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UNTANGLING GENETIC VARIABILITY OF TWENTY-ONE FIELD PEA (*PISUM SATIVUM* L. SUBSP. *ARVENSE* L.) GENOTYPES FOR GRAIN YIELD IN BILECIK, TÜRKİYE

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Abstract

Grain legumes, including field pea, contribute significantly to ensuring nutritional security; however, research gaps exist regarding their genetic potential for grain yield under the agro-ecological conditions of Bilecik, Türkiye. Therefore, a two-year screening study comparatively assessed 15 potent genotypes of field pea (KB-211, 21, 39, 55, 70, 79, 90, 95, 104, 110, 124, 141, 153, 161, and 165) and 6 varieties (Tore, Servet, Whistler, Ulubatli, Golyazi, and Kirazli). The experiment was conducted in a randomized complete block design (RCBD) with three replicates. The results showed that genotype 39 had the highest harvest index (37.7%), and the Whitler variety exhibited the maximum number of pods per plant (13.9), biological yield (8.92 t ha^{-1}), and straw yield (7.04 t ha^{-1}). However, the Golyazi cultivar showed a maximum seed yield of 2.71 t ha^{-1} (89% higher than the least performing genotype 21) owing to superior genetic potential and adaptability to soil and environmental conditions. In addition, the correlation analysis demonstrated a positive and significant association between seed yield and physiological maturity (0.537*), biological yield (0.760**), and straw yield (0.607**). Contrastingly, a negative correlation (-0.667**) between seed yield and the number of seeds per pod was recorded, probably owing to a reduction in seed weight with increasing number of seeds per plant. Moreover, the biological yield had the strongest direct association with seed yield, which in turn had linear relationships with straw yield and the number of seeds per pod. Furthermore, as per principal component analysis, PC 1 depicted the eigenvalue of 3.79 and accounted for 47.45% of the variation, while PC 2 had an eigenvalue of 2.13 and accounted for 26.70% of the variation. Based on recorded findings, Golyazi, Whitler, and genotype 39 could be recommended to field pea growers and breeders for developing high-potential cultivars with better adaptability under changing climatic scenarios of global warming and disruption of rainfall patterns.

Key words: Biological nitrogen fixation, Dual-purpose crop, Grain legumes, Correlation analysis, Principal component analysis

Introduction

Grain legumes have increasingly become vital for ensuring the food security of the human population globally (Sayed *et al.*, 2024; Ahmad *et al.*, 2025). Importantly, these hold the potential to reduce the marked deficit of protein in the human diet, along with contributing to nitrogen (N) to soil through the biological nitrogen fixation (BNF) process, which pronouncedly reduced greenhouse gas emissions from agricultural lands (Awal *et al.,* 2024; Shaddam *et al.*, 2024). The BNF process, which takes place in root nodules of legumes, tends to enrich the soil by fixing the atmospheric N with the help of the Rhizobium bacteria in the rhizosphere (Sadiq *et al.*, 2023). Compared to warm-season legumes, comparatively higher N fixation has been reported in winter-sown grain legumes (Smytkiewicz *et al.*, 2021; Iqbal *et al.*,2022). In addition, grain legumes impart resilience and sustainability to modern crop-livestock farming systems by restoring soil fertility and microbial population for organic matter decomposition (Harmankaya *et al.*, 2010). Moreover, they also occupy a special place among field crops because of their suitability for crop rotation in cereal-dominant farming systems (Iqbal *et al.*, 2023).

Recently, field pea (*Pisum sativum* L. subsp. *arvense* L.) has attained the status of one of the largest cultivated grain legumes in Europe, owing to its high yield potential and nutritional value due to abundant protein content (24-31%). Besides protein content, it has been reported to be rich in carbohydrates, amino acids (the human body cannot synthesize most of them), vitamins (A, B complex, C, and D), and minerals (calcium, phosphorus, iron, etc.) (Harmankaya *et al.,* 2010). Owing to numerous health benefits, it is consumed as fresh produce or canned and frozen foods in European countries. Interestingly, light-coloured seeds (*Pisum sativum* subsp. *sativum*) find their utilization in human food, whereas, owing to extreme difficulty in cooking, dark-coloured seeds (*Pisum sativum* subsp. *arvense*) are mostly used as a protein-rich feed for dairy animals (Karayel & Bozoğlu, 2012).

Field pea is predominantly grown in Türkiye's western regions (having a transitional climate influenced by continental Anatolian and Marmara, characterized by warm to hot summers and cold to snowy winters, along with uniformly

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distributed rainfall throughout the year) as a grain legume in winter (Sumer, 2023). Globally, it has been ranked as the third largest edible grain legume in terms of area under cultivation (over 7 billion ha), whereas its corresponding rank is fifth in Türkiye, with 679 ha of cultivated area under this crop (Anon., 2021). Besides human consumption, it has persistently gained interest over time among dairy farmers in Türkiye owing to its potential to address the deficit of good-quality forages for livestock, particularly during the winter season. Its forage is highly nutritious due to high protein (22-28%) and low fiber content, and relished by dairy animals in green succulent form, hay (air-dried feed), and silage (fermented feed) (Ouafi *et al.,* 2016). Likewise, it has been mixed with roughages in different ratios, which boosted milk production and reduced the cost of production. Additionally, it contained significantly higher digestible substances (86-87%) than many forage crops (both cereals and legumes) and has been considered as an alternative to soybean in many European countries (Çaçan *et al.,* 2018). Moreover, it is being grown in many parts of Türkiye as a green manure crop to restore soil fertility sustainably, and it has been reported that this crop contributed 50-150 kg ha^{-1} N (Tekeli & Ates, 2003; Ozkan, 2020).

