant at the 1% probability level in Drujba x Kirazlı (22.52), M65 x Kirazlı (39.91), Drujba x Kurtbey (51.48), Gölyazı x Kurtbey (109.03), M65 x Kurtbey (62.42), M65 x Naota (11.53), Gölyazı x Pleven 10 (5.88) and M65 x Pleven 10 (6.41). When heterobeltiosis values were examined, M65 x Kirazlı (22.51), Drujba x Kurtbey (1.82), Gölyazı x Kurtbey (57.28) and M65 x Kurtbey (40.07) showed a positive effect at the 1% probability level. Although positive heterosis and heterobeltiosis were present in the F_1 generation, the fact that almost all hybrids showed negative heterosis and heterobeltiosis, and that these were statistically significant, indicates that they are not suitable for high biological yield. In the study conducted by Yadav et al.

(2015), heterosis values ranged from -34.99% to 53.46% and heterobeltiosis from -35.77% to 51.86%, and they obtained similar results to ours.

When heritability in the F_1 generation was examined, broad sense heritability (H^2 = 0.82) was quite high, while narrow sense heritability (h^2 = 0.08) was low. The low narrow sense of heritability value of the biological yield character indicates that improving this character through selection may be difficult, but progress can be made through suitable hybrids (Fehr, 1987; Griffing, 1956). Biological yield is a trait in forage peas that is highly sensitive to both genotype and environmental interactions. High broad sense heritability in the F_1 generation indicates strong genetic variation and its potential for evaluation in breeding programs. Similar results have been reported in studies on *Pisum sativum* L. and other legume species (Barcchiya et al., 2018).

Table 2. Means of biological yield, specific combining ability (SCA), general combining ability (GCA), heterosis (Hs), heterobeltiosis (Hb), and heritability in the F_1 generation of parents and hybrids

F_1 Genotypes	Means (g/plant)	GCA	SCA	Hs (%)	Hb (%)
Kirazlı	95,50	16,32*			
Kurtbey	52,00	42,41**			
Mir	68,00	-31,59**			
Naota	125,50	13,41			
Pleven 10	135,00	9,41			
Taşkent	127,00	-49,93**			
Drujba	151,00	6,28			
Gölyazı	103,00	4,65			
M65	71,75	-10,93			
Drujba x Kirazlı	151,00		32,06*	22,52**	0,00
Gölyazı x Kirazlı	70,00		-47,32**	-29,47**	-32,04**
M65 x Kirazlı	117,00		15,26	39,91**	22,51**
Drujba x Kurtbey	153,75		8,72	51,48**	1,82**
Gölyazı x Kurtbey	162,00		18,59	109,03**	57,28**
M65 x Kurtbey	100,50		-27,32*	62,42**	40,07**
Drujba x Mir	110,25		39,22**	0,68	-26,99**
Gölyazı x Mir	66,00		-3,41	-22,81**	-35,92**
M65 x Mir	18,00		-35,82**	-74,24**	-74,91**
Drujba x Naota	104,25		-11,78	-24,59**	-30,96**
Gölyazı x Naota	115,00		0,59	0,66	-8,37**
M65 x Naota	110,00		11,18	11,53**	-12,35**
Drujba x Pleven10	81,25		-30,78*	-43,18**	-46,19**
Gölyazı x Pleven10	126,00		15,59	5,88**	-6,67**
M65 x Pleven10	110,00		15,18	6,41**	-18,52**
Drujba x Taşkent	15,25		-37,44**	-89,03**	-89,90**
Gölyazı x Taşkent	67,00		15,93	-41,74**	-47,24**
M65 x Taşkent	57,00		21,51	-42,64**	-55,12**
LSD %1 :40,719	Mean Hs % : -3,176		H^2 : 0,825	SE (Lineler) : 4,452	
LSD %5 :30,703	Mean Hb % : -20,194		h^2 : 0,083	SE (Testerler) : 6,296	
				SE (SCA) : 10,905	

Note: *: p<0.05 level, **: p<0.01 level, specific combining ability (SCA), general combining ability (GCA), heterosis (Hs), heterobeltiosis (Hb), least significant difference (LSD), broad sense heritability (H^2), narrow sense heritability (h^2) and standard error (SE)

Number of Pods per Plant

As with all plants, increasing seed yield is extremely important in peas. The number of pods per plant is one of the most important characteristics determining seed yield in peas. Increasing the number of pods per plant theoretically increases seed yield (Ceyhan, 2003; McPhee and Muehlbauer, 2001; Sarawat et al., 1994b).

