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The use of principal component analysis (PCA) in the selection of bread wheat (*Triticum aestivum* L.) genotypes under kahramanmaraş conditions

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Abstract
In this study, grain yield and yield-contributing agricultural traits of 50 different bread wheat genotypes (1 standard cultivar Germenicia and 49 advanced lines) were investigated, and the relationships between traits and genotypes were evaluated using Principal Component Analysis (PCA) and correlation analysis. The research was conducted during the 2024-2025 growing season at the experimental fields of the Eastern Mediterranean Transitional Zone Agricultural Research Institute in Kahramanmaraş, Turkey. Results showed significant variations among genotypes: plant height ranged from 84.00 to 106.33 cm, spike length from 8.78 to 12.88 cm, number of spikelets from 16.00 to 22.00, number of kernels per spike from 30.80 to 91.40, grain weight per spike from 1.50 to 2.81 g, and grain yield from 416.42 to 632.49 kg/da. Correlation analysis revealed a statistically significant positive relationship (r=0.416) between grain yield and plant height, while spike characteristics exhibited high internal correlations ranging from r=0.478 to 0.683. Principal Component Analysis indicated that 71.35% of the total variance was explained by the first two principal components. The First Principal Component (F1), explaining 46.97% of the variance, was defined as the "Spike Yield Components", whereas the Second Principal Component (F2), explaining 24.38%, was designated as the "Total Yield and Vegetative Growth" axis. As a result of the research, lines 208 and 209 demonstrated superiority in terms of spike size and architecture. Conversely, lines 244, 225, 233, and 207 stood out regarding maximum grain yield per unit area, manifesting excellent adaptation to the transitional zone ecology and highlighting their potential as strong cultivar candidates for future breeding programs.

Keywords: Bread wheat, transitional zone, principal component analysis (PCA), correlation, yield, breeding

Introduction
Bread wheat, which has strategic importance with a 7.1 million hectare cultivation area and an annual production of 22 million tons in Turkey, is one of the most important cultivated crops forming the foundation of food security (Kahraman *et al.*, 2021) [1]. Evaluated on a regional basis, the Eastern Mediterranean Region continues to be a strategic center, accounting for approximately 9.47% of Turkey's total wheat cultivation area and 12.12% of its production (Ezici and Hızlı, 2024) [2]. The pressure on agricultural productivity due to the growing global population and climate change makes it essential to obtain higher yields per unit area from existing production areas (Çağlar *et al.*, 2011; Yüce *et al.*, 2022) [3, 22]. Towards this goal, identifying genotypes with high yield potential and strong adaptation capabilities to environmental stress conditions in breeding programs constitutes a critical stage for sustainable production (Kurt and Yağdı, 2013) [4].

Grain yield stands out as a multi-factorial trait determined by a complex interaction of genetic capacity, plant morphology, and environmental factors (Bilgin and Korkut, 2014) [5]. In this context, analyzing the complex relationships among yield components using multivariate statistical methods directly affects the success rate of breeders in the selection process (Sönmez and Olgun, 2020) [6].

In particular, Principal Component Analysis (PCA) and biplot techniques allow for the visualization of large amounts of agricultural data and reduce the complexity of relationships among genotypes, enabling the development of a clearer selection strategy (Bayram *et al.*, 2017; Güngör *et al.*, 2022) [7, 8]. Visualizing the effects of the investigated traits on genotypic profiles, these methods provide a critical mechanism that supports decision-making processes in selecting lines demonstrating high yield potential among breeding materials (Akçura, 2011; Demirel *et al.*, 2021) [9, 10].

Various studies conducting genotypic evaluations aim to explain the variation in yield components and identify lines sensitive to genotype-environment interactions (Aktaş *et al.*, 2017; Kadıoğlu *et al.*, 2024) [11, 12]. The data obtained through such studies reveal the fundamental parameters required to accelerate modern breeding strategies by selecting high-yielding genotypes adapted to the regional conditions where the studies are conducted (Bayhan, 2022; Yorulmaz *et al.*, 2022) [13, 14].

