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Assessment of the reactions of pure lines selected from Turkish bread wheat landraces against bunt disease (*Tilletia foetida*) with the GGE-biplot method

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Abstract

The present research was conducted to determine the reactions of 200 pure lines selected from bread wheat landraces collected from 18 provinces and seven regions of Turkey against bunt disease (*Tilletia foetida*) under field conditions for 3 years. Bunt disease reactions of pure lines were assessed based on the infected spike/total spike ratio. For visually assessed materials, the GGE-biplot method, where G = genotype effect and GE = genotype-by-environment effect, was used to group the reactions against bunt disease. Fifty-nine pure lines showed high resistance (with infection rates ranging from 0.1 to 10%); 24 in the moderate resistance (with infection rates ranging from 10.1 to 25%); 75 in the moderate susceptibility (with infection rates ranging from 25.1 to 45%); 38 in the susceptibility (with infection rates ranging from 45.1 to 70%) and finally four in the highly susceptibility (with infection rates of >70.1%). PC1 and PC2 of the GGE-biplot graph created over the years explained 76.49% of the total variation. The GGE-biplot graph provided efficient identification of resistant genotypes. The lowest PC1 values and PC2 values close to 0.0 explained the resistance of pure line to bunt disease best. The resistance of pure lines to bunt disease over the biplot decreased from the first section through the last section. Based on the results of present study, 19 pure lines (located within the first circle of the biplot graph) were selected for resistance breeding programmes against the diseases.

Keywords: bunt (*Tilletia foetida*), GGE-biplot, landraces, pure line, Turkey

Introduction

Bread wheat landraces grown in Turkey exhibit great variation. Gen-Banks were established to preserve this diversity and several wheat cultivars have been collected and preserved for years (Akcura *et al*., 2016).

Mamluk *et al*. (1997) and Mamluk and Nachit (1994) assessed a series of genotypes composed of Turkey-originated local wheat cultivars through cluster and PCA analyses to find out new resistance sources against bunt disease (*Tilletia foetida* and *Tilletia caries*) in durum wheat and identified 26 new resistance sources against bunt disease. In another study investigating worldwide distributions of resistance sources against bunt disease based on geographical regions, Turkey-originated local wheat cultivars were found to have significant variation with regard to resistance to common and dwarf bunt diseases (Bonman *et al*., 2006).

Biplot method originated by Gabriel (1971), and uses were subsequently expanded by Kempton (1984) and Zobel *et al*. (1988). The extensive usefulness of GGE biplot, where G = genotype effect and GE = genotype-by-environment effect, has been clarified (Yan *et al*., 2000). The GGE biplot is a versatile tool for in plant breeding and quantitative genetic. Additionally, GGE biplot helps analyse different types of

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two-way data such as genotype-by-trait, genotype-by-marker and diallel cross (Yan and Hunt, 2001).

Recently, the GGE-biplot methodology has been used to determine the stability of disease resistance through multi-location trials, to characterize and identify stability of germplasm, breeding lines and cultivars resistant to diseases such as net blotch (*Pyrenophora teres* Drechs) in barley (Yan and Falk, 2002), spot blotch disease (*Cochliobolus sativus*) in wheat (Joshi *et al*., 2007), fusarium head blight (*Fusarium graminearum*) and powdery mildew [*Blumeria graminis* f. sp. tritici (DC.)] in wheat (Kadariya *et al*., 2008; Lillemo *et al*., 2010), ascochyta blight (*Ascochyta fabae*) in faba bean (Rubiales *et al*., 2012), ascochyta blight [*Ascochyta rabei* (Pass.) Labr.] in chickpea (Pande *et al*., 2013), fusarium wilt (*Fusarium udum*) in pigeonpea (Sharma *et al*., 2016).

The present study was conducted with 200 pure lines selected from wheat landraces collected from 18 provinces of seven geographical regions of Turkey to identify their resistance levels to bunt disease (*T. foetida*) through multi-year evaluations (2012–2014 growing seasons) using the GGE-biplot methodology.

Materials and methods

A two hundred pure-line selected from Turkish wheat landraces which stored Turkish National Gen-Bank used as experimental material in this research. While selecting research materials, care was taken to include the provinces with the greatest diversity in wheat landraces and to include material from every province in which wheat landraces were grown (Akcura, 2006). Information about the origins of pure lines and sampling locations were provided in Fig. 1; National Gen-Bank records, provincial information and selection numbers were provided in Table 1.