According to the number of pods per plant in the F_1 generations, it was determined that the parent values ranged from 32.25 pods/plant (Kurtbey) to 81.00 pods/plant (Naota), and the number of pods per plant in the F_1 generation varied between 5.25 pods/plant (Drujba x Taşkent) and 86.00 pods/plant (M65 x Pleven 10). In this regard, in a study conducted with peas, the average values for the number of pods per plant in hybrids were reported to range from 22.77-55.98 pods, in maternal parents from 13.93-51.80 pods, and in paternal parents from 28.18-51.40 pods (Halil and Uzun, 2019).

When the differences between the minimum and maximum values for the number of pods per plant are examined, it is seen that there are large differences in both hybrids and parents. On the other hand, in hybrids, the magnitude of these types of differences is an indicator of a wide variation. Because, as wide a range of variability as possible in the generational gap of hybrid populations will increase the selection efficiency in terms of the observed trait and will also have a positive effect on the success of the breeding study. Of course, these types of differences can also vary depending on the hybrid populations (Halil and Uzun, 2019).

When the general combining ability (GCA) values in the F_1 generation were examined, Kurtbey (13.89) and Naota (18.22) showed a positive and significant effect at the 1% probability level; Pleven 10 (8.64) and M65 (6.81) showed a positive and significant effect at the 5% probability level. These results show that the parents in question have a superior genetic contribution in terms of the number of pods in the plant and that this trait can be used in breeding studies (Falconer and Mackay, 1996; Singh and Chaudhary, 1981).

Table 3 shows that when the F_1 generation hybrids were examined in terms of the effects of specific combining ability (SCA) on the number of pods, M65 x Kirazlı (25.53), Drujba x Mir (35.61) and M65 x Pleven 10 (20.36) were determined to have 1% compatibility. The fact that M65 x Kirazlı showed high heterosis (77.54%) and heterobeltiosis (61.17%) indicates that genetic superiority and parental complementarity are important (Griffing, 1956). Drujba x Taşkent (-16.06) showed low SCA and very high negative heterosis (-92.95%); this indicates the dominance of genetic incompatibility or epistatic interactions. Abdou et al. (1999); Ateş and Ceyhan (2016); Ceyhan (2003); Ceyhan et al. (2008); Lejeune–Henaut et al. (1992); Sarawat et al. (1994b) and Singh and Singh (1990), who investigated the GCA and SCA effects of parent and hybrid on the number of pods in the plant, obtained similar results to our findings.

As can be seen in Table 3, the average heterosis value was -3.43%; and the heterobeltiosis value was -16.88%. Heterosis was found to be positively significant at the 1% probability level in Gölyazı x Kirazlı (20.25), M65 x Kirazlı (77.54), Drujba x Kurtbey (31.07), Gölyazı x Kurtbey (81.95), M65 x Kurtbey (36.12), Gölyazı x Naota (28.81), M65 x Naota (8.68) and M65 x Pleven 10 (69.46). All remaining hybrids showed a negative effect at a 1% probability level. When heterobeltiosis values were examined, Gölyazı x Kirazlı (13.10), M65 x Kirazlı (61.17), Gölyazı x Kurtbey (70.27), M65 x Kurtbey (10.68) and M65 x Pleven 10 (66.99) showed a positive effect at a 1% probability level. Again, all remaining hybrids were found to have a significant negative effect at a 1% probability level. This finding indicates that F_1 hybrids generally did not show a significant increase in pod number compared to parental averages, and there was a decrease in some hybrids. The fact that the heterosis and heterobeltiosis values of the hybrids varied over a very wide range also shows that this trait is greatly affected by environmental conditions (Ceyhan, 2003). Ceyhan (2003); Ceyhan et al. (2008); Lejeune–Henaut et al. (1992) and Singh et al. (1994), who examined heterosis and heterobeltiosis values for the number of pods in the plant, found significant, both negative and positive, heterosis and heterobeltiosis values for this trait.

When heritability was examined in the F_1 generation, broad sense heritability ($H^2 = 0.897$) was quite high, while narrow sense heritability ($h^2 = 0.015$) was low. The high broad sense heritability and low narrow sense heritability in the study revealed that the number of pods is also affected by the environment. The trait of the number of pods is largely determined by dominant and epistatic genes. In other words, it can be said that selection will not be effective in early generations; however, more efficient selection can be achieved in later generations with the revelation of genetic variance (Mather and Jinks, 1982). Studies on similar topics by Abdou et al. (1999); Ceyhan (2003); Ceyhan et al. (2008); and Sarawat et al. (1994b) have found moderate to high levels of broad sense heritability and low levels of narrow sense heritability for the number of pods per plant. Given the significance of non-additive gene effects in the generation studied, it can be stated that it might be better to start selection after 3-4 generations.