In Europe, field pea yield losses vary from 30-60% owing to a wide array of factors, including genetic potential of specific cultivars, inappropriate sowing time, unfavorable climatic conditions, soil fertility status, and particular locality-related ecological factors (intensity and distribution of rainfall, soil compaction, insect-pest attacks, etc.) (Mcdonald & Peck, 2009; Öten *et al.,* 2017; Kadioğlu & Tan, 2018). The optimum range of temperature for germination and growth of winter-sown field peas has been 18-22˚C. However, one of the downsides of field pea is its sensitivity to elevated temperatures because even a slight increase in temperature over 25˚C, particularly at the initiation of the flowering stage, caused significant yield losses and adversely affected the seed quality (Jiang *et al.,* 2019; Lamıchaney *et al.,* 2021; Parihar *et al.,* 2022). Contrastingly, field pea grain yield was seriously reduced in regions where elevated temperature spells occurred at the pod formation stage of the crop (Guilioni *et al.,* 2003; Bueckert *et al.,* 2015). In such scenarios, it has become vital to screen out the genotypes of field pea that might perform as per their genetic potential under the prevalent climatic conditions of specific regions and changing climatic scenarios.

Previously, it was inferred that considerable genotypic variation existed among field pea genotypes (Mayer, Giresun, Local 1, Local 2), as the Mayer genotype remained unmatched by recording the highest yield (1.95 t ha^{-1}), whereas the Giresun genotype exhibited the maximum protein content (25.6%) (Sumer, 2023). The underlying reason was the varying response of field pea genotypes to temperature, which influenced several physiological processes (photosynthesis, respiration, fertilization, and maturation). It was suggested that different genotypes had varying growth degree requirements to attain the key phenological stages, which led to variation in grain yield. Olle (2017), Devi *et al.* (2019), and Ahmed *et al*., (2020) also reported that field pea genotypes responded differently to elevated temperatures, which ultimately led to pronounced differences in grain yield produced on a per unit land area basis. Contrastingly, Rubiales *et al*., (2009) noted that field pea cultivars varied in their response to diseases in the Mediterranean environment due to genetic makeup differences among them. However, it was also reported that genotypic variation resulted in pronounced differences in the chemical composition of field pea genotypes (Wang *et al.,* 2010).

In Türkiye, the transitional climate of the Bilecik region offers suitable climatic conditions for achieving a higher grain yield of field pea; however, it could not be achieved as per the genetic potential of the cultivars (Demirbaş, 2018; Ton *et al.,* 2018). Therefore, it has become strategically vital to identify and sort out new cultivars having higher seed yield potential and adaptability to local agro-climatic conditions. Moreover, conducting fresh screening studies has become even more important to find out potent genotypes that could be utilized in cultivar breeding programs (Kumar *et al.,* 2018; Prasad *et al.,* 2018). However, there is a paucity of information on field pea genotypes having superior adaptability in the Bilecik regions of Türkiye and agronomic traits that contribute to grain yield and impart adaptation to contrasting environments. Therefore, the research hypothesis of this study entailed that field pea genotypes vary in their grain production potential by virtue of different genetic make-up, agro-botanical traits, and root architecture, which could lead to different agro-morphological responses under the same set of agro-climatic conditions and agronomic management plans. Thus, in this multi-year field investigation, many potent and geographically diversified field pea cultivars underwent comparative performance analysis with the prime objective of defining their yield potential in the Bilecik agroecological and climatic conditions.

Materials and Methods

Experimental details: Field trials were conducted at the Research and Application Center of the Faculty of Agriculture, Bilecik Şeyh Edebali University, Türkiye (39º39′N, 30º40′E, having 850 m altitude), for two seasons (2016 – 2018). The planting material included 15 field pea genotypes (KB-211, 21, 39, 55, 70, 79, 90, 95, 104, 110, 124, 141, 153, 161, and 165) that were provided by the Sivas Vocational School Cumhuriyet University, Türkiye, along with 6 commercial varieties (Tore, Servet, Whistler, Ulubatli, Golyazi, and Kirazli). In this way, the experiment included 21 genotypes of field pea, and the trial was conducted in a randomized complete block design (RCBD) using the regular arrangement with three replications for each genotype. Manual sowing was performed in mid-October each year, with P×P spacing of 4 cm. Each plot covered a net area of 6×8 meters, consisting of 20 rows with R×R spacing of 30 cm. During sowing, a composite fertilizer containing N (30 kg ha^{-1}) and P_2O_5 (60 kg ha^{-1}) was applied as a basal dose, because field pea requires less N than phosphorus owing to its potential to fix atmospheric N through the BNF process.

