

## GGE BILOT ANALYSIS IN WILD (*PISUM SATIVUM* L. SUBSP. *ELATIUS* AND SUBSP. *SATIVUM*) AND CULTIVATED PEA (*PISUM SATIVUM* L.) GENOTYPES IN NORTHERN AND SOUTHERN TURKEY

GIRGEL, U.<sup>1</sup> – COKKIZGIN, A.<sup>2\*</sup>

<sup>1</sup>Bayburt University, Aydıntepe Vocational School, 69500 Bayburt, Turkey  
(phone: +90-458-311-4426; fax: +90-458-311-4466)

<sup>2</sup>Gaziantep University, Nurdagi Vocational School, 27840 Gaziantep, Turkey  
(phone: +90-342-671-3382; fax: +90-342-671-3384)

\*Corresponding author

e-mail: [acokkizgin@gantep.edu.tr](mailto:acokkizgin@gantep.edu.tr), [acokkizgin@hotmail.com](mailto:acokkizgin@hotmail.com)

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**Abstract.** This research was carried out in the multiple-environment trials (MET) which one is in Bayburt (40°24'05.7"N 40°08'31.3"E) where the Black Sea geographical region located in the north of Turkey and in the Kahramanmaraş (37°35'24.8"N 36°48'49.4"E) where the Mediterranean geographical region located in the south of Turkey in 2016 and 2017 years. In this investigation, 6 registered pea cultivars (Bolero, Jof, Karina, Nihal, Reyna and Utrillo) and 2 wild pea genotypes (*Pisum sativum* L. subsp. *elatius* and *P. sativum* L. subsp. *sativum*) were used. The variance analysis showed a significant difference among Location (L), genotypes (G), genotypes×locations interaction (GL), genotypes×year interaction (GY), year×location interaction (YL) (all significant at P<0.01 level) and genotype×location×year interaction (GLY) (significant at P<0.05 level) interaction in terms of seed yield. Main effect genotypes (G) is explained 24.42% of total variation. This is followed by 18.78% (L), 17.87% (YL) 7.04% (GL), 4.91% (GY), 2.71% (GLY) and 1.12% (Y), respectively. Graphs were drawn according to the results of GGE biplot analysis and yield data of genotypes were evaluated according to these graphs. In accordance with GGE biplot analysis the seed yield first principal component explained 82.81% of the total variation and second principal component explained 17.19% of the total variation.

**Keywords:** multi environment (MET), stability, yield, *Pisum sativum*

### Introduction

Dry pea cultivation was carried out on 8.141.031 hectare area in the world and it has 16.205.448 tons production and 1990,6 kg/ha yield value. On the other hand green pea cultivation has 2.669.305 hectare area value, 20.699.736 tons production and 7754,7 kg/ha yield value worldwide (FAO, 2018).

Peas are the second most produced legumes in worldwide (FAO, 2018). The number of diploid chromosomes in pea is 14 (Murtaza et al., 2005) and it is a legume crops which origin is near east (Abbo et al., 2017). This region is also the source of wild pea subspecies (Symkal et al., 2015). On the other hand for further pea crop improvement the wild peas are important sources of genetic diversity in climate change context (Symkal et al., 2018).

It is known that Biplot concept started with Descartes. Also Ptolemy used to map cities in ancient times (Gower et al., 2011). Also “Biplot” is a term used by Gabriel (1971), but the first using of biplots in agricultural data was Bradu and Gabriel (1978), as popular versions of variables which were represented by directed vectors and Gower and Hand (1996), emphasized its advantages of biplots with calibrated axes.

Genotype×Environment interaction is a complicated source of variation and also makes the selection of genotype(s) difficult (Magari and Kang, 1993). Genotype by environment (GE) interaction may vary according to crops and years (Milligan, 1994). When G×E interaction is statistically significant, its nature, reason and results must be carefully examined (Magari and Kang, 1993). On the other hand, genotype environment interaction is very effective on seed yield to reveal the effectiveness of interaction; trials should have multiple years and multiple locations (Rao et al., 2011; Luo et al., 2015).

It is reported that the best method for revealing Genotype×Environment interaction is GGE-biplot analysis (Samonte et al., 2005; Fan et al., 2007). Using the graphs, GE interaction could be better understandable (Luo et al., 2015). GGE biplot technique has been used by many researchers to determine product performance such as rapeseed (Shang et al., 2006), peanut (Chen et al., 2009), millet (Zhang et al., 2016), barley (Kendal et al., 2014; Kizilgeci, 2019), oat (Zhang et al., 2010), rice (Sharifi and Motlagh, 2011), sugarcane (Luo et al., 2015), wheat (Akbarzai et al., 2017), maize (Fan et al., 2007), bean (Kang et al., 2006), chickpea (Farshadfar, 2013).

