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Forage Yield Performance of Forage Pea (*Pisum sativum* spp. *arvense* L.) Genotypes and Assessments Using GGE Biplot Analysis

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ABSTRACT

This study was conducted to evaluate the performance of forage pea (*Pisum sativum* spp. *arvense* L.) genotypes, in terms of fresh forage yield and associated traits, when grown on the Kiziltepe Plain, Mardin, Turkey. Field trials were performed during the 2007-08 and 2009-2010 growing seasons. The experiments were arranged according to randomized block design with three replications. The following trait ranges were reported: Days to 50% flowering: 147.5-162.5 days, Natural plant height and Main Stem Height: 45.58-72.75 cm, Main stem height: 52.52-100.42 cm, Main stem numbers per plant: 1.275-1.658 stems plant^{-1}, Main stem thickness: 2.913-3.703 mm, Fresh forage yield: 10.43-23.83 t ha^{-1} and Dry matter yield: 2.525-5.891 t ha^{-1}. GGE (i.e., G+GE) biplot analysis showed that the two growing seasons were markedly different, stemming exclusively from differences in rainfall amounts between the two growing seasons. Results of this study showed that the lines 88P00-1-4-9-661 (1) and P101 (6), and cultivar Kirazli (9) were superior in terms of fresh forage yield, dry matter yield, natural plant height and days to 50% flowering traits. At the same time, PC2 scores of these genotypes were found near to zero, so, they were identified as stable genotypes for the investigated traits. In conclusion, in terms of forage yield, these three forage pea genotypes are recommended for the Kiziltepe Plain growing conditions.

Keywords: Biplot analysis, Dry matter yield, Forage yield components, Genotype×year interaction, Kiziltepe Plain.

INTRODUCTION

Forage pea (*Pisum sativum* spp. *arvense* L.) is a cool-season annual-forage legume species. Its forage is of high nutritional value (Acikgoz, 2001). When mowed as recommended, its forage contains ~20% crude protein. Forage pea seeds contain 20-30% crude protein and are regarded as an excellent protein source (Acikgoz *et al.,* 2001; Sayar and Anlarsal, 2008). Forage pea is also harvested for green manure in organic farming. It is very suitable for annual crop rotations, as it provides soil nitrogen for crops that follow forage pea in a rotation (Tan *et al.,* 2012). Forage pea has cold tolerance and can be sown in the winter in many parts of Turkey (Sayar *et al.,* 2011). Additionally, when compared with other annual legume species, forage pea is known for relatively early flowering and maturity. Early maturity makes forage pea suitable for a crop rotation involving cotton (*Gossypium hirsutum* L.) and corn (*Zea mays* L.), which are the most heavily cultivated crops in the irrigated arable lands of southeastern Turkey (Sayar, 2014). Due to the outstanding features of forage pea, in recent decades, a great deal of effort has been spent by many researches in Turkey to improve new high-

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yielding cultivars by using local or introduced forage pea materials (Bilgili and Acikgoz, 1999; Tekeli and Ates, 2003; Sayar and Anlarsal, 2008, Sayar *et al*., 2009; Tan *et al*., 2012). As a result of the intensive breeding studies, many new high-yielding cultivars have been developed in recent years in the country (Sayar *et al*., 2011).

Shortage of quality forage is among the bigger problems of animal husbandry of Turkey and especially of the Southeastern Anatolia Region (Sayar *et al.,* 2010). To meet this shortage, plant breeders in the country have spent a great effort to develop and to introduce higher yield forage crops varieties (Sayar *et al.,* 2013). When selecting suitable genotypes, plant breeders consider many traits. Selecting genotypes superior for multiple traits increases the likelihood of success of breeding programs (Seker and Serin, 2004). Understanding of Genotype×Environment Interaction (GEI) is important to determine stability status of genotypes in terms of crop yield in a target production environment (Akbarpour *et al.,* 2014).

Since its first time reported by Gabriel (1971), GGE (i.e., G+GE) biplot analysis has been applied to numerous disciplines, including sociology, economics, business, medicine, genetic and ecology (Yan and Tinker, 2006). Exclusively, agricultural scientists have applied this visual data analysis method to many different crops (Yan, 2002; Kaya *et al.,* 2006; Ilker *et al.,* 2009; Ahmadi *et al.,* 2012; Kendal, 2013; Mortazavian *et al.,* 2014). In contrast to classical genotype×environment interaction and stability analyses methods, the GGE biplot analysis method enables us not only to show relationships between genotypes and environments, but also to demonstrate relationships between genotypes and traits with a simple graph (Sayar and Han, 2015).

With the hypothesis tested in the study; we aimed at determining superior forage pea genotypes in terms of fresh forage yield, dry matter yield traits, and determining some components, associated with these traits in Kiziltepe ecological conditions, one of the hottest and drought subregions of the Southeastern Anatolia and Turkey. Additionally, the study aimed to illustrate relations not only between genotypes and environments but also between genotypes and the examined traits by using GGE biplot analysis method.