Meteorological features of the experimental locality and soil physico-chemical traits: During the experiment conducted in 2016-2017 and 2017-2018, the total annual precipitation was measured as 562.2 mm, 1069.0 mm, and 512.7 mm, respectively. Relative humidity and average temperatures remained stable throughout 2016, 2017, and 2018. The precipitation and average temperature values during September and May of both growing seasons remained higher than the long-term average (Table 1). During the first year of the experiment, the field pea experienced higher average temperatures and precipitation compared to the following year. For conducting soil analysis, the samples were collected from the middle as well as all corners of the experimental block, which were thoroughly mixed and stored in Ziplock bags for further investigations. The results showed that the soil of the experimental area had low organic matter content (1.5%), medium levels of calcium carbonate (8.3%), and a strong alkaline pH (8.1).

Recording of response variables: The study analyzed various response variables of all genotypes under investigation, including seed yield, number of seeds per plant, thousand seed weight, number of pods per plant, straw yield, biological yield, physiological maturity, and harvest index (HI). Harvesting of crops for estimating yield components and seed yield was performed when the pods were fully mature. To analyze seed yield components, pod samples from 10 randomly selected plants from the interior rows within each plot were examined. The HI was estimated by the following equation 1 (Iqbal *et al.*, 2019). Moreover, the estimation of biological yield (BY) was performed by using equation 2 (Iqbal *et al.*, 2016). Furthermore, straw yield (SY) was determined by subtracting GY from BY, by following equation 3.

$$\text{HI (\%)} = \frac{\text{Grain yield}}{\text{Biological yield}} \times 100 \qquad (1)$$

$$\text{BY} = \text{Grain yield + Straw yield} \qquad (2)$$

$$\text{SY} = \text{Biological yield - Seed yield} \qquad (3)$$

Statistical analysis: The data were analyzed using the JMP Software (version Pro 13) as per the regular arrangement of the randomized complete block design (RCBD). The recorded data of response variables were subjected to statistical analysis through the analysis of variance (one-way ANOVA) technique for estimating the overall significance among field pea genotypes under investigation. To assess significance among treatment means, the least significant difference (LSD) test was applied by setting the probability level of 5% (Steel *et al.*, 1997). Additionally, the path coefficient analysis was conducted to determine both direct and indirect associations of yield attributes with the grain yield of field pea under Bilecik climatic conditions. Moreover, the principal component analyses were performed on all genotypes for the estimation of the genotypes' performance in relation to each other.

Results

The analysis of variance (ANOVA) revealed significant variations among 15 genotypes and 6 varieties of field pea for all response variables under investigation (Table 2).

Harvest index, physiological maturity, biological yield, and straw yield: In terms of the harvest index, biological yield, and straw yield, the genotype and year interaction remained nonsignificant, whereas this interaction was significant for the physiological maturity of field pea genotypes under investigation (Table 2). Among all genotypes of field pea, genotype 39 (37.7%) remained unmatched by recording the maximum HI; however, it was statistically at par with the Ulubatli (37.6%) cultivar during both years. Genotype 104 exhibited the lowest HI value of 18.9% which was even lower than the HI recorded by the most superior Genotype 39. Regarding physiological maturity (FM), the genotype KB-211 recorded the minimum number of days required to reach the FM stage, and it was followed by the genotypes 104 and 161. Contrastingly, the field pea genotypes 21, 124, Golyazi, and Whitler recorded the maximum number of days to attain the FM stage (Table 2). As per year-wise data, the results showed that in the first year, genotypes 21 and 39 had the longest FM, with 233.0 and 232.0 days, respectively. In the second year, genotypes 124, 55, and 39 had the longest FM, with 234, 231.4, and 231.6 days, respectively (Fig. 1). As far as the biological yield values of various field pea genotypes were concerned, the Whitler variety remained superior by exhibiting the highest biological yield (8.92 t ha^{-1}) closely followed by the Tore cultivar which produced only 10 kg da^{-1} lesser BY than the Whitler variety, while the genotype 39 had the lowest yield (4.01 t ha^{-1}). Interestingly, genotype 79 with BY of 8.85 t ha^{-1}, remained statistically at par with the Whitler variety, which had the highest biological yield. Moreover, significant differences were recorded among field pea genotypes in terms of straw yield. Overall, genotype 104 recorded the maximum SY value (7.04 t ha^{-1}) (Table 2). It was followed by genotype 21, which in turn performed statistically at par with the Whitler genotype. However, genotype 39 exhibited the lowest SY value (250.28 t ha^{-1}), which was 182% less than the most performing genotype 104.

Number of pods per plant, number of seeds per pod, 1000-seed weight, and seed yield: The year × genotype interactions remained non-significant for the number of pods per plant (NPP), thousand seed weight (TSW), and seed yield (SeY) of field pea genotypes, whereas a significant interactive effect was recorded for seed number in each pod (NSP) (Table 2). As far as NPP was concerned, the results indicated that the Whitler variety performed superiorly to the rest of the genotypes under investigation by recording the maximum NPP value of 13.9. Genotypes 21, 39, 141, and the Gölyazı also showed remarkable results in terms of the NPP and closely followed the most performing genotype, Whitler. The KB-211, 70, and 110 genotypes could not perform at par with to rest of the genotypes and exhibited the minimum NPP. In the first year, genotype 21 (7.7) had the highest NSP along with the varieties Gölyazi (7.6), Kirazli (7.4), and Servet (7.6), while in the second year, genotype 165 (7.8) recorded the maximum NSP along with the varieties Servet (7.4) and Tore (7.4). In the first year, Genotype 104 recorded the lowest NSP value of 3.2, while in the second year, the Whitler variety had the lowest count of 3.3 (Fig. 2). Regarding the TSW of field pea genotypes in this study, their values ranged from 110.4 g (Tore cultivar) to 226.4 g (genotype 110). However, the highest value (226.4 g) was obtained from 110 genotypes (Table 3), whereas the Whitler cultivar (225.9 g) also performed statistically at par with 110 genotypes. The data pertaining to the SeY of various field pea genotypes in Bilecik conditions of Türkiye revealed that the Golyazi cultivar remained unmatched by recording the highest SeY of 2.71 t ha^{-1} (Table 2). Genotype 110 recorded the SY of 2.37 t ha^{-1} and was grouped with the Whitler and Tore varieties. The lowest SeY was observed for genotype 165 with 1.18 t ha^{-1}.

