

Evaluation of wheat genetic resources of Azerbaijan on normal and saline fields

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Abstract: Genetic variation is a key to successful crop improvement. This study was conducted to evaluate a set of 48 accessions and two controls of hexaploid winter wheat from the gene bank of the Genetic Resources Institute (Azerbaijan) to examine genotypic variation for 11 morphophysiological traits under saline and nonsaline conditions. These accessions belonged to five different botanical groups collected from eight districts in Azerbaijan. Replicated field tests were conducted at Absheron (nonsaline) and Ujar (saline) locations for 3 years. Genotype and genotype \times environment biplot analysis was used to determine associations among the accessions and identify superior genotypes for individual traits as well as multiple traits. There were arrays of genotypic variation for plant height (PHT), peduncle length (PDL), PDL:PHT ratio, number of tillers per plant, spike length, spikelet and kernel number per spike, grain weight per spike, grain weight per plant, 1000-kernel weight, and SPAD value. Superior genotypes were identified for both saline and nonsaline conditions, which were distributed among different botanical varieties and places of collection. Based on multivariate analysis using 10 traits, the five accessions superior under both saline and nonsaline conditions were RFS08K-8 (*Graecum*), RFS08K-19 (*Milturum*), RFS08K-189 (*Erythroleucon*), RFS08K-195 (*Erythroleucon*), and RFS08K-199 (*Erythroleucon*). These accessions could be valuable as parents for wheat breeding to develop superior varieties for saline and nonsaline conditions. This largely unexplored collection of wheat accessions in Azerbaijan should provide significant diversity for the improvement of national and international germplasm.

Key words: Genetic resources, biplot, salinity, *Triticum aestivum* L., wheat

1. Introduction

There are a number of abiotic and biotic stresses negatively affecting wheat productivity in Azerbaijan and its neighboring countries in Central Asia and the Caucasus. Among biotic stresses, soil salinity is considered as an important constraint. The problem of soil salinity in Central Asia has historical perspective related to soil formation and climate (Pankova and Konyushkova, 2013). However, in modern-day agriculture, soil salinity is becoming a major constraint to crop production in the Central Asian region (Qadir et al., 2009), including Azerbaijan (<http://en.trend.az/news/society/2145515.html>). It is particularly a problem under irrigated agriculture with poor drainage conditions. Since cultivation of winter wheat on saline soils in Central Asia and the Caucasus is done by leaching to reduce salt concentration in the root zone, the problem of soil salinity is expected to be aggravated under dwindling water availability for agriculture in the region including Azerbaijan (Israfilov and Israfilov, 2010; Sutton et al., 2013).

Soil salinity could negatively affect growth and development of plants. It can adversely affect vegetative

growth and grain yields (Francois et al., 1986). In wheat, soil salinity affects germination and seedling growth (Rahman et al., 2008; Akbarimoghaddam et al., 2011), plant height and dry matter (Mirzaei et al., 2012), and grain yield and kernel weight (Turki et al., 2012). These previous reports suggest that salinity can affect all growth stages in wheat. In order to develop wheat varieties for cultivation on saline soils, genetic variations must occur in traits related to tolerance. In a study including 55 wheat accessions, Turki et al. (2012) reported genotypic variations for grain yield, protein, and 1000-kernel weight under salt treatment of leaves. Kushiev et al. (2005) reported differences among winter varieties in relative reductions in grain and spike characteristics under saline conditions. Information is scarce on identifying genotypic variations for morphophysiological traits under natural saline field conditions.

In order to develop wheat varieties tolerant to soil salinity, there is a need to identify sources of tolerance. Most of the presently cultivated winter wheat varieties in Azerbaijan and its neighboring countries are either unsuitable for saline conditions or produce lower yields.

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This study was conducted to evaluate a set of hexaploid wheat accessions from the gene bank of Azerbaijan for morphophysiological traits under saline and nonsaline conditions and to identify superior genotypes based on individual and multiple traits.