The inoculum source used in disease tests was collected in August 2012 from the experimental fields of Field Crops Central Research Institute located in Ankara/Golbasi/İkizce, and bunt disease reaction tests were carried out. Initially, the isolate was identified based on teliospore morphology in collected samples according to Goates (1996). The samples with the common bunt disease [*T. foetida* (Wall.)], which was the most common one, were reserved as inoculum source according to Akan *et al*. (2005). The present research was conducted under field conditions of İkizce location (longitude: 32°50′ E, latitude: 39°43′ N, altitude: 1225 m) in which bunt disease reaction tests of national/regional wheat breading programmes have been carried out for 10 years.

Infected wheat kernels collected before sowing were smashed in a mortar and sieved to separate the spores from plant material. For sowing, seeds of each genotype were placed in separate paper bags and inoculated with about 0.05% spores at sowing (Akan *et al*., 2005). Sowing was performed manually in the first half of November 2012, 2013 and 2014 growing seasons in two replicates over 1 m-long rows with 33 cm row spacing to 5–7 cm depth. After 10 pure lines of test materials were planted,

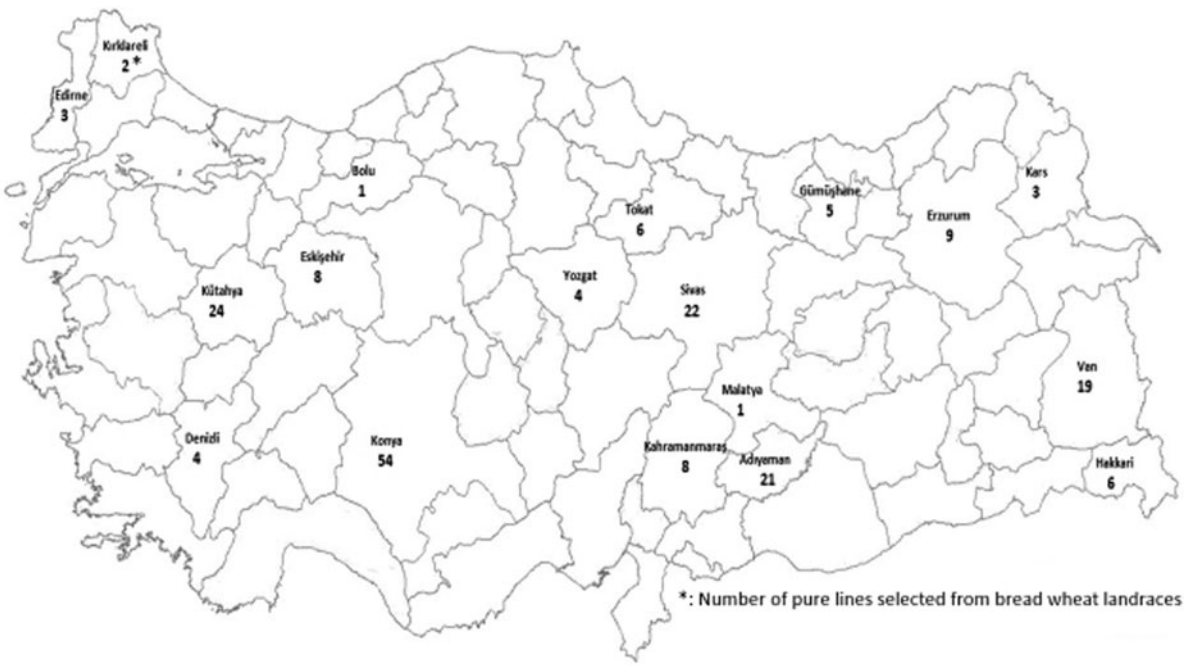

Fig. 1. Originated of pure lines selected from Turkish bread wheat landraces.

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Table 1. Turkish genbank codes, provinces, pure line number of research materials