Table 1. Mean monthly and 10-year average data of temperature and precipitation of the experimental locality (Bilecik, Türkiye) during both crop growth seasons.

Months	Temperature (°C)			Precipitation (mm)		
	2016-17	2017-18	10 years average	2016-17	2017-18	10 years average
September	25.6	21.4	18.8	26.7	0.8	23.0
October	20.0	13.2	13.9	51.6	19.8	48.5
November	13.6	8.9	8.6	39.0	14.4	40.2
December	7.8	6.7	4.5	54.0	47.8	54.6
January	6.2	3.9	2.6	46.6	23.2	49.3
February	8.2	7.3	3.6	43.8	40.0	40.7
March	12.1	10.8	6.7	50.2	55.4	46.1
April	17.3	15.9	11.6	49.6	18.6	45.3
May	22.6	20.5	16.2	41.2	20.0	43.8

Table 2. The harvest index (HI), physiological maturity (FM), biological yield (BY), straw yield (SY), number of pods per plant (NPP), number of seeds per pod (NSP), thousand seed weight (TSW), and seed yield (SeY) of field pea genotypes sown under agro-ecological conditions of Bilecik, Türkiye.

Genotypes	HI (%)	FM (Day)	BY (t ha^{-1})	SY (t ha^{-1})	NPP	NSP	TSW (g)	SeY (t ha^{-1})
21	31.1d	232.2ab	4.61n	6.63b	12.1b	5.4d	195.3eg	1.43j
39	37.7a	230.2be	4.01q	3.18k	11.9b	6.5c	178.4j	1.51i
55	33.5c	230.7bd	5.64l	2.50m	7.6ıj	6.5c	190.5h	1.89f
70	28.5fg	230.2be	7.42f	3.75j	6.6k	6.5c	197.6df	2.11d
79	25.1j	229.7de	8.85ab	5.30e	9.9cd	4.5e	203.9c	2.21c
90	29.9e	228.2e	6.66ıj	4.67fg	9.5de	3.7fg	209.3b	1.99e
95	31.5d	229.8cd	6.78gh	4.64g	10.6c	3.6fg	205.4bc	2.13d
104	18.9m	179.7ı	8.69c	7.04a	8.4fh	6.7c	180.1ıj	1.64gh
110	34.7b	185h	6.84g	4.46h	7.4jk	3.6fg	226.4a	2.37b
124	29.4ef	232.7a	6.59j	4.81f	9.1ef	3.8f	201.5cd	1.94ef
141	28.3g	228e	7.61e	5.45de	12.1b	3.5fg	198.9de	2.15d
153	28.0g	184.2h	6.01	4.34hı	8.3gı	6.7c	129.0m	1.69g
161	22.9k	178.2ı	5.57l	4.29ı	9eg	6.7c	192.7gh	1.28k
165	27.7g	184.7h	4.28p	3.09k	8hj	7.7a	183.7ı	1.18l
Golyazı	32.8c	232ac	8.27d	5.55d	11.5b	3.7fg	208.7b	2.71a
KB211	25.6ıj	162.5j	4.31p	3.21k	7.3jk	7.3b	156.3k	1.10m
Kirazli	33.3c	191.3g	4.79m	3.19k	8.3gı	7.3b	138.8l	1.59h
Servet	20.8l	194f	6.70hi	5.30e	7.9hj	7.3b	194.8fg	1.39j
Tore	26.8h	191.8fg	8.81b	6.45c	9.4de	7.6ab	110.4n	2.36b
Ulubatlı	37.6a	186.2h	4.42o	2.75l	8.6fh	6.4c	155.9k	1.66g
Whıtler	26.2hı	231.3ad	8.92a	6.59bc	13.9a	3.4g	225.9a	2.33b
Years	ns	Ns	Ns	ns	ns	ns	Ns	ns
F-Probability Genotypes	**	**	**	**	**	**		**
Years×Genotype	ns	**	Ns	ns	ns	*	Ns	ns
CV (%)	2.7	0.95	1.23	2.28	6.96	5.4	1.88	2.6

Ns = Non-significant; *= p≤0.05; **= p≤0.01 CV = Coefficient variance

Table 3. Correlation coefficients among yield attributes, biological yield, straw yield, and seed yield of twenty-one field pea genotypes sown under agro-ecological conditions of Bilecik, Türkiye.