On the other hand, the application of multivariate statistical approaches aims to increase selection success in breeding programs by more accurately revealing the relationships between the yield capacity and morphological features of genotypes (Kendal, 2026; Stojšin *et al.*, 2026) [15, 16]. As frequently emphasized in the international literature, advanced statistical models establish a reliable framework for identifying the most stable and high-yielding genotypes under different environmental conditions by clarifying complex interactions among variables during the selection process (Kendal, 2026; Stojšin *et al.*, 2026)[15]. Elevating the multifarious relationships between yield and yield components of the investigated genotypes provides breeders with a crucial roadmap in selecting lines with high regional adaptation. Such multivariate approaches enhance the efficiency and selection precision of breeding programs by more accurately defining genotypic variation (Janmohammadi *et al.*, 2014; Ali *et al.*, 2020) [17].

In this study, it was aimed to evaluate the agricultural traits of 50 different bread wheat genotypes through multivariate analyses; it was anticipated that the findings would identify the lines most suitable for regional conditions and transfer them to future generation breeding studies.

Materials and Methods

Plant Material and Experimental Design

In the study, 1 registered bread wheat cultivar (Germenicia) widely grown in the region and 49 advanced bread wheat lines originating from CIMMYT (International Maize and Wheat Improvement Center, Mexico) were used as plant material (Table 1). The field experiment was established during the 2024-2025 growing season at the experimental area of the Eastern Mediterranean Transitional Zone Agricultural Research Institute in Kahramanmaraş, Turkey, using a Randomized Complete Block Design (RCBD). Following land preparation, sowing was carried out with a seed drill at the optimal seeding rate; fertilization and agricultural maintenance practices suitable for local cultivation standards were fully applied throughout the growing season.

Table 1: Bread wheat genotypes used in the study and their pedigrees

No	GANOTYPE
201	GERMENICIA
202	KAKURU #1
203	BONSU
204	BECARD//ND643/2*WBLL1*2/3/BORL14
205	AKEPA/KASUKO//KASUKO
206	SWSR22T.B./KACHU//2*KACHU/4/2*SUP152//WBLL1*2/BRAMBLING*2/3/KSW/SAUAL//SAUAL
207	WBLL1*2/KKTS//PASTOR/KUKUNA/3/KINGBIRD #1//INQALAB 91*2/TUKURU/5/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/SAUAL*2/6/MOKUE #1
208	SAUAL/MUTUS//COPIO/3/COPIO*2/4/KACHU*2/3/ND643//2*PRL/2*PASTOR
209	KFA/2*KACHU/4/WBLL1*2/KURUKU//KRONSTAD F2004/3/WBLL1*2/BRAMBLING/5/2*BORL14*2//KFA/2*KACHU
210	KFA/2*KACHU/4/WBLL1*2/KURUKU//KRONSTAD F2004/3/WBLL1*2/BRAMBLING/5/2*BORL14*2//KFA/2*KACHU
211	SAUAL/MUTUS/4/KACHU #1//WBLL1*2/KUKUNA/3/BRBT1*2/KIRITATI/5/KASUKO/6/SAUAL/MUTUS/4/KACHU #1//WBLL1*2/KUKUNA/3/BRBT1*2/KIRITATI
212	BECARD//ND643/2*WBLL1*2/3/KSW/SAUAL//SAUAL*2/9/TACUPETO F2001/6/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/PASTOR/7/ROLF07*2/8/SAUAL/YANAC//SAUAL
213	BECARD//ND643/2*WBLL1*2/3/KSW/SAUAL//SAUAL*2/4/MOKUE #1
214	KFA/2*KACHU/4/WBLL1*2/KURUKU//KRONSTAD F2004/3/WBLL1*2/BRAMBLING/5/KASUKO
215	TACUPETO F2001/6/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/PASTOR/7/ROLF07*2/8/SAUAL/YANAC//SAUAL/9/KASUKO
216	TACUPETO F2001/6/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/PASTOR/7/ROLF07*2/8/SAUAL/YANAC//SAUAL/9/KASUKO
217	TACUPETO F2001/6/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/PASTOR/7/ROLF07*2/8/SAUAL/YANAC//SAUAL/9/KASUKO
218	TACUPETO F2001/6/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/PASTOR/7/ROLF07*2/8/SAUAL/YANAC//SAUAL/9/KASUKO
219	TACUPETO F2001/6/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/PASTOR/7/ROLF07*2/8/SAUAL/YANAC//SAUAL/9/KASUKO
220	SAUAL/MUTUS/4/KACHU #1//WBLL1*2/KUKUNA/3/BRBT1*2/KIRITATI/5/NAINA #3
221	SAUAL/MUTUS/4/KACHU #1//WBLL1*2/KUKUNA/3/BRBT1*2/KIRITATI/5/MUTUS*2/KINGBIRD #1/3/KSW/SAUAL//SAUAL
222	SAUAL/MUTUS/4/KACHU #1//WBLL1*2/KUKUNA/3/BRBT1*2/KIRITATI/5/MUTUS*2/KINGBIRD #1/3/KSW/SAUAL//SAUAL
223	TACUPETO F2001/6/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/PASTOR/7/ROLF07*2/8/SAUAL/YANAC//SAUAL/9/SHORTENED SR26 TRANSLOCATION/4/3*CHIBIA//PRLII/CM65531/3/MISR 2
224	TACUPETO F2001/6/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/PASTOR/7/ROLF07*2/8/SAUAL/YANAC//SAUAL/9/PRL/2*PASTOR//KACHU