2. Materials and methods

2.1. Field experiments

A set of 48 accessions of wheat was selected from the gene bank of the Genetic Resources Institute of the Azerbaijan National Academy of Sciences and two landraces were used as the control (Aran1 and Aran2) (Table 1). These accessions were chosen to include genotypic diversity in terms of botanical variety and geographical distribution as reflected through place of collection in Azerbaijan (Table 1; Figure 1). Prior to selection for this experiment,

the accessions had been planted for 3 years for seed multiplication, examination of purity, and identification of botanical variety.

Field experiments were conducted at Absheron (40°29'54"N, 49°22'16"E; 30 m.a.s.l.) and Ujar (40°31'06"N, 47°39'15"E; 17 a.s.l.) in the 2010/2011 (2011), 2011/2012 (2012), and 2012/2013 (2013) winter wheat growing seasons. Average rainfall in Absheron is around 200 mm compared to 295 mm for Ujar. Average temperature at Absheron is about 4 °C warmer than Ujar. Soil type at Absheron is medium loam and nonsaline with low fertility compared to clay loam, medium salinity (6 dS/m), and high fertility at Ujar. The road distance between the two locations is 230 km.

The experiment at each location was designed as an alpha lattice in two replications. Each plot consisted of

Table 1. Name and other information about the wheat genotypes used in the study.

Entry number	Accession number	Botanical variety	Place of collection	Altitude (m a.s.l.)†	Entry number	Accession number	Botanical variety	Place of collection	Altitude (m a.s.l.)†
1	RFS08K-8 ^a	<i>Graecum</i>	Shamakhi	169 ⁺	26	RFS09K-228 ^a	<i>Erythrospermum</i>	Shamaxi	168 [‡]
2	RFS08K-9 ^a	<i>Graecum</i>	Shamakhi	168 ⁺	27	RFS09K-231 ^a	<i>Erythrospermum</i>	Shamaxi	216 [‡]
3	RFS08K-10 ^a	<i>Graecum</i>	Shamakhi	53 ⁺	28	RFS09K-230 ^a	<i>Erythrospermum</i>	Shamaxi	218 [‡]
4	RFS08K-37 ^a	<i>Graecum</i>	Ter-ter	5 ⁺	29	RFS09K-238 ^a	<i>Erythrospermum</i>	Shamaxi	248 [‡]
5	RFS08K-16 ^a	<i>Graecum</i>	Sheki	61 ⁺	30	RFS09K-242 ^a	<i>Erythrospermum</i>	Zakatala	112 [‡]
6	RFS08K-18 ^a	<i>Graecum</i>	Oguz	136 ⁺	31	RFS09K-244 ^a	<i>Erythrospermum</i>	Balakan	102 [‡]
7	RFS08K-17 ^a	<i>Graecum</i>	Gabala	180 [‡]	32	RFS09K-219 ^b	<i>Lutescens</i>	Shamaxi	165 [‡]
8	RFS08K-20 ^a	<i>Graecum</i>	Gabala	158 [‡]	33	RFS09K-225 ^b	<i>Lutescens</i>	Sheki	88 [‡]
9	RFS08K-34 ^b	<i>Milturum</i>	Shamakhi	183 ⁺	34	RFS09K-220 ^b	<i>Lutescens</i>	Shamaxi	168 [‡]
10	RFS08K-36 ^b	<i>Milturum</i>	Yevlakh	5 ⁺	35	RFS09K-215 ^b	<i>Lutescens</i>	Shamaxi	216 [‡]
11	RFS08K-19 ^b	<i>Milturum</i>	Ter-ter	5 ⁺	36	RFS09K-235 ^b	<i>Lutescens</i>	Shamaxi	216 [‡]
12	RFS08K-38 ^b	<i>Milturum</i>	Ter-ter	105 ⁺	37	RFS09K-238 ^b	<i>Lutescens</i>	Shamaxi	248 [‡]
13	RFS08K-40 ^b	<i>Milturum</i>	Sheki	61 ⁺	38	RFS09K-243 ^b	<i>Lutescens</i>	Zakatala	112 [‡]
14	RFS08K-41 ^b	<i>Milturum</i>	Sheki	61 ⁺	39	RFS09K-245 ^b	<i>Lutescens</i>	Qabala	174
15	RFS08K-42 ^b	<i>Milturum</i>	Oguz	155 ⁺	40	RFS09K-189 ^c	<i>Erythroleucon</i>	Ter-ter	108 ⁺
16	RFS09K-223 ^c	<i>Ferrugineum</i>	Sheki	88 [‡]	41	RFS09K-190 ^c	<i>Erythroleucon</i>	Ter-ter	108 ⁺
17	RFS09K-229 ^c	<i>Ferrugineum</i>	Shamakhi	168 [‡]	42	RFS09K-187 ^c	<i>Erythroleucon</i>	Barda	45 ⁺
18	RFS09K-232 ^c	<i>Ferrugineum</i>	Shamakhi	216 [‡]	43	RFS09K-191 ^c	<i>Erythroleucon</i>	Sheki	61 ⁺
19	RFS09K-233 ^c	<i>Ferrugineum</i>	Shamakhi	218 [‡]	44	RFS09K-195 ^c	<i>Erythroleucon</i>	Sheki	61 ⁺
20	RFS09K-239 ^c	<i>Ferrugineum</i>	Shamakhi	248 [‡]	45	RFS09K-196 ^c	<i>Erythroleucon</i>	Sheki	66 ⁺
21	RFS09K-235 ^c	<i>Ferrugineum</i>	Balakan	102 [‡]	46	RFS09K-197 ^c	<i>Erythroleucon</i>	Oguz	155 ⁺
22	RFS09K-234 ^c	<i>Ferrugineum</i>	Gabala	160 [‡]	47	RFS09K-198 ^c	<i>Erythroleucon</i>	Absheron	162 ⁺
23	RFS09K-221 ^a	<i>Erythrospermum</i>	Shamakhi	165 [‡]	48	RFS09K-199 ^c	<i>Erythroleucon</i>	Qabala	180 [‡]
24	RFS09K-222 ^a	<i>Erythrospermum</i>	Shamakhi	165 [‡]	49	Aran 1 (LC) [*]			
25	RFS09K-226 ^a	<i>Erythrospermum</i>	Shamakhi	168 [‡]	50	Aran 2 (LC) [*]			