MATERIALS AND METHODS

Experimental Area and Plant Material

This study was conducted in two growing seasons (2007-2008 and 2009-2010) in a farmers' field of Cagıl Village, Kiziltepe, Mardin, Turkey (37^{o} 07'N, 40^{o} 40'E and altitude of 495 m). At least for two decades, the experimental field has been used by GAP International Agricultural Research and Training Centre (GAP IARTC), Diyarbakır, Turkey, as an experimental station, where the genotypes of various crops have been tested to determine their responses to high temperatures and low rainfall conditions.

The study materials consisted of seven promising lines and three control cultivars. The three of promising lines, 88P00-1-4-9-661, 88P038-4-3-683, Spring Pea 3-638 were provided from International Center for Agricultural Research in Dry Areas, Aleppo, Syria (ICARDA). The other four promising lines, namely, P57B, P51, P101, P104, and the two control cultivars Atos and Kirazlı were provided from Field Crops Department of Uludag University, Bursa, Turkey. In addition, Ozkaynak cultivar was supplied from Field Crops Department, Selcuk University, Konya, Turkey.

Soil and Climatic Conditions of Experimental Area

The research fields were flat, or nearly flat, with very little erosion, with a deep or relatively deep soil profile. According to the soil analysis, the experimental area soils had a clay loam texture, and were red-brown in

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color. Moreover, the soils were rich in terms of calcium carbonate (CaCO3) (19.24%) and potassium (0.35 t ha^{-1} K_2O) contents, whereas organic matter (1.22%) was relatively low. Additionally, phosphorus and total salt content of the soil were, respectively, 0.0904 t ha^{-1} P_2O_5 and 0.05%. Also, due to the high limestone content, the pH status of the soils was alkaline (pH 7.83).

Continental climate prevails in the Kiziltepe Plain, where summers are dry and hot and winters are moderately cool and rainy. Rainfall in the region is variable both within and among years. The long-term annual average total precipitation is 428.0 mm, approximately three-quarters of which (75-80%) falls from November to May. The region's forage and seed yields obtained from annual legume crops depend greatly on the spring rainfall (Karadag and Buyukburc, 2004; Sayar and Han, 2014). Monthly total precipitation and average temperature, relative humidity records during the study years, and the long-term averages, are summarized in Figures 1, 2, and 3, respectively (Diyarbakır Regional Directorate of Meteorology records, 2010).

Precipitation in both of the growing years was less than the long-term average (Figure 1). Rainfall during the 2009-2010 growing season was greater than for the 2007-2008 season. There was a severe drought during the 2007-2008 growing season. The plots were irrigated to field capacity at flowering and pod formation in the 2007-2008 growing season. Monthly average temperatures of the 2007-2008 growing season were lower than that of the 2009-2010 growing season and compared to long-term averages (Figure 2). Temperatures during the spring months of the 2007-2008 season were higher than in the 2009-2010 season and the long-term averages due to drought conditions. The relative humidity of both growing seasons was lower than the long-term average. The average relative humidity of the 2009-2010 season was

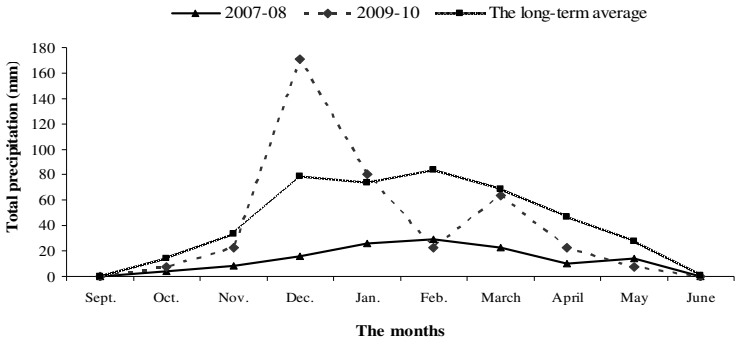

Figure 1. The monthly total precipitation records in the experimental area.

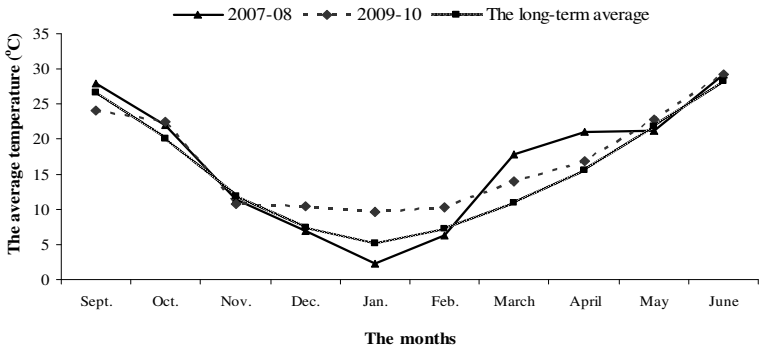

Figure 2. The monthly average temperatures records in the experimental area.