225	TACUPETO F2001/6/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/PASTOR/7/ROLF07*2/8/SAUAL/YANAC//SAUAL/9/PRL/2*PASTOR//KACHU
226	MUNAL*2//WAXWING*2/TUKURU/3/MUCUY/4/KASUKO
227	SUP152/AKURI//SUP152/3/MUCUY/4/MUTUS//WBLL1*2/BRAMBLING/3/WBLL1*2/BRAMBLING/5/KASUKO
228	KACHU/KIRITATI//2*BORL14/4/KACHU//WBLL1*2/BRAMBLING/3/KACHU/KIRITATI
229	WAXWING/2*ROLF07//BORL14/3/2*KASUKO
230	MUNAL/WESTONIA//2*BORL14/3/KASUKO
231	BAVIS//ATTILA*2/PBW65/3/KASUKO
232	PREMIO/4/CROC_1/AE.SQUARROSA (205)//KAUZ/3/PIFED*2/5/KSW/SAUAL//SAUAL/6/KASUKO
233	KACHU/BECARD//WBLL1*2/BRAMBLING*2/3/SUP152/BAJ #1/4/KASUKO
234	SW89.5277/BORL95//SKAUZ/3/PRL/2*PASTOR/4/HEILO/5/WAXWING/KRONSTAD F2004//FRNCLN/6/BORL14/7/KASUKO
235	MUKADI/KASUKO
236	KACHU/BECARD//WBLL1*2/BRAMBLING/3/KASUKO
237	KACHU/BECARD//WBLL1*2/BRAMBLING/3/KASUKO
238	ND643/2*TRCH//BECARD/3/BECARD/4/SUP152*2/TECUE #1/5/KASUKO
239	WBLL1*2/BRAMBLING//WBLL1*2/BRAMBLING/3/2*BORL14/4/KASUKO
240	ONIX/KBIRD*2//KFA/2*KACHU/3/KASUKO
241	FRANCOLIN #1/MESIA//MUNAL #1/3/SUP152/TECUE #1//SUP152/4/SUP152/BAJ #1/5/KASUKO/6/BORL14*2//KFA/2*KACHU
242	ATTILA/3*BCN*2//BAV92/3/HEILO/4/CHIBIA//PRLII/CM65531/3/MISR 2/5/TRCH/HUIRIVIS #1/6/CHIPAK/7/KASUKO/8/KASUKO
243	K9644//KIRITATI/2*TRCH/3/BECARD/QUAIU #1/4/BABAX/LR42//BABAX/3/ER2000*2/5/KUTZ//KFA/2*KACHU
244	BLOUK #1/KINGBIRD #1*2//KACHU/KIRITATI/3/BORL14//KFA/2*KACHU/4/KASUKO
245	BABAX/LR42//BABAX*2/3/SHAMA/4/KINGBIRD #1/5/QUAIU/6/2*COPIO*2/7/KUTZ//KFA/2*KACHU
246	BABAX/LR42//BABAX/3/ER2000*2/4/WBLL1*2/SHAMA//BAJ #1/5/PRL/2*PASTOR//KACHU/6/KASUKO
247	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/4/QUAIU/5/BORL14*2/6/KASUKO
248	WBLL1*2/BRAMBLING//WBLL1*2/BRAMBLING/3/2*BORL14*2/4/BORL14//KFA/2*KACHU
249	BECARD/QUAIU #1//ONIX/KBIRD/3/KASUKO/4/WBLL1*2/BRAMBLING//WBLL1*2/BRAMBLING/3/2*BORL14
250	KVZ/PPR47.89C//TACUPETO F2001*2/BRAMBLING/3/2*TACUPETO F2001*2/BRAMBLING*2/4/KOKILA/5/KASUKO/6/KASUKO