The objectives of the study were to (1) reveal genotype, location, year values, (2) determine genotype by location interaction, (3) determine genotype by year interaction, (4) determine year×location interaction, (5) determine genotype×location×year interaction, (6) reveal the stability of wild and cultivated pea genotypes in Bayburt and Kahramanmaras locations (in northern and southern part of Turkey) via GGE biplot analysis. As a result, more compatible genotypes will be obtained in future breeding studies.

## Material and Methods

### Research areas

This research was carried out in the multiple-environment trials (MET). The locations were Bayburt/Turkey (Bayburt University, Food and Agriculture and Livestock Application and Research Center area) (40°24'05.7"N 40°08'31.3"E) and Kahramanmaras/Turkey (Kahramanmaras Sutcu Imam University, Field Crops Department Treatment area) (37°35'24.8"N 36°48'49.4"E). The study was conducted at the locations in 2016 and 2017 years. These locations are located in the northern and the southern of Turkey (Table 1). Climate data of the research areas are given in Table 2. In the research, each plot consists of 5 rows, the distance between rows was 50 cm and the plot length was 5 m, total plot area is determined as 12.5 m<sup>2</sup> and plant density was 40 plant m<sup>-2</sup>.

**Table 1.** Global positions and soil properties of the research areas

Location	Soil feature	Altitude	Global position
Bayburt	Loamy soil	1650	40°24'05.7"N 40°08'31.3"E
Kahramanmaras	Loamy soil	507	37°35'24.8"N 36°48'49.4"E

### Seed materials

Two wild pea genotypes (*Pisum sativum* L. subsp. *elatius* and *P. sativum* L. subsp. *sativum*) in which they were gained from natural vegetation in Turkey and six registered pea cultivars (Bolero, Jof, Karina, Nihal, Reyna and Utrillo) were used and the study

was used in the study. The selection criterion was considered to be the genotype that can adapt to both regions.

Before the seed yield was obtained, one row on each side of the plot and 0.5 m from both ends of the plot which was evaluated as side effect were excluded from the evaluation and the central rows harvested by hand, according to Girgel (2013).

**Table 2.** Some climatical datas for research areas (Bayburt and Kahramanmaras)

<b>Long time period (1959 - 2018) climatical datas in growing period for Bayburt Province</b>					
Parameters	May	Jun	July	Aug	Sep
Average Temp. (°C)	11.8	15.5	19.2	19.0	14.8
Average Highest Temp. (°C)	18.2	22.7	27.1	27.6	23.5
Average Lowest Temp. (°C)	5.7	8.3	11.2	11.0	7.3
Average Rainy Days	16.0	10.7	5.0	4.4	5.0
Average Monthly Total Rainfall (mm)	71.8	50.5	20.2	13.9	20.5
Highest Temp.(°C)	29.6	32.9	37.0	37.2	33.7
Lowest Temp. (°C)	-4.4	-1.6	0.2	2.4	-2.1
<b>Long time period (1930-2018) climatical datas in growing period for Kahramanmaras province</b>					
Parameters	Feb	Mar	Apr	May	Jun
Average Temp. (°C)	6.6	10.8	15.5	20.3	25.2
Average Highest Temp. (°C)	11.0	15.9	21.2	26.7	31.9
Average Lowest Temp. (°C)	2.4	5.7	9.8	13.9	18.6
Average Rainy Days	11.3	11.1	9.9	7.4	2.2
Average Monthly Total Rainfall (mm)	109.9	96.3	72.8	41.9	7.4
Highest Temp.(°C)	25.3	29.8	36.0	38.0	42.0
Lowest Temp. (°C)	-9.6	-7.6	-1.8	4.7	4.9

\*(TSMS, 2019)

### Statistical analysis

In the research, for the phenotypic variation,  $P = E + G + GE$  formula was used. In the formula, the phenotype P represents the environment, the G genotype, and GE represents the genotype×environment interaction (Yan and Kang, 2003). Also, year and location factors are within environment (E).

In addition to being a multiple-environment trials (MET), the factors could be divided because it was conducted for two years (2016 and 2017). For a more detailed variance analysis (E) is divided year (Y) and location (L) factors also all interactions between G, L and Y factors were evaluated according to Comstock and Moll (1963).

The experiment was established with 3 replications in according to randomized complete block design (RCBD). Statistical analysis was performed with GenStat Release 12.1 (VSN International Ltd.) according to Gomez and Gomez (1984) and Rao (2007). And GGE biplot graphs and analysis was performed according to Gabriel (1971), Yan et al. (2000), Yan and Tinker (2006) and Kang et al. (2006) by using GenStat software (VSNI, 2009).

## Results and Discussion

### Analysis of variance

In the study, genotype, locaiton, year and their interactions were examined. The variance analysis showed a significant difference among genotypes (G), locations (L), genotypes×location interaction (GL), genotypes×year interaction (GY), year×location interaction (YL) (all significant at  $P < 0.01$  level) and genotype×location×year interaction

(GLY) (significant at  $P < 0.05$  level) in terms of seed yield (Table 3). Luo et al. (2015) reports that the factors of genotype, location, year, and all interactions between them were found to be statistically significant. And similar statistical results reported by Kan et al. (2010).