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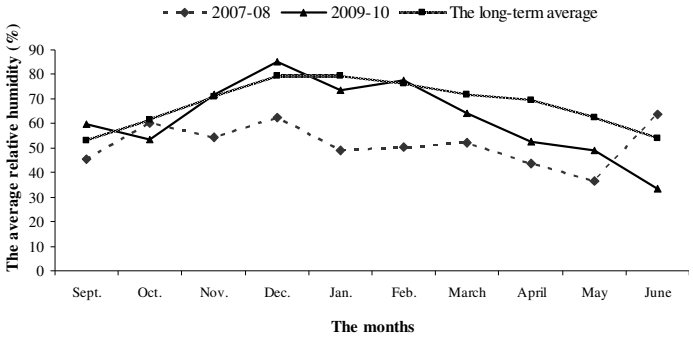

Figure 3. The monthly average relative humidity records in the experimental area.

higher for all months in comparison to the 2007-2008 growing season (Figure 3). Due to the poor climatic conditions in 2007-2008, fresh forage yield, dry matter yield, natural plant height and main stem numbers per plant were lower than in the 2009-2010 growing season.

Experimental Design and Measured Traits

The experiments were established according to a randomized complete block design with three replications. Each plot consisted of six rows 5 m in length, and rows were spaced 20 cm apart. Weeds appearing in the experimental site were controlled by hand. The seeding rate was 100 seeds m^{-2} (SRCC, 2001). The sowings were made in well-annealed soil using an experimental drill. The sowing dates of the first and second growing seasons were on November 17, 2007, and November 27, 2009, respectively. In taking experimental data, a half-meter at the beginning and end of each plot was neglected to avoid edge effects and half of each plot was harvested separately in full flowering time of the genotypes. The investigated traits in this study were determined according to the technical instructions for leguminous forage crops published by the Seed Registration and Certification Centre, Ankara, Turkey (SRCC, 2001).

Statistical Analysis

Combined the two years data were analyzed using the JMP 5.0.1 statistical software package (SAS Institute, 2002), and the differences between means were compared using the Least Significant Difference (LSD) test at the 0.05 probability level (Steel and Torrie, 1980). On the other hand, GGE biplot analyses and GGE biplot graphic were made by using GENSTAT statistical software package (VSN International, 2011) as described by Yan *et al.* (2001) and Yan and Kang (2003). At the same time, cluster analyses were made by using the same program.

RESULTS AND DISCUSSION

The combined analysis of variance over years showed that years, genotypes, and the genotype × year interaction were highly significant ($P< 0.01$) for days to 50% flowering, natural plant height, and the main stem height traits. Climatic differences between the growing seasons significantly affected ranking of the genotypes for these traits. Days to 50% flowering in the 2007-2008 growing season were higher than that in the 2009-2010 season. Sowing in the 2007-2008 growing season occurred 10 days earlier than in 2009-2010, contributing to the flowering time differences. Although days to 50% flowering and the main stem height values of the 2007-2008 growing season were higher than that of the 2009-2010 growing season, natural plant heights in 2007-2008 were lower compared with the 2009-2010 growing season (Table 1).

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Table 1. Analysis of variance for investigated traits in forage pea (*Pisum sativum* spp. *arvense* L.) genotypes.[a]

Source of variation	*df*	DTF[a]		NPH[b]		MSH[c]		MSN[d]		MST[e]		FFY[f]		DMY[g]	
		Sum of square	*F* Value	Sum of square	*F* Value	Sum of square	*F* Value	Sum o square	*F* Value	Sum of square	*F* Value	Sum of square	*F* Value	Sum of square	*F* Value
Years (Y)	1	252.150	500.5919**	2295.254	233.3251**	272.555	16.1797**	0.828	24.1763**	0.272	2.6699ns	702.982	108.9786**	59.045	146.5751**
Genotypes (G)	9	990.683	218.5331**	4325.325	48.8548**	9207.614	60.7324**	0.562	1.8221ns	2.495	2.7205*	1072.712	18.4773**	67.606	18.6473**
Replications	4	0.533	0.2647ns	51.989	1.3213ns	28.412	0.4217ns	0.585	4.2671ns	0.359	0.8799ns	153.669	5.9556**	9.007	5.59**
Y×G	9	58.683	12.9449**	2247.645	25.3873**	2779.624	18.3341**	0.378	1.2254ns	1.433	1.5628ns	568.063	9.7848**	31.183	8.601**
Error	36	18.133		354.137		606.438		1.234		3.668		232.223		14.502	
General	59	1320.183		9274.350		12894.643		3.586		8.226		2729.649		181.344	

[a] Days To 50% Flowering; [b] Natural Plant Height; [c] Main Stem Height; [d] Main Stem Numbers; [e] Main Stem Thickness; [f] Fresh Forage Yield, DMY: Dry Matter Yield. Significant at *: $P \leq 0.05$; **: $P \leq 0.01$, ns: Non-significant.

In terms of days to 50% flowering trait, the genotype×year interaction is given in Table 2. While the earliest days to 50% flowering time was recorded in 200920-10

growing season from the 88P00-1-4-9-661 (1) line (145.3 days), the highest days to 50% flowering time was recorded in 2007-2008 growing season in the Ozkaynak (10) cultivar (163.3 days). In the meantime, according to the average of the two years, the earliest and the latest flowering genotypes in the two study years remained the same (Table 2). Previously, many researchers reported that day numbers to 50% flowering in the forage pea ranged from 122 days to 175 days (Cakmakcı and Cecen, 1999; Cecen *et al.,* 2005; Sayar and Anlarsal, 2008; Sayar *et al.,* 2009; Sayar *et al.,* 2011; Sayar, 2014).