Investigated traits
In the study, the following traits were measured in the plots reaching harvest maturity (Çölkesen *et al.*, 1999) [18]:

Plant height (cm): In 10 randomly selected plants from each plot, the length from the soil surface to the tip of the spike (excluding awns) was measured and averaged.

Spike length (cm): Measured with a ruler on 10 random spikes, and the average was calculated.

Number of spikelets (number/spike): The number of spikelets present on the main stem spike was visually counted and averaged.

Number of kernels per spike (number): Kernels from 10 spikes were counted, and their averages were taken.

Grain weight per Spike (g): Kernels from 10 randomly selected spikes were individually weighed, and the average was calculated.

Grain yield (kg/da): Calculated by converting the harvested yield of the experimental plots to yield per decare (1 decare = 1000 m²).

Statistical analyses
Descriptive statistics of the raw data obtained from the research were calculated, and Pearson correlation coefficients were determined to identify the interactions among the variables. Principal Component Analysis (PCA) was performed to optimize the variance matrix and model the twodimensional distribution of the investigated traits and the 50 genotypes. Within the scope of this analysis, factor loadings, eigenvalues, and variance explanation ratios were determined.

Results and Discussion
Descriptive statistics
The minimum, maximum, and overall means of the parameters belonging to the 50 investigated wheat genotypes were calculated. The ranges of variation were determined as 84.00-106.33 cm (mean 95.46 cm) for plant height, 8.78-12.88 cm (mean 11.03 cm) for spike length, 16.0-22.0 (mean 18.90) for the number of spikelets, 30.80-91.40 (mean 53.64) for the number of kernels per spike, and 1.50-2.81 g (mean 2.07 g) for grain weight per spike (Table 2). The average grain yield was 523.38 kg/da, and the yield potential among genotypes varied between 416.42 and 632.49 kg/da, presenting a very broad genetic variation for selection. Line 208, representing the institute's working materials, exhibited a remarkable potential by reaching a capacity of 91.4 kernels per spike.
While the grain yield findings obtained in the study demonstrate parallelism with the findings of Yüce *et al.* (2022) [3] and Ezici and Hızlı (2024) [2] conducted in the same ecology, the high variation we obtained in terms of spike characteristics proves that the genetic material has a rich foundation for selection.