Especially M65 x Pleven 10 and M65 x Kirazlı are candidates for evaluation in advanced selection studies due to their high yield potential and positive heterosis values.

Table 3. Means of number of pods per plant, specific combining ability (SCA), general combining ability (GCA), heterosis (Hs), heterobeltiosis (Hb), and heritability in the F_1 generation of parents and hybrids

F_1 Genotypes	Means (pods per plant)	GCA	SCA	Hs (%)	Hb (%)
Kirazlı	42,00	0,47			
Kurtbey	32,25	13,89**			
Mir	54,75	-17,44**			
Naota	81,00	18,22**			
Pleven 10	50,00	8,64*			
Taşkent	71,00	-23,78**			
Drujba	78,00	-5,11			
Gölyazı	37,00	-1,69			
M65	51,50	6,81*			
Drujba x Kirazlı	21,50		-24,06**	-64,17**	-72,44**
Gölyazı x Kirazlı	47,50		-1,47	20,25**	13,10**
M65 x Kirazlı	83,00		25,53**	77,54**	61,17**
Drujba x Kurtbey	72,25		13,28	31,07**	-7,37**
Gölyazı x Kurtbey	63,00		0,61	81,95**	70,27**
M65 x Kurtbey	57,00		-13,89*	36,12**	10,68**
Drujba x Mir	63,25		35,61**	-4,71**	-18,91**
Gölyazı x Mir	35,00		3,94	-23,71**	-36,07**
M65 x Mir	na		na	na	na
Drujba x Naota	57,25		-6,06	-27,99**	-29,32**
Gölyazı x Naota	76,00		9,28	28,81**	-6,17**
M65 x Naota	72,00		-3,22	8,68**	-11,11**
Drujba x Pleven10	51,00		-2,72	-20,31**	-34,62**
Gölyazı x Pleven10	39,50		-17,64*	-9,20**	-21,00**
M65 x Pleven10	86,00		20,36**	69,46**	66,99**
Drujba x Taşkent	5,25		-16,06*	-92,95**	-93,27**
Gölyazı x Taşkent	30,00		5,28	-44,44**	-57,75**
M65 x Taşkent	44,00		10,78	-28,16**	-38,03**
LSD %1 : 20,914	Mean Hs % : -3,431		H^2 : 0,897	SE (Lineler) : 2,286	
LSD %5 : 15,769	Mean Hb % : -16,881		h^2 : 0,015	SE (Testerler) : 3,233	
				SE (SCA) : 5,601	

Note: *: p<0.05 level, **: p<0.01 level, na:not available specific combining ability (SCA), general combining ability (GCA), heterosis (Hs), heterobeltiosis (Hb), least significant difference (LSD), broad sense heritability (H^2), narrow sense heritability (h^2) and standard error (SE)

Number of Seeds in a Pod

The number of seeds in a pod in peas is an important yield factor in the development of high-yielding varieties. There is a positive relationship between seed yield and the number of seeds in a pod. Seed yield can be increased by increasing the number of seeds in a pod (Ceyhan, 2003).

According to the number of seeds in a pod in the F_1 generations, it was determined that the parent values ranged from 4.25 seeds (Pleven 10) to 7.50 seeds (Kirazlı), and the number of seeds in a pod in the F_1 generation varied between 2.25 seeds (Drujba x Taşkent) and 6.75 seeds (Drujba x Pleven 10). Our research findings are consistent with those of Ateş and Ceyhan (2016); Ceyhan (2003); Ceyhan and Kahraman (2013); The results of Santalla et al. (2001) and Şimşek and Ceyhan (2017) are in agreement. In studies on peas, the number of seeds in the pod has been reported to be between 3.25 and 8.60 (Avcı and Ceyhan, 2013; Ömeroğlu, 2016; Öz and Karasu, 2010; Sayar et al., 2009; Tamkoç 2007, Tan et al., 2013).

When the general combining ability (GCA) values in the F_1 generation were examined, Gölyazı (0.67) showed a positive significant effect at the 5% probability level.

Table 4 shows that when the F_1 generation hybrids were examined in terms of specific combining ability for the seed number trait in forage pea, Drujba x Mir (1.88) and Gölyazı x Mir (1.67) were found to be positively significant at the 5% probability level.