	Harvest index	Physiological maturity	Biological yield	Straw yield	Number of pods per plant	Number of seeds per pod	Thousand seed weight	Seed yield
Harvest index								
Physiological maturity	0.320							
Biological yield	-0.451*	0.288						
Straw yield	-0.621**	0.184	0.977**					
Number of pods per plant	0.138	0.579**	0.239	0.185				
Number of seeds per pod	-0.246	-0.640**	-0.416	-0.299	-0.536*			
Thousand-seed weight	-0.006	0.538*	0.267	0.225	0.309	-0.715**		
Seed yield	0.212	0.537*	0.760**	0.607**	0.326	-0.667**	0.324	

*= p≤0.05 and **= p≤0.01

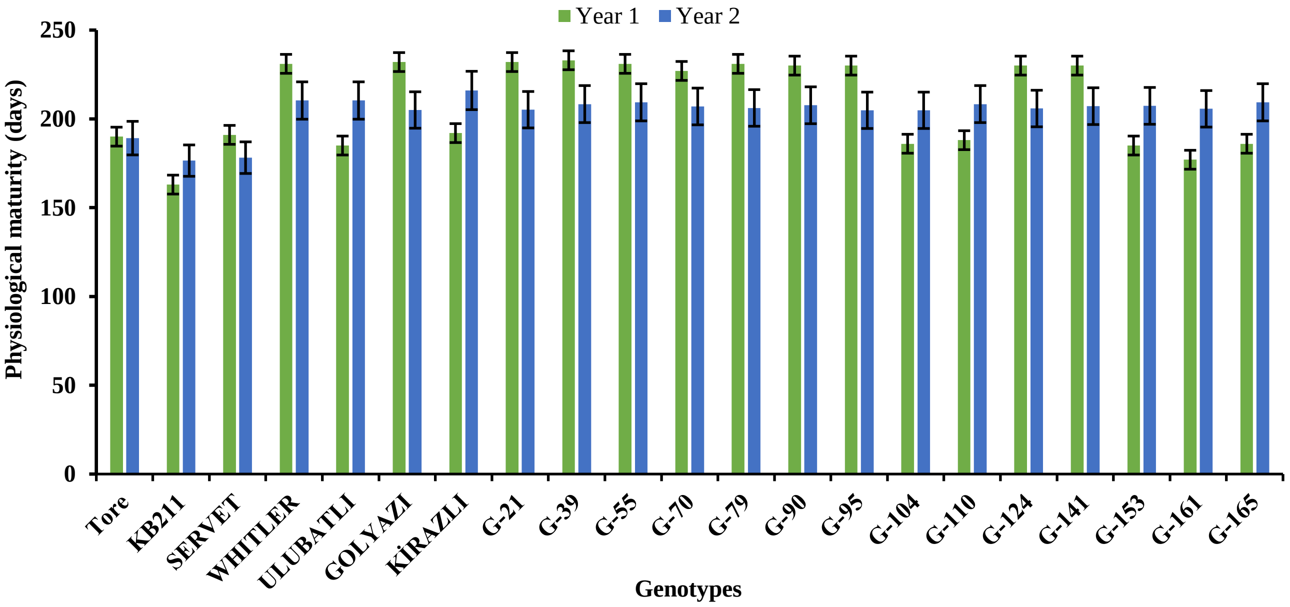

Fig. 1. Physiological maturity of twenty-one field pea genotypes sown under agro-ecological conditions of Bilecik, Türkiye during both years of study.

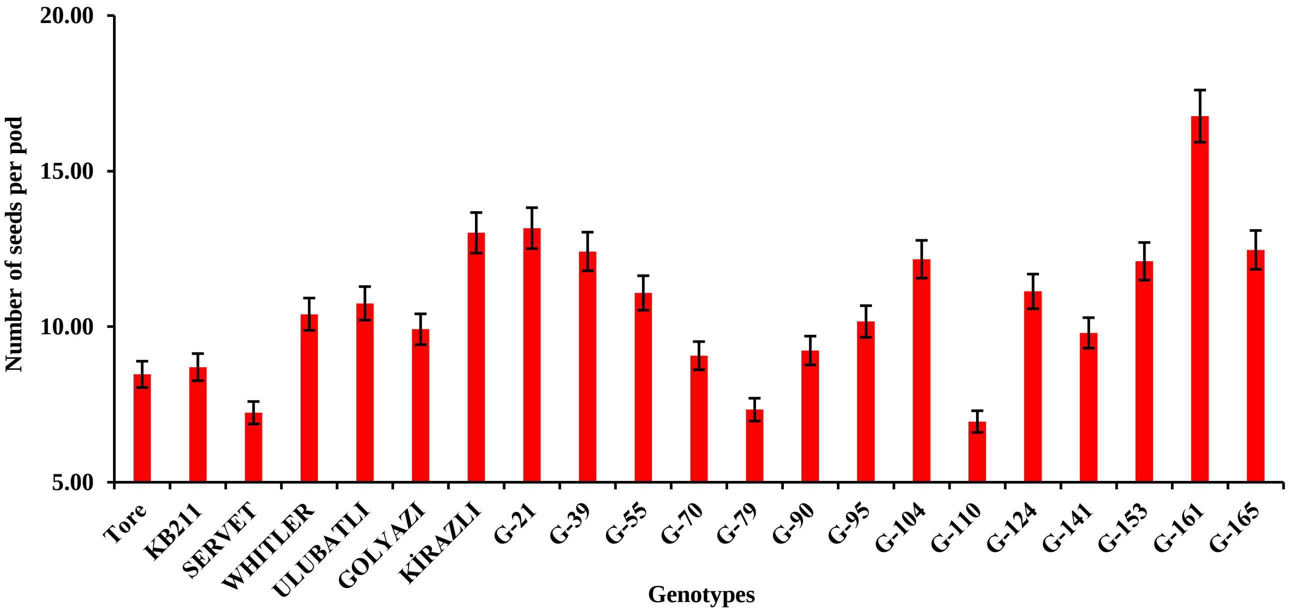

Fig. 2. Number of seeds per pod of twenty-one field pea genotypes (2-years mean) sown under agro-ecological conditions of Bilecik, Türkiye.