GN[a]	Origin[b]	GN	Origin	GN	Origin	GN	Origin
1	Adiyaman TR 49034/2	51	Gumushane TR 48039/6	101	Konya D.hisar-30/10	151	Sivas TR 53304/6
2	Adiyaman TR 50457/6	52	Hakkari TR 47981/1	102	Konya D.hisar-32/20	152	Sivas TR 48062/6
3	Adiyaman TR 50476/1	53	Hakkari TR 46763/1	103	Konya D.hisar-33/13	153	Sivas TR 55002/3
4	Adiyaman TR 50455/1	54	Hakkari TR 47988/4	104	Konya D.hisar-34/11	154	Sivas TR 46890/3
5	Adiyaman TR 46810/6	55	Hakkari TR 47982/5	105	Konya Akşehir-35/14	155	Sivas TR 53318/1
6	Adiyaman TR 49029/3	56	Hakkari TR 47981/4	106	Konya Akşehir-36/18	156	Sivas TR 53359/3
7	Adiyaman TR 50465/6	57	Hakkari TR 47987/4	107	Konya Akşehir-37/22	157	Sivas TR 46892/2
8	Adiyaman TR 49034/3	58	K.Maras M-396/6	108	Konya Akşehir-38/15	158	Sivas TR 53292/5
9	Adiyaman TR 46822/3	59	K.Maras M-397/6	109	Konya Akşehir-39/23	159	Sivas TR 53342/3
10	Adiyaman TR 50464/5	60	K.Maras TR 32009/1	110	Konya Seydisehir-4/24	160	Sivas TR 55010/1
11	Adiyaman TR 50465/1	61	K.Maras M-397/4	111	Konya Akşehir-40/2	161	Sivas TR 55002/2
12	Adiyaman TR 49040/5	62	K.Maras M-388/4	112	Konya Akşehir-41/3	162	Sivas TR 53370/6
13	Adiyaman TR 49040/4	63	K.Maras M-398/3	113	Konya D.hisar-43/16	163	Sivas TR 53318/5
14	Adiyaman TR 49040/6	64	K.Maras M-394/6	114	Konya D.hisar-44/20	164	Sivas TR 53365/4
15	Adiyaman TR 50465/4	65	K.Maras M-391/6	115	Konya D.hisar-44/19	165	Sivas TR 53313/5
16	Adiyaman TR 50476/4	66	Kars TR 48025/6	116	Konya D.hisar-45/24	166	Sivas TR 48067/6
17	Adiyaman TR 49029/5	67	Kars TR 46851/1	117	Konya D.hisar-46/20	167	Sivas TR 48062/1
18	Adiyaman TR 49029/6	68	Kars TR 45904/6	118	Konya Seydisehir-47/3	168	Sivas TR 53313/3
19	Adiyaman TR 46822/5	69	Kırklareli TR 38316/2	119	Konya Seydisehir-48/4	169	Sivas TR 53375/1
20	Adiyaman TR 49029/1	70	Kırklareli TR 33521/3	120	Konya Seydisehir-5/15	170	Sivas TR 53356/5
21	Adiyaman TR 50476/5	71	Konya TR 53342/4	121	Konya Derebucak-6/12	171	Sivas TR 53323/5
22	Bolu TR 36948/5	72	Konya TR 35409/2	122	Konya Seydisehir-7/16	172	Tokat TR 55001/5
23	Denizli TR 52859/7	73	Konya TR 63319/1	123	Konya Seydisehir-8/22	173	Tokat TR 55001/3
24	Denizli TR 52863/5	74	Konya TR 35409/4	124	Konya Seydisehir-9/23	174	Tokat TR 54989/1
25	Denizli TR 52865/3	75	Konya TR 35409/6	125	Kutahya TR 55140/5	175	Tokat TR 54989/3
26	Denizli TR 52865/2	76	Konya TR 63316/6	126	Kutahya TR 55138/6	176	Tokat TR 44431/5
27	Edirne TR 33419/2	77	Konya TR 38894/2	127	Kutahya TR 55148/3	177	Tokat TR 48371/2
28	Edirne TR 33257/3	78	Konya TR 52021/3	128	Kutahya TR 55149/6	178	Van TR 45410/4
29	Edirne TR 33419/5	79	Konya TR 38894/4	129	Kutahya TR 55125/6	179	Van TR 47966/7
30	Erzurum TR 32790/1	80	Konya TR 52021/5	130	Kutahya TR 55142/1	180	Van TR 45938/5
31	Erzurum TR 45370/5	81	Konya TR 52021/2	131	Kutahya TR 55174/3	181	Van TR 45398/6
32	Erzurum TR 45370/6	82	Konya S.şehir-1/7	132	Kutahya TR 55125/1	182	Van TR 45409/5
33	Erzurum TR 32893/1	83	Konya S.şehir-10/16	133	Kutahya TR 55146/7	183	Van TR 45410/5
34	Erzurum TR 45370/4	84	Konya Derebucak-11/6	134	Kutahya TR 55142/3	184	Van TR 45402/4
35	Erzurum TR 45370/6	85	Konya Derebucak-12/13	135	Kutahya TR 55144/3	185	Van TR 47966/3
36	Erzurum TR 32655/1	86	Konya Derebucak-13/24	136	Kutahya TR 55167/1	186	Van TR 47993/6
37	Erzurum TR 32780/3	87	Konya Derebucak-14/13	137	Kutahya TR 55148/4	187	Van TR 32275/5
38	Erzurum TR 32846/4	88	Konya Derebucak-15/7	138	Kutahya TR 55128/2	188	Van TR 48313/5
39	Eskisehir TR 55155/6	89	Konya Derbent-16/13	139	Kutahya TR 55127/1	189	Van TR 47993/2
40	Eskisehir TR 57999/6	90	Konya Derbent-17/19	140	Kutahya TR 55146/4	190	Van TR 47995/3
41	Eskisehir TR 57999/2	91	Konya Derbent-18/24	141	Kutahya TR 55212/2	191	Van TR 47966/5
42	Eskisehir TR 57999/5	92	Konya Derbent-19/3	142	Kutahya TR 55143/5	192	Van TR 45399/2
43	Eskisehir TR 55154/4	93	Konya Seydisehir-2/22	143	Kutahya TR 55174/5	193	Van TR 47995/5
44	Eskisehir TR 55155/2	94	Konya Doganhisar-22/13	144	Kutahya TR 55167/2	194	Van TR 45402/1
45	Eskisehir TR 55164/2	95	Konya Doganhisar-23/13	145	Kutahya TR 55141/2	195	Van TR 47995/4