Table 4. Means of number of seeds per pod, specific combining ability (SCA), general combining ability (GCA), heterosis (Hs), heterobeltiosis (Hb), and heritability in the F_1 generation of parents and hybrids

F_1 Genotypes	Means (number)	GCA	SCA	Hs (%)	Hb (%)
Kirazlı	7,50	0,42			
Kurtbey	4,50	0,50			
Mir	5,75	-1,25**			
Naota	5,50	0,42			
Pleven10	4,25	0,58			
Taşkent	5,25	-0,67			
Drujba	6,25	-0,04			
Gölyazı	6,25	0,67*			
M65	6,00	-0,62*			
Drujba x Kirazlı	5,50		-0,29	-20,00	-26,67*
Gölyazı x Kirazlı	6,00		-0,50	-12,73	-20,00
M65 x Kirazlı	6,00		0,79	-11,11	-20,00
Drujba x Kurtbey	6,00		0,12	11,63	-4,00
Gölyazı x Kurtbey	5,50		-1,08	2,33	-12,00
M65 x Kurtbey	6,25		0,96	19,05	4,17
Drujba x Mir	6,00		1,88*	0,00	-4,00
Gölyazı x Mir	6,50		1,67*	8,33	4,00
M65 x Mir	na		na	na	na
Drujba x Naota	5,75		-0,04	-2,13	-8,00
Gölyazı x Naota	6,00		-0,50	2,13	-4,00
M65 x Naota	5,75		0,54	0,00	-4,17
Drujba x Pleven10	6,75		0,79	28,57	8,00
Gölyazı x Pleven10	6,00		-0,67	14,29	-4,00
M65 x Pleven10	5,25		-0,12	2,44	-12,50
Drujba x Taşkent	2,25		-2,46**	-60,87**	-64,00**
Gölyazı x Taşkent	6,50		1,08	13,04	4,00
M65 x Taşkent	5,50		1,38	-2,22	-8,33
LSD %1 : 1,435	Mean Hs % : -5,959		H^2 : 0,911	SE (Lineler) : 0,157	
LSD %5 : 1,081	Mean Hb % : -15,083		h^2 : -0,029	SE (Testerler) :0,221	
				SE (SCA) : 0,384	

Note: *: p<0.05 level, **: p<0.01 level, na:not available specific combining ability (SCA), general combining ability (GCA), heterosis (Hs), heterobeltiosis (Hb), least significant difference (LSD), broad sense heritability (H^2), narrow sense heritability (h^2) and standard error (SE)

As can be seen in Table 4, when the heterosis and heterobeltiosis values of the hybrids in the F_1 generation are examined, the average heterosis value is -5.95%; and the heterobeltiosis value is -15.08%. Ateş and Ceyhan (2016); Avcı and Ceyhan (2006); Ceyhan (2003); Ceyhan et al. (2008); Lejeune–Henaut et al. (1992); Mishra et al. (1993); Sharma et al. (1999) and Singh et al. (1994), who examined the heterosis and heterobeltiosis values for the seed number trait in pea, stated that they generally detected low heterosis and heterobeltiosis values.

The broad sense heritability calculated for the seed number in forage pea in the F_1 generation was determined as 0.91, and the narrow sense heritability was determined as -0.029. Ceyhan (2003), who examined the heritability of seed number in faba bean; Ceyhan et al. (2008); Sarawat et al. (1994b) and Sharma et al. (1999) determined similar results to this research. If it is theoretically assumed that yield increases with increasing seed number in forage peas, then it would be more appropriate to start selection in later generations due to the importance of non-additive gene effects and low hybrid vigor.

Gölyazı stands out as a stable and promising parent with a high GCA value in terms of yield. Drujba x Mir and Gölyazı x Mir hybrids can be included in breeding programs as superior genetic hybrids in terms of seed yield.

Number of Seeds Per Plant

In pea, the number of seeds per plant is an important yield factor in developing high-yielding varieties. Seed yield can be increased by increasing the number of seeds per plant (Ceyhan, 2003).

According to the number of seeds per plant in the F_1 generations, it was determined that the parent values ranged from 114.50 (Kurtbey) to 351.50 (Drujba), and the number of seeds per pod in the F_1 generation varied between 10.25 (Drujba x Taşkent) and 455.00 (M65 x Naota). Our research findings are in agreement with the results of Dalgıç (2018).

When the general combining ability (GCA) values in the F_1 generation were examined, Kurtbey (83.58) and Naota (135.17) showed a significant positive effect at the 1% probability level. Parents with positive and insignificant GCA indicate that they did not adequately pass this trait on to the hybrids. This shows that the Naota and Kurtbey lines have high additive gene effects in terms of seed number.