**Table 3.** Variance analysis for seed yield of pea genotypes in two years (2016 and 2017) and two locations (Bayburt and Kahramanmaraş)

Source of Variation	DF	SS	MS	F pr.	Explained (%)
G	7	45612.4	6516.1	<.001	24.42
Y	1	299.3	299.3	0.294	1.12
L	1	5009.8	5009.8	<.001	18.78
GY	7	9162.3	1308.9	<.001	4.91
GL	7	13142.9	1877.6	<.001	7.04
YL	1	4767.2	4767.2	<.001	17.87
GLY	7	5056.3	722.3	0.016	2.71
Residual	64	17891.2	940.9		
Total	95	100941.5			

DF: Degree of freedom, SS: Sum of square, MS: Mean square, F pr.: Probability

In the investigation, variance analysis showed that the genotypes had greater effect on seed yield than the factors location or year. Genotype, environment and year factors and their interactions explain 76.85% of the total variance (Table 3). In here the greatest variance value is due to main effect genotypes (G) and it is explained 24.42% of total variation. This is followed by 18.78% (L), 17.87% (YL) 7.04% (GL), 4.91% (GY), 2.71% (GLY) and 1.12% (Y), respectively. On the other hand, least significant difference statistical groups (LSD) for all measurement interactions and factors were determined with the help of MSTAT-C software package program (v2.10) (MSTAT-C, 1994) (Table 4).

Environmental factors and primarily genetic structure are the main factors in determining the phenotype. As a result of the interactions of these factors reveals the amount of seed yield. Yan and Kang (2003) reported that phenotypic variation consists of genotype and environment and their interaction. Sabaghnia et al. (2011) reported that when there are no different locations, the year factor explained the large proportion of the total variation. On the other hand, similar results gained by Noerwijati et al. (2014).

According to GGE biplot analysis results for the seed yield first principal component explained 82.81% of the total variation and second principal component explained 17.19% of the total variation. The PCA (Principle Component Analysis) model based on the GGE biplot explains further variation (Yan and Kang, 2003).

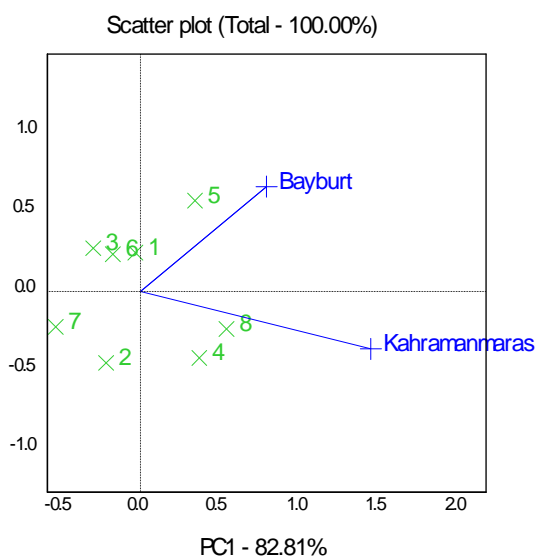
### Scatter plot results

According to the scatter plot graph for ranking of locations and genotypes, it can be said that there is almost none correlation the between Bayburt and Kahramanmaraş locations due to the acute angle value is very close to the right angle (Fig. 1). In the analysis, the cosine of the angle between vectors shows that correlation between vectors i.e. obtuse angles shows that negative association and acute angle indicate positive association and at right angles there is no relationship between vectors (Yan, 2014; Dallo et al., 2019).