Continued

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Table 1. (*Cont.*)

GN[a]	Origin[b]	GN	Origin	GN	Origin	GN	Origin
46	Eskisehir TR 57999/3	96	Konya Doganhisar-24/21	146	Kutahya TR 55144/5	196	Van TR 39676/4
47	Gumushane TR 14861/1	97	Konya Doganhisar-26/16	147	Kutahya TR 55166/6	197	Yozgat TR 53863/5
48	Gumushane TR 14861/4	98	Konya Doganhisar-28/1	148	Kutahya TR 55138/5	198	Yozgat TR 45308/4
49	Gumushane TR 14861/6	99	Konya Doganhisar-29/3	149	Malatya TR 31894/1	199	Yozgat TR 45303/3
50	Gumushane TR 46871/1	100	Konya Seydisehir-3/18	150	Sivas TR 53312/3	200	Yozgat TR 45306/5

[a]Codes used in biplot graph.
[b]Province/genbank codes/pure line selection number.

the bunt infested cultivar Little Club (LC) was planted in every 10th rows as a susceptible positive control. Around the experimental plots also, the susceptible cultivars Yakar-99 and LC were sown in four rows as described above. Fertilizer (chemical or organic) and irrigation were not performed in all three growing seasons.

A differential set (CB-DIFF Common Bunt) composed of 17 genotypes with including bunt-resistance genes [*Bt0* to *Bt15*; Heines VI (*Bt-0*), SEL 2092 (*Bt-1*), SEL 1102 (*Bt-2*), Ridit (*Bt-3*), Turkey 1558 (*Bt-4*), Hohenheimer (*Bt-5*), Rio (*Bt-6*), Sel 50077 (*Bt-7*), M78–9496 (*Bt-8*), M82-2098 (*Bt-9*), M82-2102 (*Bt-10*), P.I. 178383 (*Bt-8,9,10*), M82-2123 (*Bt-11*), P.I. 119333 (*Bt-12*), P.I. 181463 (*Bt-13*), Doubi (*Bt-14*), Carlton (*Bt-15*)] was used to identify the gene/genes controlling the resistance to disease race/races. The differential set was also sown in the field as the research material.

The experiments were performed in clay-loam soils with a pH of 7.7 under rainfed conditions. The climate in İkizce is semi-arid with cold winters, rainy springs, hot and dry summers. Since both the prevailing northerly winds and the common southerly winds were dry, Ankara/Golbasi/İkizce Basin usually had a relative humidity below 50% during the experimental seasons. The total precipitation was about 200–250 mm.

Statistical analyses

In each growing season, healthy and infected spikes were counted in each genotype of the tested pure line and the differential set between the end of July and the beginning of August when the spikes were matured. Then, percentage of disease incidence was calculated by using the following equation (Akan *et al.*, 2005; Dumalasova and Bartos, 2007, 2010; Dumalasova *et al.*, 2014).

$$\%\ \text{Disease incidence} = \frac{\text{No. of infected spikes}}{\text{Total no. of spikes}} \times 100.$$

By using resultant average percentages of 3 years, they were grouped as: immune (0.0% incidence), resistant (0.1–10.0% incidence), moderately resistant (10.1–25.0% incidence), moderately susceptible (25.1–45% incidence), susceptible (45.1–70.0% incidence) and highly susceptible (>70.1% incidence).