†m a.s.l. = meters above sea level. ^aCollected by Rana Jafarova. ^bCollected by Fatma Sheykzamanova. ^cCollected by Svetlana Rzayeva.

^{*}Collected in 2006. [‡]Collected in 2008. ⁺ = local control.



Figure 1. Map of Azerbaijan showing locations from where the wheat accessions used in this study were collected.

a single row of 2 m long with each row planted with 50 seeds, thinned to 40 plants after germination. The row-to-row distance was 20 cm in each experiment. Planting was done in the second week of November in each year, which is considered the optimum seeding time for wheat in Azerbaijan. The trial management practices were consistent with good crop husbandry recommendations for the region.

All data were recorded on five randomly tagged plants in each plot and averaged. Days to heading was recorded when spikes on the main tiller were completely out of boot. Genotypic response to stripe rust and powdery mildew was recorded during the grain development stage. Plant height was measured from the soil level to the tip of the spike without considering awn. Peduncle length was measured from the upper most node to the base of the spike. The ratio of peduncle length to plant height (PDL:PHT) was determined. Number of spike-bearing tillers of each plant (TLN) was recorded. Spike length, number of spikelets per spike (SPKLTN), and kernels per spike (KPS) were measured on the main tillers. SPAD value was measured on flag leaves of the main tillers with the help of a self-calibrating Minolta chlorophyll meter (SPAD-502) according to the procedure outlined by Rosyara et al. (2010). SPAD is used to measure leaf chlorophyll content

(Balasubramanian et al., 1999), which was recorded in Minolta-defined SPAD values (Minolta Co., 1999). SPAD value was recorded during grain-filling stage only in 2013 at both locations. Grain weight was recorded on main tillers (GWPSPK) as well as on a per-plant basis (GWPLT). One thousand kernels were randomly counted from each plot seed bag and weighed to record TKW.