**Table 4.** Means and the least significant difference (LSD) groups for all measurement interactions and factors\*

Location	Genotype**	Year		Location×Genotype Interaction	Means of Location
		2016	2017		
Bayburt	1	106.0 <sup>b-f</sup>	86.00 <sup>c-i</sup>	96.00 <sup>BC</sup>	88.56 <sup>A</sup>
	2	67.00 <sup>g-l</sup>	59.00 <sup>i-l</sup>		
	3	89.00 <sup>c-i</sup>	82.00 <sup>d-j</sup>		
	4	99.00 <sup>c-h</sup>	80.00 <sup>e-k</sup>		
	5	138.0 <sup>ab</sup>	110.00 <sup>a-e</sup>		
	6	101.0 <sup>c-h</sup>	78.00 <sup>e-k</sup>		
	7	61.00 <sup>i-l</sup>	54.00 <sup>i-m</sup>		
	8	118.0 <sup>a-c</sup>	89.00 <sup>c-i</sup>		
	Location×Year Interaction	97.38 <sup>A</sup>	79.75 <sup>B</sup>		
Kahramanmaras	1	66.00 <sup>h-l</sup>	67.53 <sup>g-l</sup>	66.77 <sup>DEF</sup>	74.12 <sup>B</sup>
	2	45.00 <sup>k-n</sup>	86.67 <sup>c-i</sup>		
	3	17.67 <sup>n</sup>	72.67 <sup>f-k</sup>		
	4	115.70 <sup>a-d</sup>	107.50 <sup>a-f</sup>		
	5	107.00 <sup>a-f</sup>	72.87 <sup>f-k</sup>		
	6	74.80 <sup>f-k</sup>	36.67 <sup>l-n</sup>		
	7	23.27 <sup>mn</sup>	49.43 <sup>j-n</sup>		
	8	101.30 <sup>e-g</sup>	141.80 <sup>a</sup>		
	Location×Year Interaction	68.83 <sup>B</sup>	79.40 <sup>B</sup>		
Year×Genotype Interaction	1	86.00 <sup>CD</sup>	76.77 <sup>DE</sup>	Means of Genotype	
	2	56.00 <sup>EFG</sup>	72.83 <sup>DEF</sup>	1	81.38 <sup>B</sup>
	3	53.33 <sup>EFG</sup>	77.33 <sup>DE</sup>	2	64.42 <sup>BC</sup>
	4	107.30 <sup>ABC</sup>	93.75 <sup>BCD</sup>	3	65.33 <sup>B</sup>
	5	122.50 <sup>A</sup>	91.43 <sup>BCD</sup>	4	100.50 <sup>A</sup>
	6	87.90 <sup>CD</sup>	57.33 <sup>EFG</sup>	5	107.00 <sup>A</sup>
	7	42.13 <sup>G</sup>	51.72 <sup>FG</sup>	6	72.62 <sup>B</sup>
	8	109.60 <sup>ABC</sup>	115.4 <sup>AB</sup>	7	46.92 <sup>C</sup>
Means of Year		83.10 <sup>NS</sup>	79.57 <sup>NS</sup>	8	112.50 <sup>A</sup>

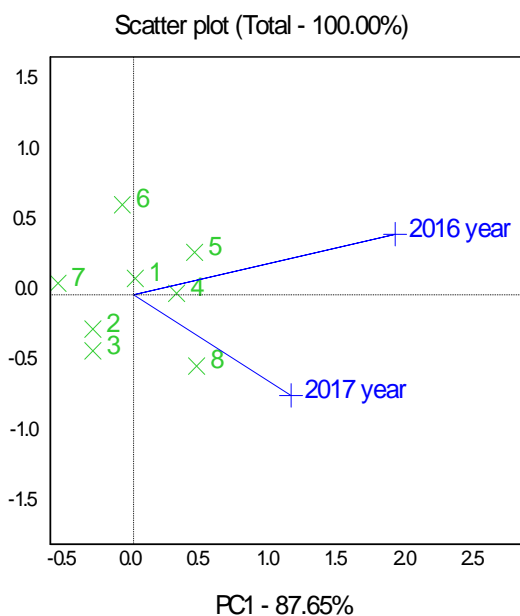
\* Differences between means that share same letter was not statistically significant.  
\*\* 1. Bolero, 2. Jof, 3. Karina, 4. Nihal, 5. Reyna, 6. ssp. sativum, 7. ssp. elatius, 8. Utrillo



**Figure 1.** GGE scatter biplot graph shows that ranking of genotypes over the environments (x: shows wild and cultivated genotype scores and +: shows environment scores) (1. Bolero, 2. Jof, 3. Karina, 4. Nihal, 5. Reyna, 6. ssp. sativum, 7. ssp. elatius, 8. Utrillo)

Narrow angle, indicates a correlation between genotypes. Similar opinions have been reported by Yan (2002) and Kang et al. (2006). Utrillo cv. was found to be most yielding genotype but *Pisum sativum* subsp. *elatius* was determined as the lowest yielding but the most stable genotype.

In terms of the years the first principal components (PC1) and second principal components (PC2) of the seed yield accounted as 87.65 and 12.35, respectively (Fig. 2). The years was similar to each other due to the narrow angle and there is a very small amount positive correlation. In other words, the conditions of the years are similar. It is reported that in such graphs, there is a correlation between the parameters examined when there is a narrow angle (Yan, 2002).