Before biplot analysis, per cent values of disease reactions of pure lines were subjected to arcsine transformation to normalize the percentile data. The GGE-biplot technique was used to create a genotype-focused GGE-biplot graph to assess the reactions of the pure lines against bunt disease statistically and to select resistant materials for national/regional disease resistance genetic sources (Yan and Falk, 2002; Yan, 2014). The statistical theory of GGE-biplot methodology was explained in detail previously (Yan, 2014).

The GGE model used to determine the resistance of pure line across years was:

$$Y_{ij} - \mu - \beta_j = \lambda_1\ \xi_{i1}\ \eta_{1j} + \lambda_2\ \xi_{i2}\ \eta_{2j} + \varepsilon ij,$$

where Y_{ij} = the expected value for pure line i in year j; μ = the grand mean of all pure line–year combinations; β_j = the main effect of year j; λ_1 and λ_2 are the singular values of first and second largest principal components, PC1 and PC2, respectively; ξ_{i1} and ξ_{i2} are the eigenvectors of pure line i for PC1 and PC2, respectively; η_{1j} and η_{2j} are the eigenvectors of year j for PC1 and PC2, respectively, and ε_{ij} = the residue for each pure line–year combination not explained by PC1 and PC2.

The biplot was constructed by plotting the first two principal components (PC1 and PC2) derived from singular value decomposition of the year-centred data (Yan and Falk, 2002; Yan, 2014).

In order to assess the resistance of genotypes, the average environment coordinate (AEC) was plotted by taking the mean of PC1 and PC2 scores for years. A performance line passing through the origin of the biplot was used to determine the mean performance of the genotype. The circles created as taking the AEC axis as the focus improved the efficiency of biplot graph in selecting the ideal pure lines. There were six sections in the graph composed of nested circles and these sections were associated with reaction groups. Based on annual performance of pure lines and variations in bunt disease reactions, the location of pure lines on the graph either moved close to or away from the AEC axis. Furthermore, among genotypes with close disease reaction

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averages in three growing seasons, the location of the ones with high or low infection rates in any one of the growing seasons moved away from the centre of the graph. While highly resistant ones were in the first section, highly susceptible ones were located in the sixth section.

Results

Bunt disease was developed in the tested genotypes throughout the growing seasons of 2012–2013, 2013–2014 and 2014–2015. In all three growing seasons, 90–100% of bunt infections were observed in the susceptible control cultivars of LC and Yakar-99. Such an outcome indicated the success of inoculation and ruled out that a genotype was falsely classified as resistant due to the lack of viable and infective inoculum.

Among the resistance genes in differential set, the inoculum of disease source was virulent/effective on *Bt0*, *Bt2*, *Bt3*, *Bt4*, *Bt6* and *Bt7* and avirulent/ineffective on *Bt-1*, *Bt-5*, *Bt-8*, *Bt-9*, *Bt-10*, *Bt-8,9,10*, *Bt-11*, *Bt-12*, *Bt-13*,

Table 2. Provincial and regional grouping of pure lines based on their reactions against bunt disease

Province	Number of pure lines					
	Second group	Third group	Fourth group	Fifth group	Sixth group	
	Resistance	Moderately resistant	Moderately susceptible	Susceptible	Highly susceptible	
	0.1–10.0%	10.1–25.0%	25.1–45%	45.1–70.0%	>70.1%	Total
Adiyaman	7	3	1	8	2	21
Bolu	0	0	0	1	0	1
Denizli	2	0	1	0	1	4
Edirne	0	0	1	2	0	3
Erzurum	1	1	4	3	0	9
Eskisehir	4	2	2	0	0	8
Gumushane	1	0	3	1	0	5
Hakkari	0	1	2	3	0	6
Kahramanmaraş	0	1	4	2	1	8
Kars	0	1	1	1	0	3
Kirklareli	1	0	0	1	0	2
Konya	17	8	21	8	0	54
Kutahya	15	0	8	1	0	24
Malatya	1	0	0	0	0	1
Sivas	3	2	13	4	0	22
Tokat	0	1	4	1	0	6
Van	7	3	7	2	0	19
Yozgat	0	1	3	0	0	4
Total	59	24	75	38	4	200
%	30	12	37	19	2	100
Region						
Marmara (Trachea)	1	0	1	3	0	5
Aegean	17	0	7	3	1	28
Mediterranean	0	1	2	4	1	8
Central Anatolia	24	13	33	18	0	88
Southeast Anatolia	7	3	1	8	2	21
Eastern Anatolia	9	6	10	13	0	38
Black Sea	1	1	4	6	0	12
Total	59	24	75	38	4	200
%	30	12	37	19	2	100

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Bt-14, *Bt-15*, provincial and regional grouping of the pure lines based on their reactions against bunt disease provided in Table 2.