Table 4. Regression analysis for seed yield and different vital yield components of twenty-one field pea genotypes sown under agro-ecological conditions of Bilecik, Türkiye.

	Unstandardized coefficients		T
	B	Std. Error	
Constant	12.148	7.479	1.624
Biological yield	0.963	0.029	32.729**
Straw yield	-0.959	0.034	-27.935**
Number of seed per pod	-1.134	0.669	-1.695

** Significant at probability level of 1%

Correlation, regression, path, and principal component analyses: More than any other yield attribute, the seed yield of field pea genotypes tends to be a complex trait that depends on several yield-contributing traits. Therefore, direct selection for seed yield is generally inaccurate, and this study aimed to determine the association of yield components with seed yield using correlation coefficients (Table 3). A notable positive correlation was found between seed yield and physiological maturity (r=0.537*), biological yield (r=0.760**), and straw yield (r=0.607**). On the other hand, there was a negative correlation between the number of seeds per pod and seed yield (r=-0.667**). The harvest index showed a significant inverse correlation with both biological yield (r=-0.451*) and straw yield (r=-0.621**). Moreover, the strongest correlation was observed between biological yield and straw yield (r=0.977**). Furthermore, the number of seeds per pod exhibited a negative and significant correlation with both thousand seed weights (r=-0.715**) and seed yield (r=-0.667**).

Likewise, in this study, regression analysis revealed the type and degree of influence of each independent variable on the dependent variables. The yield contributing traits, including biological yield, straw yield, and number of seeds per pod, were subjected to the regression analysis for estimating their direct effects, whereas path analysis was employed to determine their indirect effects (Table 4). The results indicated that biological yield had the greatest direct effect on seed yield with a coefficient of 3.52 (Table 5). Contrastingly, straw yield (-2.854) had a negative effect on grain yield, followed by the number of seeds per pod (-0.054). Moreover, the impact of biological yield on seed yield was also indirectly determined by the number of seeds per pod through path analysis.

The principal component analysis (PCA) identified key traits that accounted for the largest variability in field pea genotypes (Table 6). The first two eigenvectors exhibited eigenvalues that surpassed one, contributing to a cumulative explanation of about 74.15% of the overall variation observed among field pea genotypes (Fig. 3). PC 1 depicted the eigenvalue of 3.79 and accounted for 47.45% of the variation, while PC 2 had an eigenvalue of 2.13 and accounted for 26.70% of the variation. The correlation analysis revealed that the first principal component was positively associated with physiological maturity, biological yield, straw yield, number of pods per plant, thousand seed weight, and seed yield. Similarly, the PC 2 was positively correlated with harvest index, physiological maturity, and number of pods per plant.

Table 6. Principal component analysis for the field pea yield contributing traits and seed yield.

Principal components	PC1	PC2
Eigenvalue	3.79	2.13
Total Variance (%)	47.45	26.70
Cumulative Variance (%)	47.45	74.15
Factor loading by parameters		
Harvest index	-0.033	0.870
Physiological maturity	0.722	0.467
Biological yield	0.788	-0.588
Straw yield	0.694	-0.713
Pods per plant	0.591	0.338
Seeds per pod	-0.833	-0.358
Thousand-seed weight	0.646	0.251
Seed yield	0.843	-0.013

Table 5. Path coefficients for seed yield components of twenty-one field pea genotypes sown under agro-ecological conditions of Bilecik, Türkiye.

Variable	Direct effect	Indirect effect			Correlation coefficient
		Biological yield	Straw yield	Number of seed per pod	
Biological yield	3.526**		-2.789	0.022	0.759**
Straw yield	-2.854**	3.445		0.015	0.606**
Number of seed per pod	-0.054	-1.467	0.853	-	-0.667**