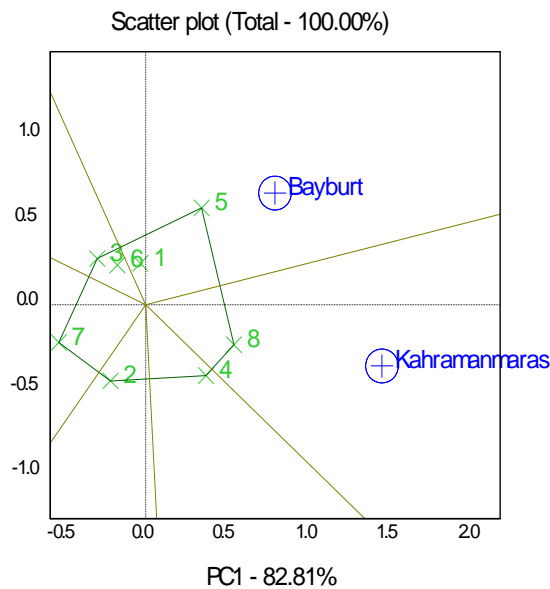
**Figure 2.** GGE scatter biplot graph shows that ranking of genotypes over the years (x: shows wild and cultivated genotype scores and +: shows year scores) (1.Bolero, 2.Jof, 3.Karina, 4.Nihal, 5.Reyna, 6.ssp.sativum, 7.ssp.elatius, 8.Utrillo)

Pea plants showed better adaptation under the first year environmental conditions and the first year point was close to the stability line than second year. On the other hand, the Nihal variety was determined as the genotype closest to the stability line (Fig. 2). Snoad and Arthur (1974), point out that repeated trials for many years reveal genotype-environment interaction in a more understandable way.

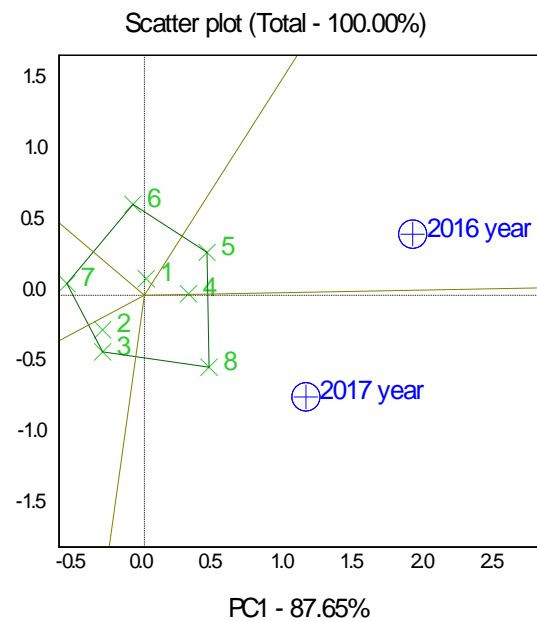
According to polygonal Genotype×Environment interaction scatter biplot graph, under the conditions of Kahramanmaras, Utrillo genotype is environmentally compatible and under the Bayburt conditions, Reyna and bolero genotypes are located in the same sectors and emerged as high performance varieties that are compatible with this environment (Fig. 3). Genotype×Environment interaction is very important for genotype selection and therefore, repeating the experiments at different years and locations provides accurate genotypic results. Similar opinions reported by Weber et al. (1996). On the other hand, Yan and Kang (2003) recommended a biplot polygon graph to better understanding the genotype environment interaction.

According to polygonal Genotype×Year interaction scatter biplot graph, in the first year Reyna and Nihal, in the second year, Utrillo and Nihal varieties appeared as the

highest performance genotypes (Fig. 4). In the graph, the polygon was divided into 5 parts and the years had taken place in different sections. As a rule, polygon edges and axes were at right angles to each other. If the locations are not taken into consideration, in terms of years, the cv. Bolero was located at the center of the axis in the graph and had been the least affected by the environmental conditions of that year. However, this genotype had less seed yield. On the other hand, cv. Nihal was determined to be stable regardless of locations and it had higher seed yield from cv. Bolero.



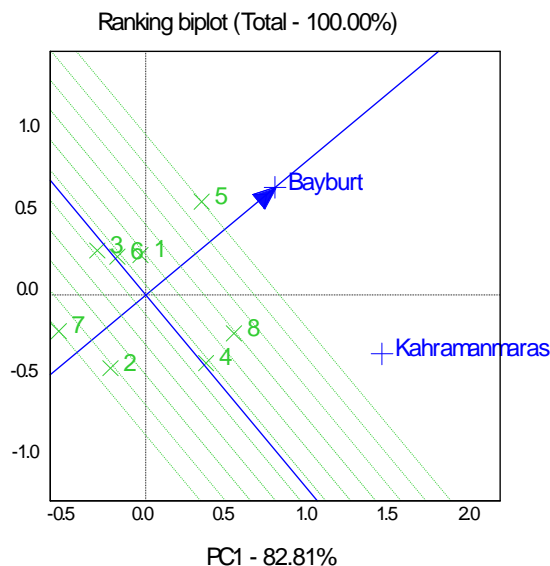
**Figure 3.** Polygon graph of Genotype×Environment interaction for genotypes over the environments (x: shows wild and cultivated genotype scores and +: shows environment scores) (1.Bolero, 2.Jof, 3.Karina, 4.Nihal, 5.Reyna, 6.ssp.sativum, 7.ssp.elatius, 8.Utrillo)