Significant differences were observed among the 200 pure lines. The disease incidences of pure lines against the bunt disease ranged from 0.0 to 98.3% in the first growing year, from 0.0 to 94.9% in the second year and from 0.0 to 96.2% in the third growing year.

When 3-year research results were assessed together, it was observed that none of the pure lines was immune; 59 pure lines were resistant; 24 pure lines were moderately resistant; 75 pure lines were moderately susceptible; 38 pure lines were susceptible and four pure lines were highly susceptible.

Biplot graph explained 76.49% of the total variation. The GGE-biplot method has recently been used in disease assessment of different plants (Yan, 2014; Sharma *et al.*, 2016) and was used for the first time in the assessment of bunt disease in wheat. Low PC1 values (negative values) and PC2 values close to 0.0 in biplot explained the resistance of genotypes to bunt disease in the best fashion. The circles created taking the AEC axis as the focus improved the efficiency of biplot graph in selecting the ideal genotype. There were six sections in the graph composed of nested circles and these sections were associated with reaction groups. Resistance of the pure lines decreased from the first section through the last section. While the most resistant genotypes were located within the inner section indicated by the first circle (with disease infection rates of between 1.8 and 5.4%), the most susceptible genotypes (with an infection rate of ≥70.1%) were located in the outer circle. The disease resistant group (with infection rates of between 0.1 and 10%; composed of 59 genotypes) was located within the second circle.

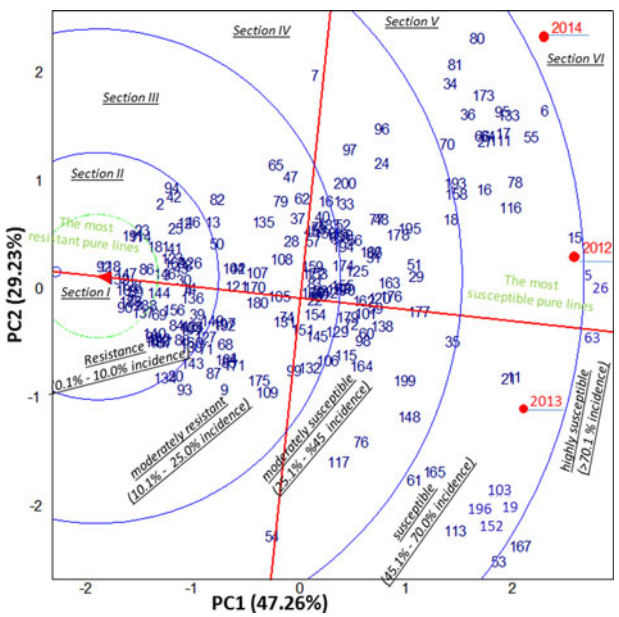

Fig. 2. Genotype, genotype–environment (GGE)-biplot graph created based on disease infection rates of the pure lines selected from Turkish bread wheat landraces.

Discussion

In this study, bunt disease infection rates in susceptible control cultivars (% infected spikes) were close to 100%. In tested pure lines, the greatest infection rate observed was 98.3% in the first year, 94.9% in the second year and 96.2% in the third year. Current findings obtained without chemicals and fertilizers applications and are therefore, unbiased by these factors. The infection rate was relatively lower in the second year. Compared with long-term averages of the Ankara–İkizce location, winter season of the second year was warmer and wetter. Therefore, plants grew faster after a certain period with higher seasonal temperatures. Rapid growth allowed plants to abstain from the systemic disease to some extent. Recently, GGE biplot has been used to characterize and determine stability of germplasm, breeding lines and cultivars resistance to diseases

Table 3. Bunt disease reactions (%) of the most resistant pure lines placed in the first section of GGE biplot