There were significant differences between the years and the forage pea genotypes in terms of natural plant height and the main stem height traits. Natural plant height and main stem height values of forage pea genotypes ranged between 44.17-86.50 cm and 48.04-102.17 cm, respectively. The highest natural plant height was recorded for P57B (4) and P101(6) lines in 2009-2010 growing season, while the lowest natural plant height and main stem height were recorded in Atos cultivar in 2009-2010 growing season. With the highest main stem height values, P101(6) line in 2009-2010 growing season, and P101(6), Kirazli (9) and Ozkaynak (10) cultivars in 2007-2008 growing season took part in the same statistical group (Table 2). The data on natural plant height and the main stem height were found mostly lower than those previously cited by researchers in forage pea (Tekeli and Ates, 2003; Timuragaoglu *et al.,* 2004; Sayar *et al.,* 2011; Tan *et al.,* 2012). According to Tan *et al.* (2012), Murray and Swensen (1985) reported that unfavorable environmental conditions led to the lower plant heights in forage pea genotypes, since forage pea is a typical cool season plant and its height increases under favorable, cool and moist

Table 2. Days to 50% flowering, natural plant height and main stem height values of the forage pea (*Pisum sativum* spp. *arvense* L.) genotypes.[a]

Genotypes	Days to 50% flowering (days)			Natural plant height (cm)			Main stem height (cm)		
	2007-2008	2009-2010	Mean	2007-2008	2009-2010	Mean	2007-2008	2009-2010	Mean
1-88P00-1-4-9-661	149.7 k	145.3 m	147.5 g	63.67 f-h	75.97 cd	69.82 a-b	93.33 b-c	85.10 e-f	89.22 b-c
2-88P038-4-3-683	151.7 g-ı	147.7 l	149.7 f	55.00 j-l	70.37 e	62.68 c	88.33 c-f	86.40 d-f	87.37 c
3-SPRING PEA 3-638	151.3 h-j	147.7 l	149.5 f	46.67 mn	65.07 fg	55.87 d	82.00 f-g	75.97 g	78.98 d
4-P57B	159.0 c	150.3 j-k	154.7 b	50.33 lm	86.50 a	68.42 b	62.67 h-ı	94.33 b-c	78.50 d
5-P51	152.7 e-g	150.7 ı-k	151.7 d	57.33 ı-k	54.07 kl	55.70 d	89.67 c-e	67.23 h	78.45 d
6-P101	156.3 d	152.3 f-h	154.3 b	59.67 h-j	83.23 ab	71.45 a-b	98.67 a-b	102.17 a	100.42 a
7-P104	153.3 e-f	147.7 l	150.5 e	61.00 g-ı	77.50 c	69.25 a-b	92.67 b-d	86.13 d-f	89.40 b-c
8-ATOS	151.7 g-ı	146.7 l	149.2 f	47.00 mn	44.17 n	45.58 e	57.00 ı	48.04 j	52.52 e
9-KİRAZLI	153.7 e	151.7 g-ı	152.7 c	67.00 ef	78.50 bc	72.75 a	98.33 a-b	88.17 c-f	93.25 b
10-ÖZKAYNAK	163.3 a	161.7 b	162.5 a	71.67 de	67.67 ef	69.67 a-b	96.67 a-b	83.17 e-f	89.92 b-c
Mean	154.3 a	150.2 b		57.93 b	70.30 a		85.93 a	81.67 b	
CV (%)	0.47			4.90			4.89		
LSD (0.05)									
Year	0.18**			0.81**			1.06**		
Genotype	0.41**			1.81**			2.37**		
Genotype×Year	0.58**			2.56**			3.35**		

[a] Means with different letters in the same column are significantly different (P< 0.05). Significant at *: $P \leq 0.05$; *: $P \leq 0.01$, ns: Non-significant.

conditions. Despite having fertile soil conditions, deep profile, smooth slope, and without stone, Kiziltepe plain unfavorable climatic conditions, with high temperatures and low rainfall and relative humidity, verified this statement.

ANOVA indicated that differences between the two growing seasons for the number of main stems per plant and differences among the means of genotypes for main stem thickness were found statistically significant (P< 0.05). However, differences between the two growing seasons for main stem thickness and differences among the means of genotypes for main stem numbers per plant were found statistically non-significant (P> 0.05). In the same way, genotype×year interaction for the main stem numbers per plant and main stem thickness were non-significant (Table 1). The non-significance of the genotype×year interaction indicated that the ranking of forage pea genotypes in terms of main stem numbers per plant and main stem thickness were not significantly affected by changing the years.

The numbers of the main stem of forage pea genotypes in the 2009-2010 growing season were higher than those of the 2007-2008 season (Table 3). The 2009-2010 growing season had more suitable climatic conditions compared with the 2007-2008 growing season (Figures 1, 2, 3), which may have contributed to the differences in the number of main stem per plant. Tekeli and Ateş (2003) reported main stem numbers per plant in forage pea as 3.473- 5.650 stems plant^{-1}, whereas Sayar *et al.* (2011) reported 1.21 - 1.78 stems plant^{-1}, and Sayar (2014) reported 1.67-213 stems plant^{-1}. Main stem thickness of forage pea genotypes was between 2.913 and 3.703 mm. According to the two-year averages, Atos (8) and P101 (6) had the thickest main stem, whereas 88P038-4-3-683 (2) had the lowest thickness mean (Table 3). Our data for the main stem thickness were consistent with those presented by Sayar and Anlarsal (2008), Sayar *et al.* (2011), and Sayar (2014), but lower than the findings reported by Tekeli and Ateş (2003). Differences between growing seasons and genotypes contributed to the deviations from previous reports.