**Figure 4.** Polygon graph of Genotype×Year interaction for genotypes over the years (x: shows wild and cultivated genotype scores and +: shows year scores)

### Ranking biplot results

GGE ranking biplot graph shows the status of genotypes by Bayburt location (Fig. 5). In the graph a line representing the province of Bayburt was drawn through the biplot origin and another a line perpendicular to the Bayburt axis was drawn from each genotype. The Bayburt line represented the axis for the Bayburt province. Yan and Tinker (2006) reported that the seed yield in the direction of the arrow increases and genotypes closer to the arrow line are more stable. When the GGE ranking biplot graph was examined, Reyna variety showed the highest performance in Bayburt province, followed by Utrillo variety, but it was found that Reyna, which is close to the axis in terms of stability, was more convenient (Fig. 5).



**Figure 5.** GGE ranking biplot graph showed according to Bayburt province the ranking of the genotypes yield (x: shows wild and cultivated genotype scores and +: shows environment scores) (1.Bolero, 2.Jof, 3.Karina, 4.Nihal, 5.Reyna, 6.ssp.sativum, 7.ssp.elatius, 8.Utrillo)

In the GGE ranking biplot graph the Kahramanmaraş line represented the axis for the Kahramanmaraş province. Yan and Tinker (2006) pointed that the seed yield in the direction of the arrow increases and genotypes closer to the arrow line are more stable. When the GGE ranking biplot graph was examined, under the Kahramanmaraş conditions, the Utrillo variety was determined as highest seed yield and the most stable genotype in terms of seed yield (Fig. 6).

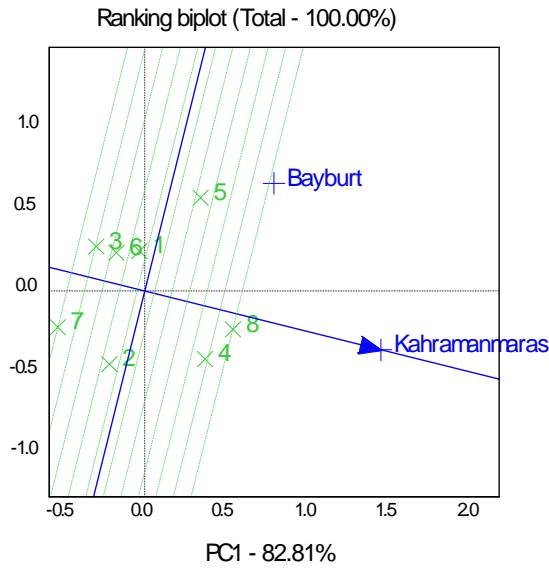
### Comparison biplot results

By using the ideal environment as the center in order to visualize the distance between Bayburt and Kahramanmaraş locations concentric circles were drawn (Yan et al., 2000; Yan and Rajcan, 2002).

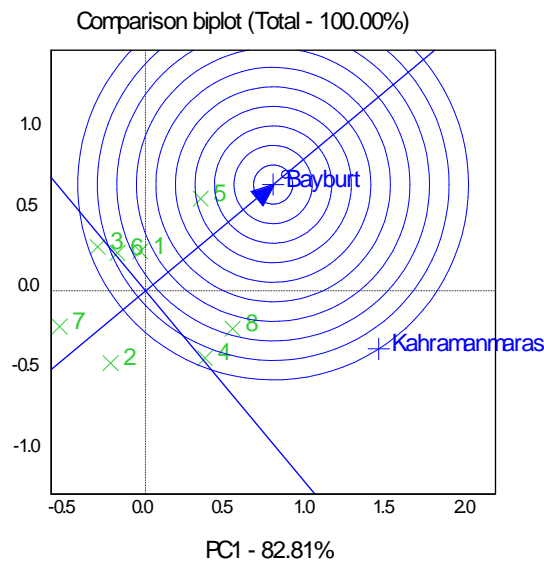
The comparison biplot graph assumes that the province of Bayburt has ideal environmental conditions and draws from the center towards the outer ring suitability for genotypes. Concentric circles were drawn so that the ideal environment is in the center (Yan et al., 2000; Yan and Rajcan, 2002). Bayburt ecological conditions were considered as an ideal environment; Reyna variety was found to be most suitable. In



addition, Bolero and Utrillo varieties and wild genotype *Pisum sativum* subsp. *sativum* can be evaluated. Jof cultivar and *Pisum sativum* subsp. *elatius* wild cultivar were not suitable for the region (Fig. 7). Our results are in agreement with other observational study of Yihunie and Gesesse (2018).