Table 2: Descriptive statistics of agricultural traits investigated in bread wheat genotypes

Investigated Trait	Minimum	Maximum	Mean	Standard Deviation
Plant Height (cm)	84.00	106.33	95.46	4.98
Spike Length (cm)	8.78	12.88	11.03	0.93
Number of Spikelets	16.00	22.00	18.90	1.32
Number of Kernels per Spike	30.80	91.40	53.64	9.32
Grain Weight per Spike	1.50	2.814	2.078	0.36
Grain Yield (kg/da)	416.417	632.492	523.387	48.96

Correlations among traits

According to the results of the Pearson correlation analysis among the investigated traits (Table 3), spike characteristics (spike length, number of spikelets, number of kernels per spike, and grain weight per spike) showed positive and highly significant relationships among themselves (ranging from *r*= 0.478 to 0.683). On the other hand, the direct relationship between spike characteristics and grain yield per unit area was negative and non-significant for spike length and number of spikelets (*r*=-0.135 and *r*=-0.048, respectively), and positive but non-significant for the number of kernels per spike and grain weight per spike (*r*=0.136 and *r*=0.174, respectively).

Table 3: Pearson correlation coefficients among the investigated agricultural traits

Investigated Trait	Spike Length (cm)	Number of Spikelets	Number of Kernels per Spike	Grain Weight per Spike	Grain Yield (kg/da)
Plant Height (cm)	-0.239	-0.051	-0.166	-0.107	0.416
Spike Length (cm)		0.644	0.478	0.515	-0.135
Number of Spikelets			0.650	0.576	-0.048
Number of Kernels per Spike				0.683	0.136
Grain Weight per Spike					0.174

Correlation coefficients in bold are statistically significant ($p < 0.05$)

The parameter showing a positive and significant correlation with grain yield was plant height (*r*=0.416). The fact that the relationships between plant height and spike characteristics remained statistically no significant indicates that height increase does not exert a negative pressure on spike architecture; conversely, the positive and significant correlation (*r*=0.416) between plant height and grain yield proves that lines with strong vegetative habitus (due to stem reserves) have an advantage under terminal stress conditions in the Mediterranean/Transitional zone ecology.

Although modern wheat breeding generally targets short stature to prevent lodging, the direct correlation of yield with plant height rather than spike size reflects the stress-based physiological dynamics of the Eastern Mediterranean transitional zone ecology. In Mediterranean climate locations subjected to drought or heat stress during the grain filling period, it is known that taller genotypes with strong vegetative habitus accumulate more water-soluble carbohydrates (WSC) in their stems (del Pozo *et al.*, 2016) [19]. As emphasized in similar studies in the literature, taller genotypes rapidly translocate these reserves accumulated in their stems to the grain during terminal stress when photosynthesis is suppressed, creating a physiological shield and preserving their yield per unit area (Bainsla *et al.*, 2020) [20]. This situation explains why, in the study, the highest yield was obtained not from the largest spiked genotypes, but from vigorous lines that could maximize plant height development.

Principal Component Analysis (PCA) and Classification of Genotypes

In the PCA test, applied to reduce dimensions and explain traits and genotypes, two "Principal Components" (F1 and F2) with eigenvalues greater than 1 were obtained, and these two components explained 71.35% of the total variance (Table 4, Figure 1).

Table 4: Eigenvalues and explained variance ratios of Principal Component Analysis (PCA)

	F1	F2	F3	F4	F5	F6
Eigenvalues	2.818	1.463	0.696	0.446	0.345	0.232
Variability (%)	46.974	24.381	11.596	7.426	5.752	3.872
Cumulative (%)	46.974	71.355	82.951	90.377	96.128	100.00

Factor 1 (F1 - Spike Components Axis): It solely explained the major part of the total variance (46.97%). The highest positive contributions to this axis came from the parameters *Number of Spikelets* (0.852), *Number of* Kernels per Spike (0.847), Grain Weight per Spike (0.827), and Spike Length (0.792), respectively (Table 5). Because the loadings belonged entirely to spike architecture, this axis was designated as the "Spike Yield Components Axis" in the study (Figure 2).