When the specific combining ability (SCA) values in the F_1 generation were examined, M65 x Kirazlı (122.58) and Drujba x Mir (167.50) were found to be significantly positive at the 1% probability level. These results show that the dominant gene effects are prominent in these hybris, and these hybrids can be evaluated for further breeding studies (Griffing, 1956). On the other hand, the Drujba x Taşkent (-91.17) hybrid showed a significant negative effect at the 1% probability level; and the Drujba x Kirazlı (-80.17) hybrid showed a significant negative effect at the 5% probability level. This situation indicates that these hybrids may have genetic incompatibility or negative hybrids effects. In Dalgıç's (2018) study on the effect of GCA and SCA on seed number in plants, they identified parents and hybrids showing significant GCA and SCA effects in varying numbers in the generation they examined.

As can be seen in Table 5, when the heterosis and heterobeltiosis values of the hybrids in the F_1 generation were examined, the average heterosis value was 21.09%, and the heterobeltiosis value was 0.45%. When examined in terms of seed number in plants in the F_1 generation, heterosis showed a significant positive effect in eleven hybrids and heterobeltiosis in eight hybrids at a 1% probability level. These values reveal that the superior parental effect is successfully carried in hybrids (Sharma, 2006).

The broad sense heritability calculated for seed number in plants in the F_1 generation was determined as 0.874, and the narrow sense heritability as 0.060. The fact that the heritability of the seed number in the plant is calculated as high in the broad sense and low in the narrow sense indicates that the effect of genotype variance on this trait is low.

Table 5. Means of number of seeds per plant, specific combining ability (SCA), general combining ability (GCA), heterosis (Hs), heterobeltiosis (Hb), and heritability in the F_1 generation of parents and hybrids

F_1 Genotypes	Means (number)	GCA	SCA	Hs (%)	Hb (%)
Kirazlı	241,00	17,50			
Kurtbey	114,50	83,58**			
Mir	227,00	-68,67**			
Naota	297,50	135,17**			
Pleven 10	168,00	-29,08			
Taşkent	251,50	-138,50**			
Drujba	351,50	-5,00			
Gölyazı	138,00	-6,00			
M65	167,00	11,00			
Drujba x Kirazlı	177,25		-80,17*	-40,17**	-49,57**
Gölyazı x Kirazlı	214,00		-42,42	12,93**	-11,20**
M65 x Kirazlı	396,00		122,58**	94,12**	64,32**
Drujba x Kurtbey	368,00		44,50	57,94**	4,69**
Gölyazı x Kurtbey	333,00		10,50	163,76**	141,30**
M65 x Kurtbey	284,50		-55,00	102,13**	70,36**
Drujba x Mir	338,75		167,50**	17,11**	-3,63**
Gölyazı x Mir	190,00		19,75	4,11**	-16,30**
M65 x Mir	na		na	na	na
Drujba x Naota	320,75		-54,33	-1,16**	-8,75**
Gölyazı x Naota	364,50		-9,58	67,39**	22,52**
M65 x Naota	455,00		63,92	95,91**	52,94**
Drujba x Pleven10	224,50		13,67	-13,57**	-36,13**
Gölyazı x Pleven10	183,00		-26,83	19,61**	8,93**
M65 x Pleven10	240,00		13,17	43,28**	42,86**
Drujba x Taşkent	10,25		-91,17**	-96,60**	-97,08**
Gölyazı x Taşkent	149,00		48,58	-23,49**	-40,76**
M65 x Taşkent	160,00		42,58	-23,54**	-36,38**
LSD %1 : 106,183	Mean Hs % : 21,099		H^2 : 0,874	SE (Lineler) : 11,609	
LSD %5 : 80,063	Mean Hb % : 0,451		h^2 : 0,060	SE (Testerler) :16,418	
				SE (SCA) : 28,436	

Note: *: p<0.05 level, **: p<0.01 level, na:not available specific combining ability (SCA), general combining ability (GCA), heterosis (Hs), heterobeltiosis (Hb), least significant difference (LSD), broad sense heritability (H^2), narrow sense heritability (h^2) and standard error (SE)

Seed Yield (g/plant)

Seed yield is the ultimate economic character and has shown positive correlations with pod number, seed per plant, biological yield, and 1000-seed weight in most studies (Greveniotis et al., 2021; Uhlarik et al., 2022). Although single-plant seed yields are used to determine the seed yields of genotypes, the significant influence of environmental conditions on this trait makes a precise assessment difficult (Ceyhan, 2003).