All of the interactions were highly significant (P< 0.01) both for fresh forage yield and dry matter yield (Table 1). Fresh forage and dry matter yields among the years showed great differences, and the yields obtained in the 2009-2010 growing season were found higher than those obtained in the 2007-2008 growing season (Table 4). According to Mortazavian *et al.* (2014), climatic and soil conditions cause large fluctuations in yield performance of crops. In this study, the lower rainfall and relative humidity in all of the months and higher temperatures during spring months can be considered as a cause of lower fresh forage and dry matter yields in the 2007-2008 growing season. Similarly, Acıkgoz *et al*. (1986), Karadag and Buyukburc (2004), and Sayar *et al.* (2011) have reported that forage yields of annual forage legumes greatly depend on suitable climatic conditions in the spring months of the growing seasons. When genotype × year interaction were examined (Table 4) for fresh forage and dry matter yield traits, 88P00-1-4-9-661 (1) and P101 (6) forage pea lines and Kirazli (9) cultivar showed a great performance in terms of fresh forage and dry matter yield in Kiziltepe Plain conditions for both of the growing seasons. In fact, especially 32.03 t ha^{-1} fresh forage yield, and 7.939 t ha^{-1} dry matter yield obtained from forage pea line 88P00-1-4-9-661 (1) was a great result for Kiziltepe Plain conditions. On the other hand, the lowest fresh forage yield (8.65 t ha^{-1}) and dry matter yield (2.243 t ha^{-1}) were determined in Spring Pea 3-638 (3) line in 2009-10 growing season (Table 4).

The findings related to fresh forage yield (8.65-32.03 t ha^{-1}) were consistent with previous findings in the forage pea genotypes for fresh forage yield trait (14.48-28.57 t ha^{-1}) by Tekeli and Ates (2003), Timuragaoglu *et al.* (2004): 8.09-20.22 t ha^{-1}, Cecen *et al.* (2005): 12.19 t ha^{-1}, Sayar and Anlarsal (2008): 8.85-16.48 t ha^{-1}, Sayar *et*

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Table 3. Main stem numbers per plant and main stem thickness values of the forage pea (*Pisum sativum* spp. *arvense* L.) genotypes.[a]

Genotypes	Main stem numbers per plant			Main stem thickness (mm)		
	2007-2008	2009-2010	Mean	2007-2008	2009-2010	Mean
1-88P00-1-4-9-661	1.133	1.600	1.367	3.100	3.197	3.148 b-c
2-88P038-4-3-683	1.150	1.533	1.342	3.128	2.697	2.913 c
3-SPRING PEA 3-638	1.150	1.400	1.275	3.297	3.133	3.215 b-c
4-P57B	1.350	1.467	1.408	3.008	3.217	3.113 b-c
5-P51	1.317	1.600	1.458	2.847	3.317	3.082 b-c
6-P101	1.483	1.467	1.475	3.140	3.360	3.250 b-c
7-P104	1.583	1.733	1.658	3.362	3.450	3.406 a-b
8-ATOS	1.400	1.400	1.400	3.793	3.613	3.703 a
9-KİRAZLI	1.283	1.600	1.442	2.778	3.403	3.091 b-c
10-ÖZKAYNAK	1.267	1.667	1.467	3.000	3.413	3.207 b-c
Mean	1.312 b	1.547 a		3.145	3.280	
CV (%)		8.28			6.96	
LSD (0.05)						
Year		0.97**			ns	
Genotype		ns			0.365*	
Genotype×Year		ns			ns	

[a] Means with different letters in the same column are significantly different (P< 0.05). Significant at *: $P \leq 0.05$; *: $P \leq 0.01$, ns: Non-significant.

Table 4. Fresh forage and dry matter yields of the forage pea (*Pisum sativum* spp. *arvense* L.) genotypes.[a]

Genotypes	Fresh forage yield (t ha^{-1})			Dry matter yield (t ha^{-1})		
	2007-2008	2009-2010	Mean	2007-2008	2009-2010	Mean
1-88P00-1-4-9-661	15.63 e-f	32.03 a	23.83 a	3.843 d-e	7.939 a	5.891 a
2-88P038-4-3-683	13.48 f	13.13 f	13.31 d-e	3.246 e-f	3.538 d-e	3.392 d
3-SPRING PEA 3-638	12.22 f-g	8.650 g	10.43 e	2.808 e-f	2.243 f	2.525 e
4-P57B	13.58 f	24.57 c	19.08 c	3.254 e-f	6.116 b-c	4.685 c
5-P51	14.08 f	13.63 f	13.86 d	3.279 e-f	3.547 d-e	3.413 d
6-P101	19.50 d-e	25.48 b-c	22.49 a-b	4.559 d	7.060 a-b	5.809 a
7-P104	15.27 f	24.50 c	19.88 b-c	3.581 d-e	6.115 b-c	4.848 b-c
8-ATOS	15.06 f	22.37 c-d	18.71 c	3.623 d-e	5.747 c	4.685 c
9-KİRAZLI	15.73 e-f	29.15 a-b	22.44 a-b	3.756 d-e	7.366 a	5.561 a-b
10-ÖZKAYNAK	15.50 e-f	25.00 b-c	20.25 b-c	3.560 d-e	5.678 c	4.619 c
Mean	15.01 b	21.85 a		3.551 b	5.535 a	
CV (%)		13.78			10.69	
LSD (0.05)						
Year		1.339**			0.331**	
Genotype		2.984**			0.743**	
Genotype×Year		4.202**			1.052**	

[a] Means with different letters in the same column are significantly different (P< 0.05). Significant at *: $P \leq 0.05$; *: $P \leq 0.01$, ns: Non-significant.