Table 5: Factor loading values of the investigated traits on the principal component axes (>0.25)

Variables	F1	F2	F3	F4	F5	F6
Plant Height	-0.253	0.771	-0.541	-0.130	0.124	-0.125
Spike Length	0.792	-0.193	-0.276	0.480	0.019	-0.170
Number of Spikelets	0.852	0.042	-0.337	-0.125	-0.230	0.301
Number of Kernels per Spike	0.847	0.155	0.225	-0.301	-0.195	-0.282
Grain Weight per Spike	0.827	0.215	0.214	-0.064	0.457	0.103
Grain Yield	0.003	0.871	0.342	0.297	-0.172	0.083

Factor 2 (F2 - Vegetation and Yield Axis): It explained 24.38% of the total variance. The factor loadings dominating this axis were Grain Yield (0.871) and Plant Height (0.771).

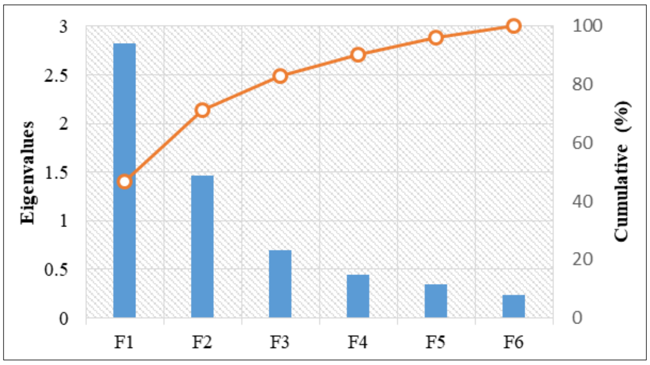

Fig 1: Line graph showing eigenvalues of principal components and cumulative variance ratios explained

When the distributions and factor score values of the genotypes on the PCA graph (biplot) are examined; the positions of the genotypes and investigated traits on the PCA axes are presented in Figure 3, and their joint distribution on the biplot graph is presented in Figure 4. Analyzing the positions in these graphs reveals:

Genotypes with dominant spike structure: Genotypes 208 (Score: 4.531) and 209 (Score: 4.292), which obtained very high scores on the F1 axis, clearly differentiated from their competitors in terms of spike size, forming a "Macro Spiked" cluster.

High grain yield genotypes: Genotypes performing along the F2 axis provided a direct increase in decare yield. Under the ecological conditions of Kahramanmaraş, lines 244 (632.49 kg/da), 225 (624.25 kg/da), 233 (621.42 kg/da), and 207 (606.52 kg/da) exhibited superior environmental adaptation and reached the top ranks in yield. This biplot distribution proves that the relationship between grain yield and morphological components separates at the genotype level; while some lines exhibit high yield potential, others specialize in traits focused on spike architecture (Bayram *et al.*, 2017; Kahraman *et al.*, 2021) [7, 1].

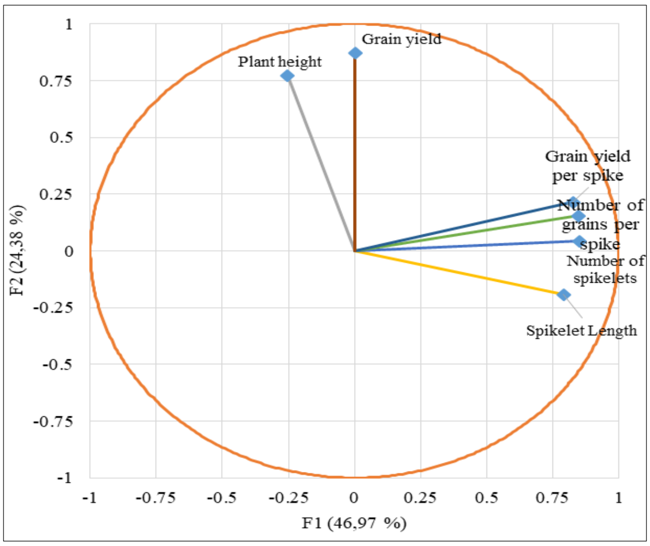

Fig 2: Distribution of the investigated agricultural traits on the first two principal component (F1 and F2) axes and the correlation circle