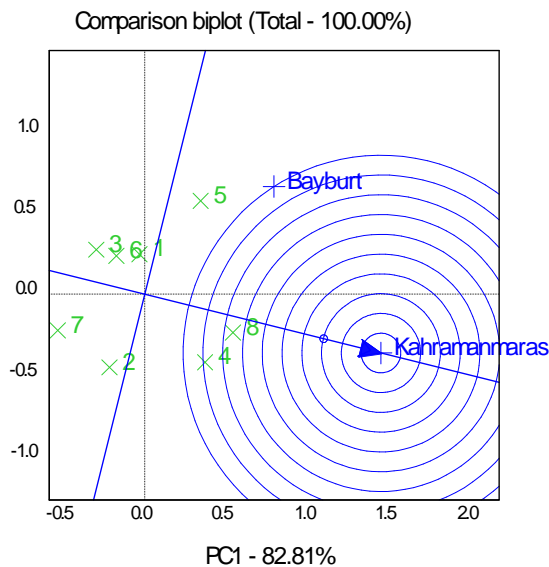
**Figure 6.** GGE ranking biplot graph shows according to Kahramanmaras province the ranking of the genotypes yield (x: shows wild and cultivated genotype scores and +: shows environment scores) (1.Bolero, 2.Jof, 3.Karina, 4.Nihal, 5.Reyna, 6.ssp.sativum, 7.ssp.elatius, 8.Utrillo)



**Figure 7.** GGE Comparison biplot graph shows the ranking of the genotypes as an ideal environment Bayburt province (x: shows wild and cultivated genotype scores and +: shows environment scores) (1.Bolero, 2.Jof, 3.Karina, 4.Nihal, 5.Reyna, 6.ssp.sativum, 7.ssp.elatius, 8.Utrillo)

Kahramanmaras as the ideal environment according to the comparison biplot graph, Utrillo and Nihal varieties are found to be appropriate (Fig. 8). The rings moving away

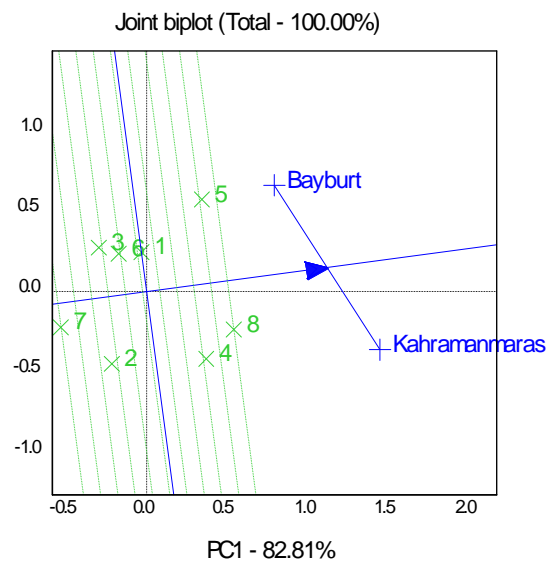
from the center of Kahramanmaras in the comparison biplot graph show that the genotype is less suitable for the province.



**Figure 8.** GGE Comparison biplot graph shows the ranking of the genotypes as an ideal environment Kahramanmaras province (x: shows wild and cultivated genotype scores and +: shows environment scores) (1.Bolero, 2.Jof, 3.Karina, 4.Nihal, 5.Reyna, 6.ssp.sativum, 7.ssp.elatius, 8.Utrillo)

### Joint biplot results

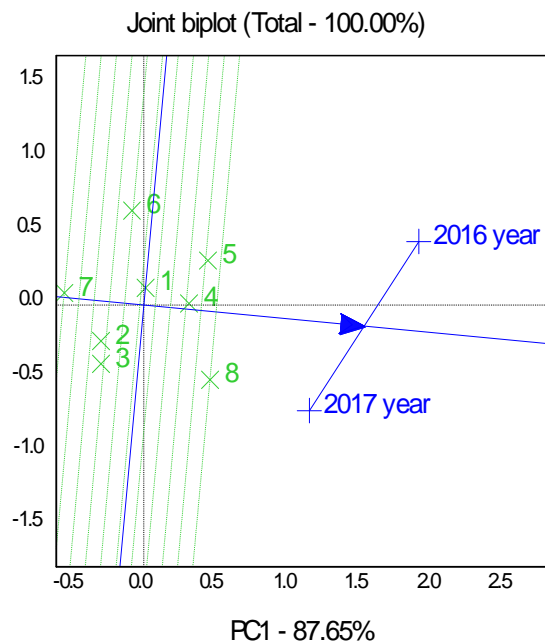
When the provinces were evaluated together according to the joint biplot graph, it was determined that Utrillo was a more stable variety on the other hand Reyna showed higher yield differences (Fig. 9).



**Figure 9.** GGE Joint biplot graph shows stability of genotypes according to evaluation of two provinces (x: shows wild and cultivated genotype scores and +: shows environment scores) (1.Bolero, 2.Jof, 3.Karina, 4.Nihal, 5.Reyna, 6.ssp.sativum, 7.ssp.elatius, 8.Utrillo)

Two genotype or two locations can be visually compared by connecting them with a linear line in a GGE biplot (Yan and Tinker, 2006). When the two provinces are evaluated together, the yield ranking of the varieties is as follows; Utrillo > Reyna > Nihal > Bolero > *Pisum sativum* subsp. *sativum* > Karina > Jof > *Pisum sativum* subsp. *elatius*. However, Reyna Jof and Nihal varieties were located further away from the stability line.