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al. (2009): 11.56-16.58 t ha^{-1}, Bilgili *et al.* (2010): 16.07-35.97 t ha^{-1}, Sayar *et al.* (2011): 11.34-19.67 t ha^{-1} and Sayar (2014): 24.35-25.30 t ha^{-1}. However, our fresh forage yield findings partly consisted with fresh forage yield findings of Bilgili *et al.* (2010) (16.07-35.97 t ha^{-1}). On the other hand, the findings in the study related to dry matter yield (2.243-7.939 t ha^{-1}) were consistent with those previously reported for the forage pea genotypes by Tekeli and Ates (2003): 3.440-7.383 t ha^{-1}, Timuragaoglu *et al.* (2004): 2.290-5.420 t ha^{-1}, Cecen *et al.* (2005): 3.17 t ha^{-1}, Sayar *et al.* (2009): 2.79-4.10 t ha^{-1}, Sayar *et al.* (2011): 2.78-4.58 t ha^{-1}, and Sayar (2014): 6.33.8-6.935 t ha^{-1}. However, our dry matter yield findings were found partly lower and partly consistent with dry matter yield findings of Acıkgoz *et al.* (2009): 2.366-8.613 t ha^{-1}, and Uzun *et al.* (2012): 6.533-7.947 t ha^{-1}. Moreover, our dry matter findings were partly higher and partly consistent with the results of Sayar and Anlarsal (2008). The partly inconsistence between the cited dry matter yields and our dry matter yield scores probably stemmed from the differences between the studies conducted ecological conditions and the used genotypes.

Assessments with GGE Biplot Analyses

PC1 (the first Principal Component) and PC2 (the second Principal Component) accounted for 83.53% and 16.47%, of the total variation, respectively (Figure 4). This indicated the existence of a good variation between the growing years and the genotypes. Similarly, Asfaw *et al.* (2012) stated that PC1 and PC2 explained 90.4% of the total Genotype plus Genotype by Environment (G+GE) variation. And, this indicated a biplot constructed by plotting PC1 scores of genotypes and the environments against their respective scores for PC2 scores adequately capturing the environment-centered data. According to Yan *et al.* (2007) and Firincioglu *et al.* (2012), the higher PC1 and PC2 values contribute to more reliable interpretation of GGE biplots.

Genotype×year interactions of forage pea genotypes in terms of all of the examined traits with different GGE biplot graphic indicated in Figure 4. The two growing seasons were found to be significantly

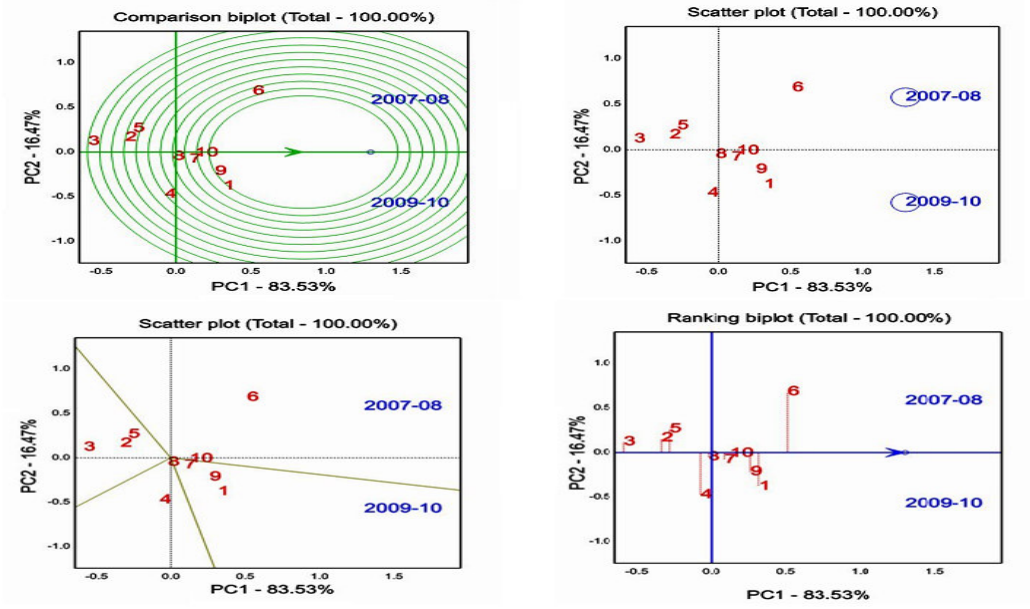

Figure 4. The explanation of genotype×year interactions in forage pea genotypes with different GGE biplot graphic.