In our research, the accumulation of spike components on the first principal component (F1) is consistent with the PCA findings of Ali *et al.* (2020), Stojšin *et al.* (2026) [16], and Çokkızgın *et al.* (2026) [23], which reported that genotypic variance in bread wheat primarily derives from spike architecture.

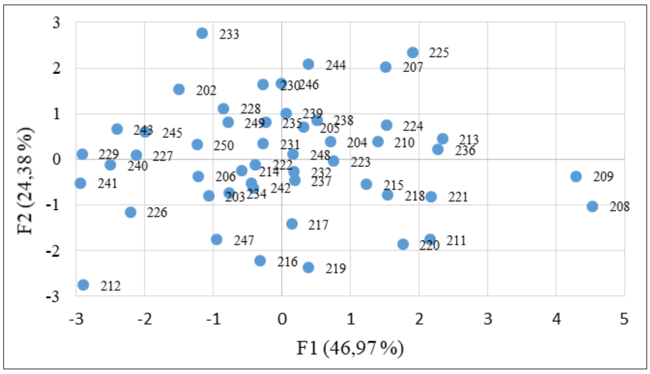

Fig 3: Factor score distributions of bread wheat genotypes on the first two principal component (F1 and F2) axes

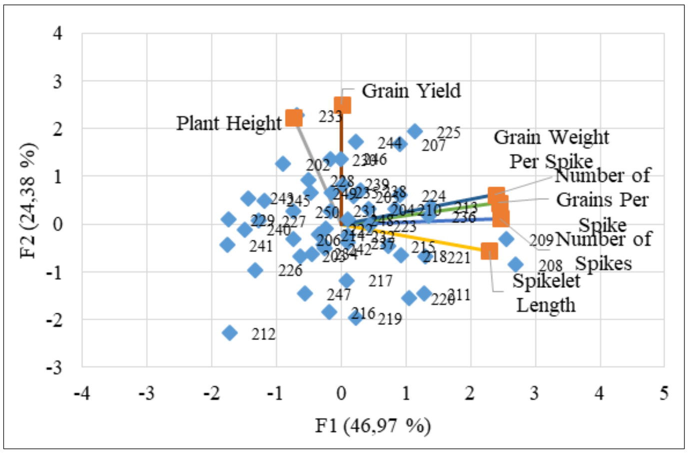

Fig 4: Joint distribution of the investigated traits and bread wheat genotypes on the first two principal component axes (Biplot graph)

The standard cultivar Germenicia (yield 483.47 kg/da) lagged behind most lines, remaining in the minus (negative) region on both component axes. This confirms that the new breeding lines are much more promising than the current standards.

Conclusion

The fundamental philosophy in wheat breeding is to translate the plant's genetic performance into maximum yield, even under challenging environmental conditions. As a result of this research conducted with 50 different bread wheat genotypes at the Eastern Mediterranean Transitional Zone Agricultural Research Institute, it was determined that the advanced lines used harbor high genetic potential/possess a rich genotypic variation in terms of plant habitus and spike architecture.

In light of the analyses, the following conclusions have been reached for future breeding and registration strategies: in genetic studies to be conducted to enlarge spike physiology and increase kernel-holding capacity per spike to record levels in bread wheat, lines 208 and 209 should absolutely be utilized as parents (donors).

Lines 244, 225, 233, and 207, which adapted well to the region's ecology and directly increased the final grain yield and vegetative vigor in the field, can be said to be promising for introduction to Regional/National agriculture.

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