** Significant at probability level of 1%

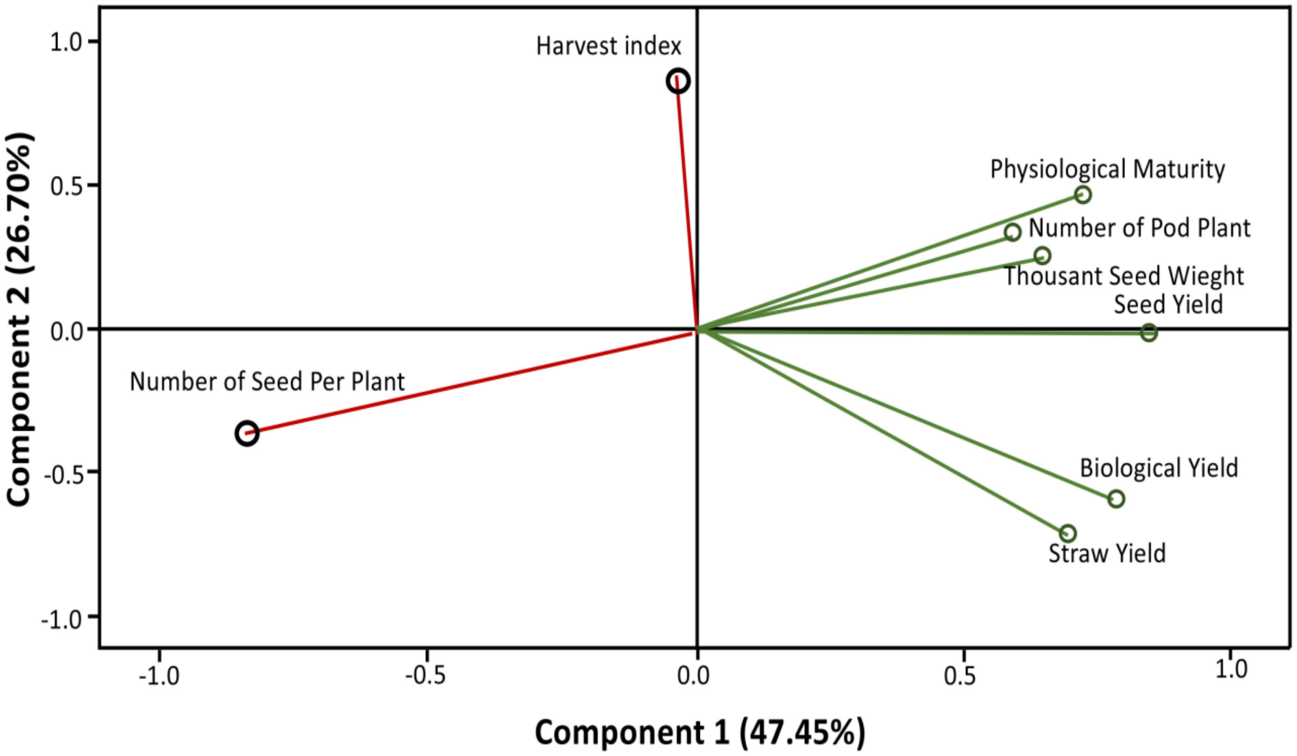

Fig. 3. Distribution of field peas investigated traits across the first two components based on principal component analysis.

Discussion

The recorded findings of this multi-year field trial indicated a significant genetic variation among field pea genotypes for yield-contributing traits and seed yield. The harvest index value represents the proportion of seed production in the total biological yield produced by that particular genotype. Our results demonstrated that genotype 39 and Ulubatli variety had the highest harvest index, the Whitler variety recorded the maximum biological yield of 892.6 kg da^{-1}, while genotype 104 exhibited the maximum straw yield (704.73 kg da^{-1}). It might be inferred that by their genetic makeup, few genotypes of field pea produced more grain than the rest of the genotypes under investigation, and ultimately, their HI values remained unmatched. Similar to these results, it was inferred that the harvest index of field pea varieties differed significantly in terms of HI values that ranged from 11.3% to 35.6% (Konuk & Tamkoc, 2018). Contrastingly, Tan *et al*., (2012) inferred that the HI of field pea genotypes ranged from 27.5% to 33.6%. The difference in HI values recorded in our study and those of previous studies might be attributed to different genotypes of field pea and atypical agro-climatic conditions. Similar to the results recorded in this study, Temel and Yazıcı (2021) reported a BY range of 501.7-760.4 kg da^{-1} of field pea genotypes, whereas another study has reported the BY range of 234.8-1359.2 kg da^{-1} among field pea genotypes (Konuk & Tamkoc, 2018). The existence of high variation between genotypes in terms of the BY of field pea genotypes might be attributed to genetic makeup variations. Moreover, this study reported pronounced differences among field pea genotypes for their potential to produce SY that were in accordance with a previous research study (Çaçan *et al.,* 2018).

In this study, the Whitler variety had the highest pods per plant (13.9), the 110 genotype exhibited the maximum thousand seed weight (226.4 g), and Golyazi and Whitler cultivars recorded the maximum seed yield. Our findings showed a similar trend to that of Singh *et al*., (2012), who found a significant and positive correlation between the number of pods and seed yield in field pea. In contradiction to our findings, Tan *et al*., (2012) reported a range of 7.9-13.8 pods per plant; however, greater pods per plant exhibited reduced grain weight, which led to a significant decline in seed yield. The pronounced variation in the number of pods produced by different genotypes of field pea might be owing to differences in their genetic potential, agronomic management plan, and climatic conditions. On the other hand, Dumanoğlu *et al*., (2021) reported a lower value of 191.9 g for the thousand-seed weight than the corresponding values recorded in the present study. Moreover, our results pertaining to the seed yield of field pea genotypes were inconsistent with those of Kadioglu *et al*., (2020), who reported a seed yield range of 145.6-322.0 kg da^{-1}, while another similar study conducted by Uzun *et al*., (2012) reported the SeY between 257.4-362.0 kg da^{-1}. Furthermore, the results of this study exhibited a significant genotype × year interaction for the number of seeds per pod of field pea genotypes under investigation. Genotypes showed varying values for the number of seeds per pod across years. These results are in agreement with those of Kadioğlu *et al*., (2020), who reported 5.4-5.9 seed numbers, while Uzun *et al*., (2012) reported a wider range of seed numbers (4.3-6.5) in different genotypes of field pea. The lack of result alignment pertaining to the number of seeds per pod of field pea genotypes could be due to genetic differences among genotypes and different agronomic management practices.