No	Pure lines	Growing seasons			Mean
		2012	2013	2014	
23	Denizli TR 52859/7	7.0	0.0	7.4	4.8
73	Konya TR 63319/1	8.1	3.1	0.0	3.7
86	Konya Derebucak-13/24	2.4	2.9	6.3	3.9
89	Konya Derbent-16/13	2.7	3.6	2.3	2.9
90	Konya Derbent-17/19	3.7	3.7	0.0	2.5
92	Konya Derbent-19/3	5.3	0.0	0.0	1.8
114	Konya Doganhisar-44/20	7.1	0.0	5.4	4.2
118	Konya Seydisehir-47/3	5.8	0.0	0.0	1.9
128	Kutahya TR 55149/6	1.6	2.7	2.2	2.2
137	Kutahya TR 55148/4	7.2	4.6	0.0	4.0
139	Kutahya TR 55127/1	6.0	0.9	0.0	2.3
144	Kutahya TR 55167/2	7.1	4.3	2.9	4.8
146	Kutahya TR 55144/5	5.8	3.6	6.3	5.2
147	Kutahya TR 55166/6	0.0	2.1	3.8	2.0
181	Van TR 45398/6	7.7	1.2	7.4	5.4
186	Van TR 47993/6	5.4	3.1	0.0	2.8
188	Van TR 48313/5	10.0	3.7	0.0	4.6
189	Van TR 47993/2	6.7	1.9	0.0	2.9
191	Van TR 47966/5	3.4	0.0	6.3	3.2
	Mean	5.4	2.2	2.6	3.4

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Table 4. Bunt disease reactions (%) of the pure lines placed in the second section of GGE biplot

No	Pure lines	Growing seasons			Mean
		2012	2013	2014	
2	Adiyaman TR 50457/6	5.8	6.7	10.0	7.5
3	Adiyaman TR 50476/1	2.8	5.1	10.0	6.0
4	Adiyaman TR 50455/1	6.1	7.8	10.0	8.0
8	Adiyaman TR 49034/3	9.2	4.9	11.8	8.6
12	Adiyaman TR 49040/5	5.7	10.3	10.3	8.9
13	Adiyaman TR 49040/4	4.4	4.2	20.6	9.7
14	Adiyaman TR 49040/6	5.9	7.4	10.0	7.8
20	Adiyaman TR 49029/1	5.9	15.8	0.0	7.2
25	Denizli TR 52865/3	7.4	5.1	10.0	7.8
30	Erzurum TR 32790/1	6.1	6.1	9.8	7.3
39	Eskisehir TR 55155/6	5.4	10.5	9.1	8.3
41	Eskisehir TR 57999/2	2.4	3.6	15.1	7.0
42	Eskisehir TR 57999/5	7.4	9.4	10.0	8.9
43	Eskisehir TR 55154/4	6.7	6.6	10.0	7.7
46	Eskisehir TR 57999/3	0.0	3.8	20.6	8.1
50	Gumushane TR 46871/1	5.2	6.2	16.0	9.1
69	Kirklareli TR 38316/2	3.2	7.6	3.2	4.7
84	Konya Derebucak-11/6	5.9	9.8	3.4	6.4
88	Konya Derebucak-15/7	6.4	10.0	5.8	7.0
91	Konya Derbent-18/24	6.7	8.3	0.0	5.0
94	Konya Doganhisar-22/13	10.0	4.2	10.0	9.1
104	Konya Doganhisar-34/11	6.7	11.3	4.3	7.4
122	Konya Seydisehir-7/16	6.5	8.8	0.0	5.1
123	Konya Seydisehir-8/22	1.4	7.1	10.0	6.2
124	Konya Seydisehir-9/23	3.2	12.2	6.8	7.4
126	Kutahya TR 55138/6	11.1	4.1	10.0	8.4
127	Kutahya TR 55148/3	7.4	10.0	9.7	9.0
130	Kutahya TR 55142/1	6.9	10.4	5.6	7.7
134	Kutahya TR 55142/3	6.4	10.8	0.0	5.7
136	Kutahya TR 55167/1	6.1	8.3	8.3	7.6
140	Kutahya TR 55146/4	6.6	7.7	0.0	4.8
141	Kutahya TR 55212/2	5.3	9.0	0.0	4.7
142	Kutahya TR 55143/5	7.0	8.6	0.0	5.2
143	Kutahya TR 55174/5	7.7	15.5	1.4	8.2
149	Malatya TR 31894/1	9.8	10.0	9.1	9.7
156	Sivas TR 53359/3	3.6	8.1	5.1	5.6
160	Sivas TR 55010/1	5.3	10.0	7.2	7.5
169	Sivas TR 53375/1	6.9	3.4	8.8	6.4
185	Van TR 47966/3	7.9	10.9	4.2	7.6
187	Van TR 32275/5	6.7	9.3	0.0	5.3
	Mean	6.03	8.22	7.41	7.24

such as anthracnose in water yam (Egesi *et al.*, 2009), chocolate spot disease in faba bean (Villegas *et al.*, 2009), white rust in brassica (Sandhu *et al.*, 2015), dry root rot and stunt disease in chickpea (Kumar *et al.*, 2017), yellow mosaic disease in mungbean (Parihar *et al.*, 2017), grey leaf spot in maize (Acorsi *et al.*, 2017). When the first section of the

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biplot was assessed separately from the entire graph, it was observed that 19 pure lines were placed in this section (Fig. 2). The average values for disease reactions of these genotypes for three growing seasons were provided in Table 3. These genotypes had quite low infection rates (ranging between 1.8 and 5.4%) in all 3 years. Year-based average disease epidemy was identified as 3.4%.