2.2. Statistical analysis

An analysis of variance was computed for each location in each year using GenStat (2013) software to determine the significance of genotypic differences for various traits measured. After testing the homogeneity of variance (Gomez and Gomez, 1984), a combined analysis of variance over two locations and 3 years was conducted for each trait.

Multivariate analysis was accomplished using genotype and genotype \times environment (GGE) biplot software (Yan and Kang, 2002) to determine superior genotypes for individual traits as well as for all traits combined. GGE biplot analysis has been widely used to identify superior genotypes for single and multiple traits (Yan et al., 2007; Roozeboom et al., 2008; Sharma et al., 2010). There is an option in the GGE biplot analysis that permits comparison among genotypes with a reference (ideal) genotype. Several concentric circles are generated using the ideal genotype

at the concentric center. The ideal genotype is used as a reference to rank the other genotypes based on their distance from the center. Similarly, an option of 'which won where' allows identification of superior genotypes for one or a set of traits. This option creates a polygon, which is divided into different sectors. The vertex genotype of the polygon in a sector is the most superior for the traits that fall within that sector.

3. Results

The wheat accessions used in the study represented diverse origins in terms of their botanical group, place of collection in Azerbaijan, and altitude (Table 1). The 48 experimental genotypes belonged to five botanical varieties, collected from eight districts in Azerbaijan. The altitude of the places of collection ranged from 5 to 248 m above sea level.

There was a significant effect of year on all traits except GWSPK (Table 2). The effect of location was significant for plant height, peduncle length, PDL:PHT ratio, spike length, KPS, GWPPLT, and TKW. Year \times location interaction was significant for plant height, peduncle length, PDL:PHT ratio, KPS, and GWPPLT. The 50 genotypes differed significantly for all traits. Genotype \times year interaction was significant for plant height and TLN. Genotype \times location and genotype \times year \times location interactions were nonsignificant for all traits.

There were arrays of variation for each trait at both locations as reflected through range of values (Table 3). There were no clear trends for a greater range of values for all traits between the two locations. In general, the range of values for individual traits was comparable between the

two locations. However, the overall mean values differed significantly between the two locations for plant height, spike length, KPS, GWPPLT, and SPAD value.

Plant height, peduncle length, PDL:PHT ratio, and TKW significantly differed across years at both locations (Table 3). Spikelets per spike and KPS differed significantly across years only at the Ujar location. Grain weight per plant differed significantly in 3 years only at the Absheron location.

Two or more of the 50 genotypes significantly differed for mean values of all traits except GWPPLT between two locations. The numbers of genotypes with significant differences between the two locations were 18, 19, and 23 for plant height, PDL:PHT ratio, and SPAD value, respectively. The corresponding numbers were fewer for peduncle length (2), TLN (3), spike length (6), SPKLTN (2), KPS (2), GWPPLT (4), and TKW (2).

Multivariate biplot analysis based on 10 traits identified four groups among the 50 genotypes at both locations but grouping was more discrete for Absheron than Ujar (Figure 2). Certain genotypes remained separated from each other at both locations, whereas a few other genotypes fell into different groups at the two locations. For example, genotypes #10 and #2 were together in a group and #15 and #47 were in another group at the opposite end of the linear map at both locations. On the other hand, genotype #4 switched positions to the two contrasting groups at the two locations.

Multivariate analysis was also used to identify the most superior genotype (Figure 3). The genotypes closer to the center of the concentric circle are considered more

Table 2. Analysis of variance for various traits recorded for 50 wheat accessions from the gene bank evaluated at two sites in 3 years, 2011–2013, Azerbaijan.