Previously, it has been inferred that seed yield was a complex trait that remained dependent on yield-contributing traits, and, therefore, the selection of high-yielding cultivars could not be made based on seed yield only. Therefore, it was suggested to study the association of yield components with SeY using correlation, regression, path analysis, and principal component analysis. This study found a significant and positive correlation between SeY and FM (r=0.537*), biological yield (r=0.760**), and straw yield (r=0.607**). However, a negative correlation was observed between the number of seeds per pod (r=-0.667**). Kaya *et al*., (2004) found significant correlations between SeY and biological yield (r=0.621**), number of pods per plant (r=0.655**), number of grains per pod (r=0.948**), and hundred-grain weight (r=0.353**). Similarly, Çaçan *et al*., (2018) established a positive correlation between SeY and SY (0.528**) as well as thousand-grain weight (0.231*). Similar to our findings, Andales *et al*., (2007) suggested that the regression analysis (a statistical technique to measure the relationship between the dependent variable and several independent variables or traits) identified biological yield, straw yield, and number of seeds per pod as significantly and directly associated traits. Likewise, BY had the highest direct effect on SeY (3.526), while SY (-2.854) had a direct negative effect on SeY. Likewise, the number of seeds per pod (-0.054) also had a negative direct effect on SeY. Similar to these results, Pekşen & Gülümser (2005) found that seeds per plant, seed weight, and pods per plant were the major yield-contributing factors due to their high direct and positive effects on SeY. In a study on grass pea (*Lathyrus sativus* L.), Öten *et al*., (2023) recorded the negative effects of BY with SeY, but a direct positive effect between BY and SY. Singh *et al*., (2012) also stated significant positive correlations between the seed number per pod and thousand seed weight with SeY of field pea genotypes. Moreover, similar to our findings regarding the grouping of field pea genotypes into different clusters by the cluster analysis, three groups were identified in grass peas (*Lathyrus sativus* L.). Furthermore, Öten *et al*., (2023) also performed cluster analysis for alfalfa (*Medicago sativa* L.) that effectively determined the interaction between the morphological traits and SeY of the crop.

The principal component analysis (PCA) has been termed as the multivariate statistical technique for exploring the genotypic divergence among genotypes of field crops (Demirkol *et al.,* 2019). In this study, PCA distinguished the productivity of genotypes and effectively analyzed the structure of observations regarding the response of variables of field pea under investigation. Moreover, the results of the current study depicted that the first two eigenvectors recorded eigenvalues higher than one and together contributed over 74.15% of the total variation. Therefore, the results of the present study demonstrated that pronounced variability among the field pea genotypes could be utilized for selecting the high-potential genotypes and subsequent use of various genotypes from distant clusters as parent material in different hybridization programs for developing high-seed-yielding cultivars, as reported by Khan *et al*., (2016). Similar to our results, Arif *et al*., (2020) also reported that PCA remained effective in revealing the Euclidean distance among landraces to distinguish the productivity potential of genotypes (Ton *et al.*, 2022). Furthermore, these findings were also in line with those of previous studies, whereby 81-86% of the total variance was attributed to seed yield contributing traits, particularly 1000 grains weight and seeds number in each pod, and it was suggested that genetic variability existed among filed crops genotypes could be exploited to boost their production under changing climate (Iqbal *et al.*, 2017; Yavuz, 2017).

Conclusions

The recorded findings of this multi-year field trial completely corroborate the research hypothesis because all field pea genotypes under investigation differed significantly in their potential for seed yield under the agro-climatic conditions of Bilecik, Türkiye. The greatest variations among all genotypes were observed for the biological yield, seed yield, and straw yield, suggesting the potential of these field pea genotypes for use in seed breeding programs to develop potent cultivars. Overall, genotype 39 exhibited the highest harvest index value, while the Whitler variety remained superior by exhibiting the highest biological yield. Additionally, the Golyazi cultivar remained unmatched in producing the maximum seed yield, and it was closely followed by the Whitler variety. The correlation coefficients of seed yield with vital yield contributing traits showed significant variations, while significantly positive correlations were found between seed yield and physiological maturity, biological yield, and straw yield. Moreover, the findings of this study suggested that harvest index and biological yield could be used as the primary selection criteria for selecting the field pea genotypes with higher seed production potential. These findings could serve as a baseline to utilize the identified field pea genotypes (Golyazi, Whitler, and 39 genotypes) in breeding programs to develop potent cultivars having unmatched seed production potential and better climatic adaptability in Türkiye and European countries. The most performing field pea cultivars must be tested in the adjacent regions having a Mediterranean climate for a wide-scale adaptability in the region. Moreover, future studies need to optimize the nutrient doses and sources (organic, mineral, and nanofertilizers, etc.) for these genotypes of field pea, along with determining the harvesting stage association with grain nutritional quality under prevailing agro-ecological conditions of Türkiye.

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