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different (Figure 4). The genotypes P101 (6) and Ozkaynak (10) performed well during the 2007-2008 season, whereas 88P00-1-4-9-661 (1), Kirazli (9) and P104 (7) performed well during the 2009-2010 growing season. However, performance of 88P038-4-3-683 (2), Spring Pea 3-638 (3), P57B (4), P51 (5) were not associated with the two growing seasons.

As a result of GGE biplot analysis, the investigated traits were grouped by taking into consideration the angles between vectors in the GGE biplot (Figure 5). When a narrow angle (< 90°) was identified between traits vectors, these traits took part in the same group (Yan, 2002; Yan and Kang, 2003; Ilker *et al*., 2009; Kendal, 2013). Accordingly, GGE biplot analysis divided the traits into four groups. Fresh forage yield, dry matter yield, days to 50% flowering, and natural plant height traits were in the first group. 88P00-1-4-9-661 (1), P101 (6), Kirazli (9) and Ozkaynak (10) genotypes were found to be superior for the first group of traits. Main stem height was close to the first group of traits, but was assigned to a second group without other traits. Only P104 (7) was placed in this second group. Main stem numbers comprised the third group, in which P57B (4) was the only line. Main stem thickness was the only trait in the fourth group, accompanied by the cultivar Atos (8). The lines 88P038-4-3-683 (2), Spring Pea 3-638 (3), and P51 (5) lines were not assigned to any of the groups.

Fresh forage yield, dry matter yield, days to 50% flowering, and main stem numbers per plant were the most stable traits (Figure 5). Conversely, main stem thickness, main stem height, and natural plant height were the least stable in the Kiziltepe climatic conditions. The line 88P00-1-4-9-661 was the most stable genotype (Figure 5). In terms of stability, it was followed by P101 (6), P57B (4) and P51 (5). Due to the lower PC1 score of P51 (5), it was not recommended for forage production in Kiziltepe

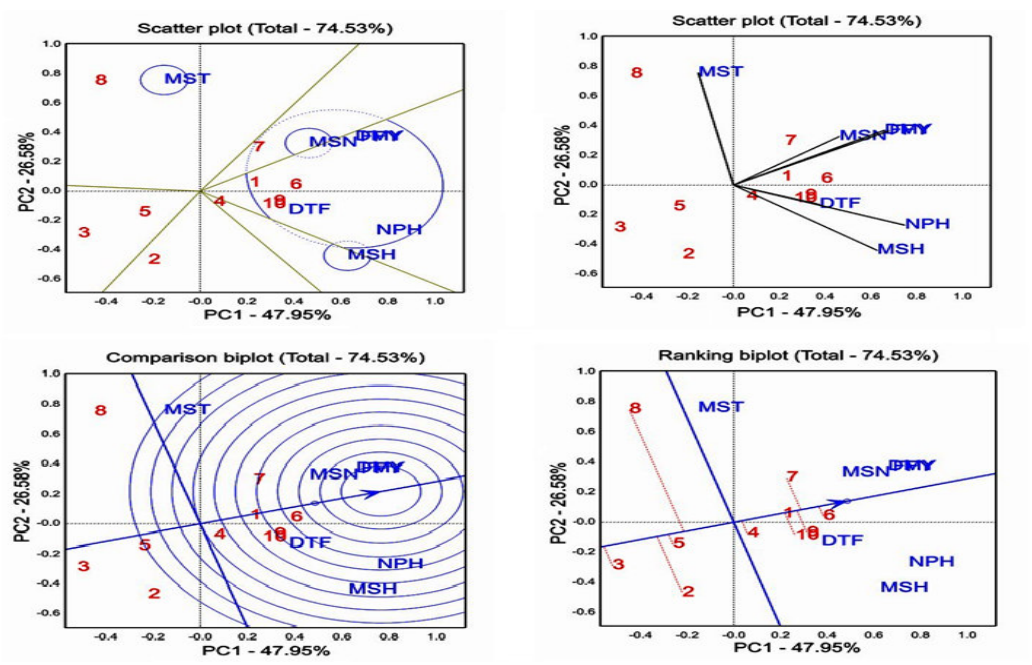

Figure 5. The explanation of relations between forage pea genotypes and the investigated traits also stability status of the genotypes and the traits with different GGE biplot graphic. (FFY: Fresh Forage Yield; DMY: Dry Matter Yield; DTF: Days To 50% Flowering; NPH: Natural Plant Height; MSH: Main Stem Height; MSN: Main Stem Numbers, MST: Main Stem Thickness).

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conditions. A lower PC1 score indicated that this line had low yields of fresh forage and dry matter. The PC2 scores of the Atos (8) and 88P038-4-3-683 (2) lines were the most distant from the average PC2 scores; therefore, these two genotypes showed poor stability for the investigated traits.