Source	df	Plant height	Peduncle length	Ped:Ht ratio†	Spike number per plant	Spike length	Spikelet number	Kernel per spike	Grain weight per spike	Grain weight per plant	1000-kernel weight	SPAD value†	
												df	Mean square
Year (Y)	2	77,060**	9189**	0.075**	6.44**	19.9**	150.6**	880**	0.2	20.3**	3218**		
Loc (L)	1	25,327**	65	0.338**	0.02	144.2**	3.2	1392**	1.1	9.4*	10	1	2793**
Y \times L	2	7836**	6227**	0.418**	0.27	24.7	18.6	711**	0.7	7.6*	11		
Rep (Y L)	6	383	619	0.031	0.98	11.9	7.4	53	0.2	1.4	16	2	74
Block/Rep/(Y L)	108	731	178	0.003	0.41	2.2	7.4	139	0.4	1.0	97	36	41
Genotype (G)	49	2808**	583**	0.003**	0.46**	7.5**	24.4**	441**	1.2**	3.0**	142**	49	26**
G \times Y	98	259**	45	0.002	0.33*	2.9	5.0	65	0.2	0.9	41		
G \times L	49	198	41	0.002	0.22	1.0	4.2	25	0.1	0.3	17	49	9
G \times Y \times L	98	84	26	0.001	0.17	0.9	2.4	14	0.1	0.3	15		
Error	186	156	42	0.002	0.23	2.3	5.2	53	0.2	0.7	40	62	8

*, ** Significant at $P = 0.05$ and $P = 0.01$, respectively.

†Peduncle length:Plant height ratio.

Table 3. Mean values for different traits recorded for 50 winter wheat genotypes evaluated at two locations in Azerbaijan, 2011–2013.

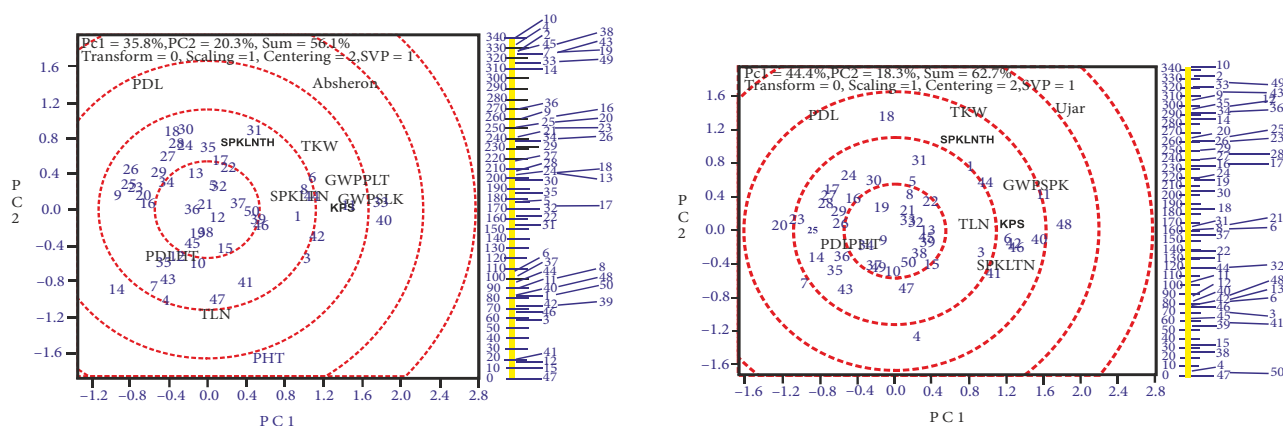
Trait	Mean across years		Mean range		Mean values at Absheron			Mean values at Ujar		
	Absheron	Ujar	Absheron	Ujar	2011	2012	2013	2011	2012	2013
Plant height (cm)	105b†	118a	79–139	79–156	92c‡	104b	119a	92 A§	120B	143A
Peduncle length (cm)	49a	50a	31–63	33–67	43b	53a	50a	43B	43B	63A
Peduncle:Plant height	0.47a	0.42b	0.39–0.51	0.38–0.46	47a	51a	42b	46A	36B	44aB
Tiller number per plant	3.1a	3.1a	2.5–3.8	2.3–3.7	3.0a	3.2a	3.2a	2.9A	3.2A	3.3A
Spike length (cm)	10.2a	9.3b	8.4–12.4	7.6–13.1	10.2a	10.3a	10.2a	10.0A	8.7A	9.0A
Spikelets per spike	19a	18a	15–22	15–27	19.0a	17.9a	18.9a	19.0A	17.1B	19.3A
Kernels per spike	39.7a	36.6b	25–61	26–51	40.0a	39.4a	39.5a	39.2A	32.0B	38.6A
Grain weight per spike (g)	1.7a	1.6a	1.1–2.7	1.0–2.5	1.6a	1.8a	1.7a	1.6A	1.5A	1.7A
Grain weight per plant	2.7a	2.5b	1.5–4.4	1.6–4.2	2.4b	3.3a	2.5b	2.4A	2.6A	2.4A
1000-kernel weight	39.1a	38.8a	29.1–48.9	28.3–47.2	36.1b	43.9a	37.3b	35.8C	43.2A	37.6B
SPAD value£	48.6a	41.2b	37.5–57.0	33.3– 48.4			48.6			41.2