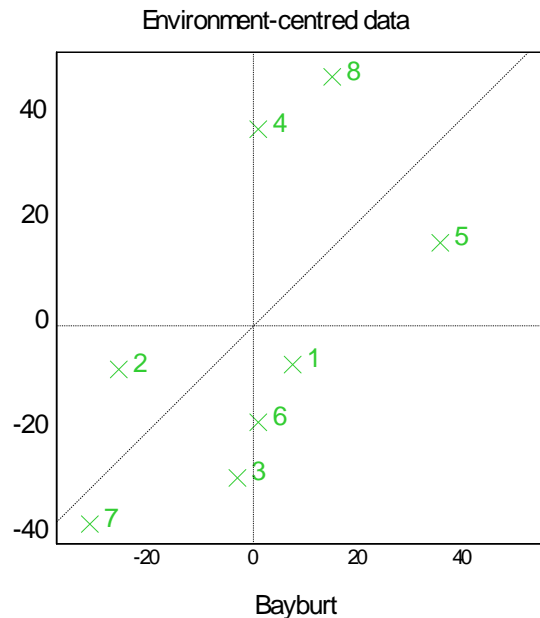
Considering the biplot graph based on an average of two years, genotypes showed as follows ranking; Utrillo > Reyna > Nihal > Bolero > *Pisum sativum* subsp. *sativum* > Karina > Jof > *Pisum sativum* subsp. *elatius* (Fig. 10). Subsp. *sativum* was the closest wild species to the cultivars, so yield levels were higher than some cultivars. Nihal, *Pisum sativum* subsp. *elatius* ve Bolero genotypes were determined to be highly stable, regardless of locations, according to two year averages. Repeated trials for many years reveal GEI in a more understandable way (Snoad and Arthur, 1974).



**Figure 10.** GGE Joint biplot graph shows stability of genotypes according to evaluation of two years (2016 and 2017) (x: shows wild and cultivated genotype scores and +: shows year scores) (1.Bolero, 2.Jof, 3.Karina, 4.Nihal, 5.Reyna, 6.ssp.sativum, 7.ssp.elatius, 8.Utrillo)

### Environment-centered data results

According to environment-centered data graphs, when two locations were taken into consideration, Utrillo, Jof, Nihal performed better in Kahramanmaras, while Reyna, Bolero, *Pisum sativum* L. subsp. *sativum*, Karina and *Pisum sativum* L. subsp. *elatius* had better performance in Bayburt province (Fig. 11). Subsp.*sativum* was the closest wild species to the cultivars, so yield levels were higher than some cultivars. To select superior genotypes and increase efficiency in selection, the biplot analysis is a good method (Dallo et al., 2019).



**Figure 11.** Environment-centered data graph shows that sorting genotypes by environment (x: shows wild and cultivated genotype scores) (The right side of the diagonal represents Bayburt province and the left side of the diagonal represents Kahramanmaras province) (1.Bolero, 2.Jof, 3.Karina, 4.Nihal, 5.Reyna, 6.ssp.sativum, 7.ssp.elatius, 8.Utrillo)

## Conclusion

Biplot analysis is an important technique in crop improvement and agricultural research. GGE biplot is an appropriate method for genotype selection and data analysis for agronomists, geneticists and breeders of the plant.

According to variance analysis main effect genotypes (G) explained 24.42%, main effect locations 18.78% (L) and main effect year 1.12% (Y). On the other hand, year×location interaction explained 17.87% (YL) of total variation and it is followed by other interactions 7.04% (GY), 4.91% (GY), 2.71% (GLY) and respectively.

According to GGE biplot analysis results for the seed yield first principal component explained 82.81% of the total variation and second principal component explained 17.19% of the total variation.

In Bayburt province Reyna cultivar was highest yielding and most stable genotype, in Kahramanmaras province Utrillo cv. highest yielding and most stable genotype. When evaluated together for two years, ranking of the wild and cultivated pea genotypes such as Utrillo > Reyna > Nihal > Bolero > *Pisum sativum* subsp. *sativum* > Carina > Jof > subsp. *elatius*. Considering the two-year results obtained from Bayburt and Kahramanmaras, ranking of the genotypes such as Utrillo > Reyna > Nihal > Bolero > *Pisum sativum* subsp. *sativum* > Carina > Jof > *Pisum sativum* subsp. *elatius*.

According to all these results, it would be more appropriate to use Utrillo variety. On the other hand, wild genotype *Pisum sativum* subsp. *sativum* has higher seed yield from some standard varieties (Karina and Jof) and as an important result it can be used to provide gene in breeding studies.

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