Cluster Analysis of All Investigated Traits

To reveal similarity between genotypes, hierarchical cluster analysis was applied to the study data for the investigated traits (Figure 6). All forage pea genotypes were at least 70% similar. At higher levels of similarity, the genotypes were divided into two groups. The first group included 88P00-1-4-9-661 (1), 88P038-4-3-683 (2), Spring Pea 3-638 (3) and Ozkaynak (10). The remaining six genotypes comprised the second group. Among the genotypes, the highest similarity was between 88P038-4-3-683 (2) and Spring Pea 3-638 (3) in the first group, and between P51 (5) and P101 (6) in the second group, with over 95% similarity. The lines 88P038-4-3-683 (2) and Spring Pea 3-638 (3) originated from ICARDA. These lines were similar in many traits, including seed and flower colors, plant height, and seed size and shape. Both P51 (5) and P101 (6) were obtained from the Field Crops Department of Uludag University, Bursa, Turkey.

CONCLUSIONS

Results of the study showed that there were highly significant differences among the forage pea genotypes in terms of the investigated traits. According to the two years average, the highest fresh forage yield and dry matter yield were obtained from, respectively, 88P00-1-4-9-661 (1), P101 (6) and Kirazlı genotypes. Additionally, GGE biplot analysis showed that the three genotypes took part in the same examined traits group. This meant that the genotypes not only for fresh forage yield and dry matter yield but also for natural plant height and days to 50% flowering traits were found superior to the other genotypes. Therefore, we recommended that when forage yield aimed in the forage pea cultivations, 88P00-1-4-9-661 (1), P101 (6) and Kirazlı genotypes should be preferred in the Kiziltepe conditions, respectively.

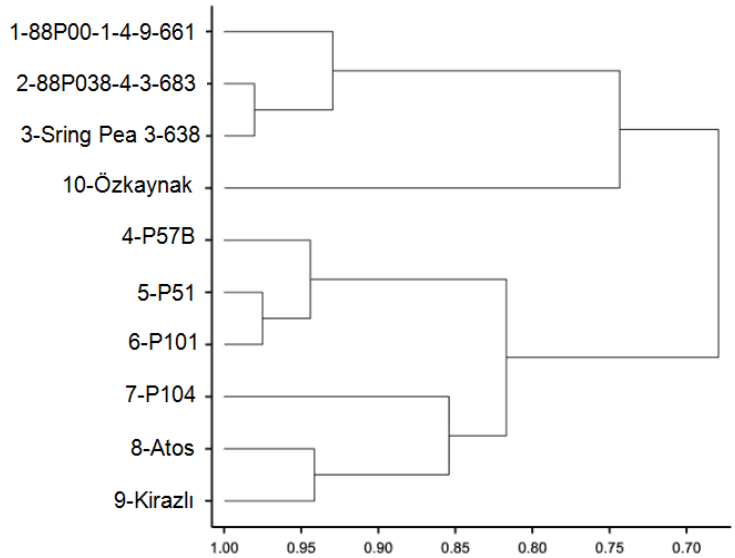

Figure 6. Classification of forage pea (*Pisum sativum* spp. *arvense* L.) genotypes with cluster analysis.

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عملکرد ژنوتیپ های نخود علوفه ای (*Pisum sativum* spp. *arvense* L.) و ارزیابی آن ها با استفاده از تجزیه بای پلاتGGE

م. ص. سیار، و م. هان

چکیده

هدف اجرای این پژوهش ارزیابی عملکرد ژنوتیپ های نخود علوفه ای (Pisum sativum spp. arvense L.) از نظر عملکرد علوفه تر و صفات همراه آن در دشت قزل تپه در منطقه ماردین ترکیه بود. آزمایش های مزرعه ای طی دو فصل زراعی در سال های ۸-۲۰۰۷ و۱۰-۲۰۰۹ اجرا شد. طرح آزمایش ها بلوک های تصادفی با سه تکرار بود. نتایج صفات اندازه گیری شده به این شرح گزارش شد: تعداد روز تا مرحله ۵۰٪ گلدهی : 147.5-162.5روز، ارتفاع طبیعی بوته ها: 45.58-72.75 سانتی متر،ارتفاع ساقه اصلی:52.52-100.42 cm، تعداد ساقه های اصلی هر بوته: 1.275-1.658، ضخامت ساقه اصلی:2.913-3.703 mm، عملکرد علوفه تر: 10.43-23.83تن در هکتار، و عملکرد ماده خشک: 2.525-5.891 t ha-1. سپس، با استفاده از تجزیه GGE(منظور G+GEاست) به روش بای پلات آشکار شد که دوفصل زراعی مزبور به طور قابل ملاحظه ای با هم تفاوت داشتند و این تفاوت منحصرا از تفاوت در مقدار بارندگی در این دو فصل ناشی می شد. نتایج این پژوهش نشان داد که رگه های (1) 88P00-1-4-9-661و (6) P101 و کولتیوار Kirazli (9)از نظر صفات عملکرد علوفه تر، عملکرد ماده خشک، ارتفاع طبیعی بوته، و تعداد روز تا مرحله ۵۰٪ گلدهی بر ژرم پلاسم های دیگر برتری داشتند. در عین حال، امتیاز های تجزیه جزء اصلی۲ (PC2) این ژرم پلاسم ها نزدیک به صفر بود، بنا بر این، آن ها از نظر صفات مطاله شده ژنو تیپ هایی پایدار بودند. نتیجه گیری کلی این بود که از نظر عملکرد علوفه، این سه ژنوتیپ نخود علوفه ای برای دشت قزل تپه توصیه می شوند.

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