Based on seed yield in the F_1 generation, it was determined that the parent values ranged from 13.00 g/plant (Pleven 10) to 42.83 g/plant (Drujba), and the seed yield in the F_1 generation ranged from 0.39 g/plant (Drujba x Taşkent) to 56.22 g/plant (M65 x Naota). The findings of this study are in agreement with those of Ateş and Ceyhan (2016); Ceyhan (2003); Ceyhan and Avcı (2005); Ceyhan (2006); Ceyhan et al. (2008); Ceyhan and Kahraman (2013); Lejeune–Henaut et al. (1992); Sarawat et al. (1994a); Sarawat et al. (1994b); Sarawat et al. (1994c) and Şimşek and Ceyhan (2017).

When the general combining ability (GCA) values in the F_1 generation were examined, Kurtbey (18.43) and Naota (13.69) showed a significant positive effect at the 1% probability level. These findings indicate that Kurtbey and Naota are lines with strong overall suitability towards high yield and can be considered as yield-enhancing parents in further breeding studies.

When the specific combining ability (SCA) values in the F_1 generation were examined, M65 x Kirazlı (16.94) and Drujba x Mir (17.48) were found to be significant in a positive direction at the 1% probability level; Gölyazı x Mir (9.87) and M65 x Naota (8.79) were found to be significant at the 5% probability level. These results show that the effects of dominant genes are significant in these hybrids, and these hybrids can be evaluated for further breeding studies. Many studies have been conducted on the effects of GCA and SCA on pea, and researchers have identified parents and hybrids showing varying numbers of significant GCA and SCA effects on seed yield in the generations they examined (Ateş and Ceyhan, 2016; Avcı and Ceyhan, 2006; Ceyhan, 2003; Ceyhan and Avcı, 2005; Ceyhan, 2006; Ceyhan et al., 2008; Singh and Singh, 1990; Lejeune–Henaut et al., 1992; Sarawat et al., 1994b; Sharma et al., 1999).

As can be seen in Table 6, when the heterosis and heterobeltiosis values of hybrids in the F_1 generation are examined, the average heterosis value is 32.687%; and the heterobeltiosis value is 8.91%. When seed yield in the F_1 generation was examined, heterosis was found to be significant in twelve hybrids and heterobeltiosis in ten hybrids at a 1% probability level. In cases where non-additive gene effects are significant, efforts are made to identify parents and hybrids exhibiting heterosis. Many studies on this subject have determined that F_1 hybrids obtained from high-yielding parents of different origins yield higher yields (Abdou et al., 1999; Ateş and Ceyhan, 2016; Avcı and Ceyhan, 2006; Ceyhan, 2003; Ceyhan and Avcı, 2005; Ceyhan, 2006; Ceyhan et al., 2008; Lejeune–Henaut et al., 1992; Mishra et al., 1993; Sarawat et al., 1994b; Sharma et al., 1999; Singh and Singh, 1990; Singh et al., 1994; Stelling et al., 1990).

The heritability for seed yield in the F_1 generation was determined to be 0.89 in the broad sense and 0.102 in the narrow sense. Abdou et al. (1999); Ceyhan (2003); Ceyhan et al. (2008), Ceyhan and Kahraman (2013); and Sarawat et al. (1994a), who investigated the inheritance of seed yield in peas, found that the heritability for this trait was high in the broad sense and low in the narrow sense. The low narrow sense heritability for seed yield and the identification of non-additive gene effects in the inheritance of this trait reduce the chances of success of selection in early generations for seed yield. For these reasons, selecting for highly heritable and clearly evident traits instead of seed yield in early generations may increase the chances of success. The high H^2 value and strong heterosis effect in the F_1 generation indicate that the seed yield character is largely controlled by dominant genes and that early selection can be applied. When evaluated from a breeding perspective; due to their high compatibility and positive heterosis values, Kurtbey and Naota genotypes are recommended as preferred parents in high-yielding line development studies.

Table 6. Means of number of seed yield, specific combining ability (SCA), general combining ability (GCA), heterosis (Hs), heterobeltiosis (Hb), and heritability in the F_1 generation of parents and hybrids