As the average of 3 years, the lowest bunt infection rates were observed in line numbers 92 (Konya Derbent-18/24), 118 (Konya Seydisehir-47/3), 147 (Kutahya TR 55166/6), 128 (Kutahya TR 55149/6) and 139 (Kutahya TR 55127/1) numbered pure lines (respectively with 1.8, 1.9, 2.0, 2.2 and 2.3%) (Table 3). These pure lines were placed right into the centre of the first section as the most resistant genotypes (Fig. 2). The position of the pure lines in the biplot graph varied based on disease reaction rates of growing seasons. For the first section, such a case indicated the best by the pure lines of 23 (Denizli TR 52859/7), 181 (Van TR 45398/6) and 188 (Van TR 48313/5). The genotypes located over the circle line of the first section (23, 181 and 188-numbered pure lines) had higher infection rates than the others in the most resistant group.

There were 40 pure lines in the second section of the biplot graph. Year-based disease infection rates of these genotypes were provided in Table 4. The average infection rate was 7.2% with the lowest value of 5.3% and the greatest value of 9.7%. The pure lines in this section were resistant to bunt disease. However, they were separated from the first group (the most resistant group) located in the first circle. The second group can be considered as the ideal genetic source to create a variation in disease-resistant sources in wheat breeding programmes. Thus, in bunt disease breeding studies, the genotypes with 10% or less infection rates were assessed as resistant in several studies (Akan *et al.*, 2005; Dumalasova and Bartos, 2007, 2010; Dumalasova *et al.*, 2014).

Among the investigated genotypes, 75 pure lines (with infection rates of between 25.1 and 45%) were categorized as moderately susceptible. All of these genotypes were placed within the fourth section of the biplot graph (Fig. 2). The most significant issue in breeding programmes for resistance to diseases in wheat was the identification of resistance sources based on the groups created by the breeders. Therefore, infection rates may vary in the assessment of moderately susceptible group of fungal disease resistance researches. Thus, in some studies, the genotypes with disease infection rates between 10.1 and 20% were accepted as moderately resistant and the ones with infection rates between 20 and 40% were accepted as susceptible (Dumalasova and Bartos, 2007, 2010; Dumalasova *et al.*, 2014; Sharma *et al.*, 2016).

All of the susceptible genotypes were placed in the fifth section of biplot graph (Fig. 2). Highly susceptible ones were placed in the sixth section. Based on this assessment, the pure line 92 (Konya Derbent-19/3) with the lowest average disease reaction was placed on far-left over AEC and the pure line 63 (Kahramanmaras M-398/3) with the greatest disease reaction was placed on far-right.

According to 3-year averages, among the pure lines, 59 lines were identified as resistant to bunt disease (0.1–10%). Considering the provinces from where the research materials were collected, it was observed that there were resistant genotypes among the pure lines of 11 provinces (Adiyaman, Denizli, Erzurum, Eskisehir, Gumushane, Kirklareli, Konya, Kutahya, Malatya, Sivas and Van), while no resistant genotypes among the pure lines of seven provinces (Bolu, Edirne, Hakkari, Kahramanmaras, Kars, Tokat and Yozgat). In a study assessing the resistance of USDA – ARS national genetic materials to different bunt diseases (*Tilletia tritici*, *Tilletia laevis* and *Tilletia controversa*), resistance sources included the materials collected from Turkey (Bonman *et al.*, 2006). That study was quite similar to the presented study with regard to identification of resistant materials in bread wheat materials. *Tilletia foetida* was the most common bunt disease in Turkey (Iren *et al.*, 1982). With this study, pure lines selected from Turkish bread wheat landraces, of which the reactions against bunt disease have not been tested previously, were assessed.

The study results indicated that GGE-biplot method could efficiently be used to group bunt disease-resistant genotypes. Based on the present results, among the genotypes, 19 pure lines identified as the most resistant to bunt disease were transferred to resistance breeding programmes.

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