† Means for the same trait at two sites followed by different letters differ significantly based on LSD_{0.05}.

‡ At Absheron the means for the same trait followed by different letters differ significantly based on LSD_{0.05}.

§ At Ujar the means for the same trait followed by different capital letters differ significantly based on LSD_{0.05}.

£ Data for SPAD value recorded in 2013 only.

**Figure 2.** Grouping of 50 genotypes at Absheron (top) and Ujar (bottom) based on 10 traits recorded over 3 years.

superior than those located further out. The most superior genotypes based on the 10 traits were #40, #48, #10, #44, #8, #6, #1, and #42 at Absheron and #11, #44, #1, #48, and #40 at Ujar.

Biplot analysis was used to identify the genotypes most superior for an individual trait or a set of traits (Figure 4). At the Absheron location #40 and #48 were the most superior genotypes for GWPPPLT, KPS, and SPKLTN. Genotypes #31, #18, and #14 were most superior for spike

length, peduncle length, and PDL:PHT ratio, respectively. Genotype #47 was most superior for plant height and TLN. At the Ujar location #48 and #11 were the most superior genotypes for the set of traits comprising GWPPSPK, GWPPPLT, KPS, TLN, and SPKLTN. Genotype #18 was most superior for TKW, spike length, and peduncle length. Genotypes #20 and #4 were most superior for PDL:PHT ratio and plant height.