F1 Genotypes	Means (g/plant)	GCA	SCA	Hs (%)	Hb (%)
Kirazlı	41,58	4,33			
Kurtbey	15,03	18,43**			
Mir	21,45	-6,38*			
Naota	29,78	13,69**			
Pleven 10	13,00	-5,29*			
Taşkent	21,23	-24,79**			
Drujba	42,83	-1,47			
Gölyazı	23,59	0,74			
M65	20,49	0,74			
Drujba x Kirazlı	20,00		-15,85**	-52,61**	-53,30**
Gölyazı x Kirazlı	36,98		-1,08	13,50**	-11,05**
M65 x Kirazlı	55,00		16,94**	77,23**	32,29**
Drujba x Kurtbey	55,35		5,39	91,35**	29,24**
Gölyazı x Kurtbey	48,85		-3,32	152,98**	107,06**
M65 x Kurtbey	50,09		-2,08	182,05**	144,44**
Drujba x Mir	42,63		17,48**	32,64**	-0,47
Gölyazı x Mir	37,23		9,87*	65,33**	57,82**
M65 x Mir	na		na	na	na
Drujba x Naota	44,69		-0,52	23,11**	4,35
Gölyazı x Naota	39,14		-8,28	46,67**	31,43**
M65 x Naota	56,22		8,79*	123,67**	88,78**
Drujba x Pleven10	26,07		-0,16	-6,61	-39,13**
Gölyazı x Pleven10	32,33		3,89	76,71**	37,05**
M65 x Pleven10	24,72		-3,72	47,63**	20,64**
Drujba x Taşkent	0,39		-6,34	-98,78**	-99,09**
Gölyazı x Taşkent	7,86		-1,08	-64,93**	-66,68**
M65 x Taşkent	16,36		7,42	-21,57**	-22,94**
LSD %1 : 13,317	Mean Hs % : 32,687		H2 : 0,893	SE (Hatlar) : 1,456	
LSD %5 : 10,042	Mean Hb % : 8,914		h2 : 0,102	SE (Testerler) :2,059	
				SE (SCA) : 3,566	

Note: *: p<0.05 level, **: p<0.01 level, na:not available specific combining ability (SCA), general combining ability (GCA), heterosis (Hs), heterobeltiosis (Hb), least significant difference (LSD), broad sense heritability (H^2), narrow sense heritability (h^2) and standard error (SE)

1000-Seed Weight (g)

1000-seed weight is critical for quality and marketability and often shows a positive correlation with yield (Yimam et al., 2024). In peas, 1000-seed weight is an important yield factor that directly affects yield (Ceyhan, 2003).

Based on the 1000-seed yield in the F_1 generations, it was determined that the parent values ranged from 70.73 g (Pleven 10) to 165.25 g (Kirazlı), and the 1000-seed yield in the F_1 generation ranged from 38.03 g (Drujba x Taşkent) to 179.55 g (Gölyazı x Mir). Some researchers have obtained similar results (Ateş and Ceyhan, 2016; Avcı and Ceyhan, 2006; Avcı and Ceyhan, 2013; Ceyhan, 2003; Ceyhan and Avcı, 2005; Ceyhan et al., 2008; Ceyhan et al., 2012; Kranup, 1995; Şimşek and Ceyhan, 2017).

When the general combining ability (GCA) values in the F_1 generation were examined, Kirazlı (20.76), Kurtbey (42.93) and Gölyazı (20.09) showed a significant positive effect at the 1% probability level.

When the hybrids of the F_1 generation were examined in terms of their specific combining ability (SCA), Gölyazı x Mir (179.55) and M65 x Taşkent (54.43) were found to have a significant positive effect at the 1% probability level. Abdou et al. (1999); Avcı and Ceyhan (2006); Ateş and Ceyhan (2016); Ceyhan (2003); Ceyhan and Avcı (2005); Ceyhan et al. (2008); Lejeune–Henaut et al. (1992); Sarawat et al. (1994b); Sharma et al. (1999) and Singh and Singh (1990) identified genotypes with significant positive GCA and SCA for 100-seed weight in their studies.

When the heterosis and heterobeltiosis values of the hybrids in the F_1 generation were examined, the average heterosis value was -8.49%; and the heterobeltiosis value was -21.18%. When examined in terms of 1000-seed yield in the F_1 generation, heterosis showed a significant positive effect in nine hybrids; and heterobeltiosis showed a significant positive effect in four hybrids at the 1% probability level. Abdou et al. (1999); Ateş and Ceyhan (2016); Avcı and Ceyhan (2006); Ceyhan (2003); Ceyhan and Avcı (2005); Ceyhan et al. (2008); Lejeune–Henaut et al. (1992); Sarawat et al. (1994b); Sharma et al. (1999) and Singh and Singh (1990) reported that they determined different heterosis and heterobeltiosis values for 100-seed weight. The values determined in this study are among the values determined by these researchers.

The broad sense heritability calculated for seed yield in the F_1 generation was determined as 0.87, and the narrow sense heritability was determined as 0.026. Dalgıç (2018), who examined the inheritance of 100-seed weight in peas, found that the broad sense heritability was high and the narrow sense heritability was also high for this trait in the F_2 generation. The high narrow sense heritability is also an indication of the presence of additive gene effects. Ateş and Ceyhan (2016); Ceyhan (2003); Ceyhan and Avcı (2005); Ceyhan et al. (2008); Ceyhan and Kahraman (2013); Kranup (1995); Sarawat et al.

(1994b); Sharma et al. (1999) and Şimşek and Ceyhan (2017), who investigated the inheritance of 100 seed weights, obtained similar results to this research.

Table 7. Means of 1000-seed weight, specific combining ability (SCA), general combining ability (GCA), heterosis (Hs), heterobeltiosis (Hb), and heritability in the F_1 generation of parents and hybrids

F_1 Genotypes	Averages (g)	GCA	SCA	Hs (%)	Hb (%)
Kirazlı	165,25	20,76**			
Kurtbey	147,50	42,93**			
Mir	82,17	-13,51			
Naota	106,65	6,50			
Pleven 10	70,73	-9,26			
Taşkent	85,47	-47,43**			
Drujba	124,75	-6,32			
Gölyazı	153,31	20,09**			
M65	126,41	-13,77*			
Drujba x Kirazlı	101,78		-25,69	-29,81**	-38,41**
Gölyazı x Kirazlı	176,60		22,72	10,87**	6,87**
M65 x Kirazlı	123,00		2,98	-15,66**	-25,57**
Drujba x Kurtbey	153,25		3,61	12,58**	3,90**
Gölyazı x Kurtbey	169,40		-6,65	12,63**	10,50**
M65 x Kurtbey	145,24		3,05	6,05**	-1,53*
Drujba x Mir	119,03		25,82	15,04**	-4,59**
Gölyazı x Mir	179,55		59,93**	52,50**	17,12**
M65 x Mir	-		-	-	-
Drujba x Naota	120,33		7,12	4,00**	-3,55**
Gölyazı x Naota	121,96		-17,66	-6,17**	-20,45**
M65 x Naota	116,30		10,54	-0,20	-8,00**
Drujba x Pleven10	107,84		10,39	10,33**	-13,56**
Gölyazı x Pleven10	98,70		-25,15	-11,89**	-35,62**
M65 x Pleven10	104,75		14,76	6,27**	-17,13**
Drujba x Taşkent	38,03		-21,25	-63,82**	-69,52**
Gölyazı x Taşkent	52,50		-33,18*	-56,03**	-65,76**
M65 x Taşkent	106,26		54,43**	0,30	-15,94**
LSD %1 : 42,449	Mean Hs % : -8,499		H^2 : 0,874	SH (Lineler) : 4,641	
LSD %5 : 32,007	Mean Hb % : -21,180		h^2 : 0,026	SH (Testerler) :6,563	
				SH (SCA) : 11,368	

Note: *: $p<0.05$ level, **: $p<0.01$ level, na:not available specific combining ability (SCA), general combining ability (GCA), heterosis (Hs), heterobeltiosis (Hb), least significant difference (LSD), broad sense heritability (H^2), narrow sense heritability (h^2) and standard error (SE)

Conclusion

Seventeen different morphological traits were examined in the F_1 generation. Line × Tester analysis results showed statistically significant genetic variation among the hybrids. This indicates that the evaluated population has sufficient genetic diversity for breeding studies.

In the evaluation of gene effects, it was determined that all traits in the F_1 generation were under the influence of non-additive gene effects. The fact that all traits examined in the F_1 generation were controlled by non-additive gene effects shows that phenotypic expression in this generation is predominantly shaped by dominance and intergenetic interactions. This indicates that the high performance observed in the F_1 generation is largely due to heterosis and that genetic interactions specific to the hybrid combination are more prominent than the individual genetic contributions of the parents.

These results are consistent with studies in literature reporting that non-additive gene effects become dominant in the F_2 and early initiation generations of self-pollinating plants. From a breeding strategy perspective, the findings of this study indicate that while the F_1 generation is a crucial stage for identifying potential superior parent and hybrid combinations in feed pea for yield and yield components, permanent selection decisions should be based on the F_2 and subsequent generations. It has been determined that parents with high general combining ability in the F_1 generation excel in certain traits, and these parents can be used as valuable genetic material in forage pea breeding.

Additional Declaration

This study was prepared based on the doctoral thesis of Gülten Sağlam who is Aydın Adnan Menderes University, Institute of Natural and Applied Sciences, Aydın, Türkiye.

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Author Contributions

In this study, the contribution of the authors was equal; both authors contributed equally to the development of the research idea, data analysis, writing and proofreading stages.

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Responsible Artificial Intelligence Statement

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Conflicts of Interest

The authors declare that there are no conflicts of interest related to the publication of this study.

Ethics Approval

In all processes of this study, the principles of Pen Academic Publishing Research Ethics Policy were followed.

This study does not require ethics committee approval as it does not involve any direct application on human or animal subjects.

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