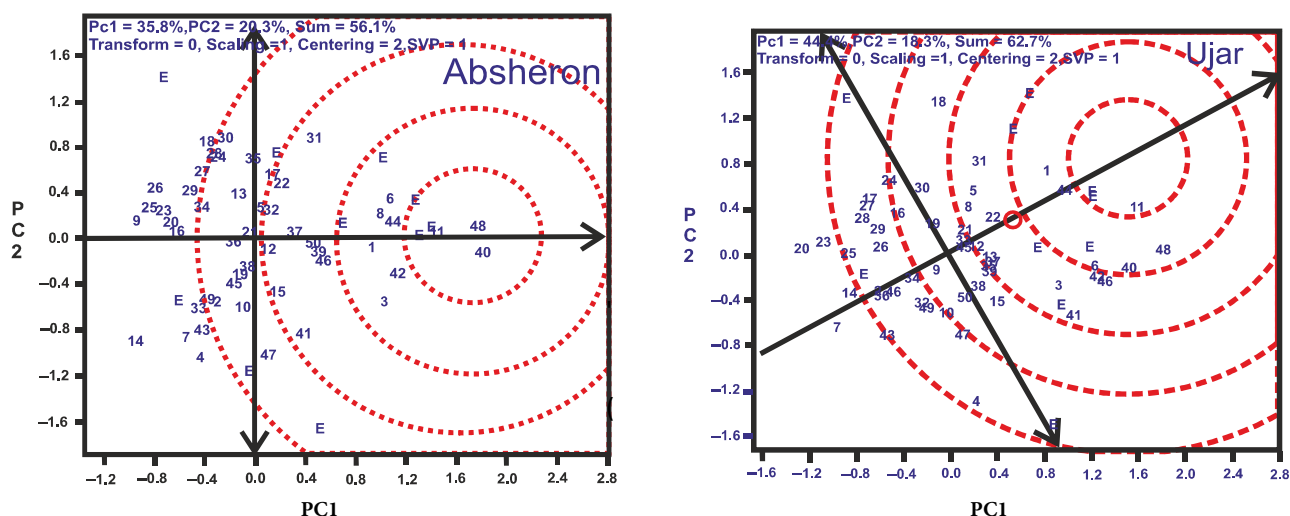


Figure 3. Superior genotypes (close to the center) at Absheron (top) and Ujar (bottom) based on 10 traits recorded over 3 years.

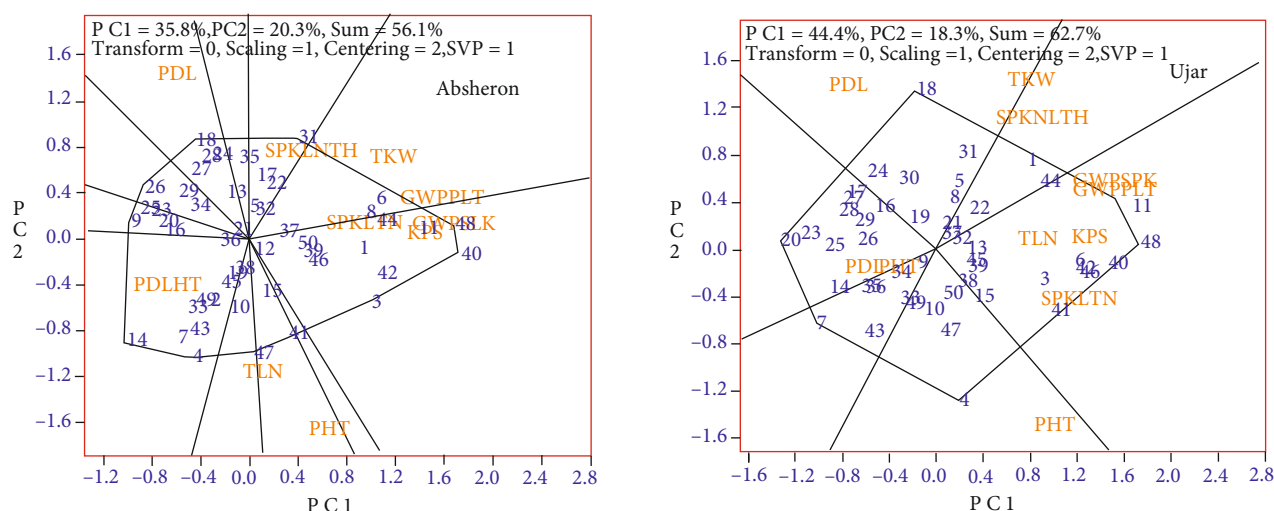


Figure 4. Genotypes superior for individual traits or a set of traits at Absheron (top) and Ujar (bottom) recorded over 3 years. The genotype located at the vertex of the polygon in different segments is the most superior for the trait(s) falling within that segment.

4. Discussion

The two locations differed in terms of their soil and climatic conditions, which was reflected through significant effects of location on seven traits. Expression of different traits differed between years and between locations. However, difference between years for various traits was more evident than between the two locations. There was significant year \times location interaction for several traits, suggesting that the relative differences between locations for these traits differed in 3 years.

The 50 wheat genotypes showed arrays of variation in all 10 traits at both locations, suggesting that superior genotypes could be selected for individual traits. This finding is in agreement with previous report of Turki et

al. (2012), who also reported the presence of genotypic variation for grain yield and TKW. The absence of significant genotype \times year and genotype \times location interactions suggests that relative differences between genotypes for various traits did not change significantly between locations and over years. The number of genotypes showing significant difference between two locations was different for different traits, suggesting that conditions at the two locations differently influenced different traits. Also, a genotype showing superior performance at both locations could be considered tolerant to salinity compared to those showing significantly different performance at the two locations.

Association among genotypes based on multiple traits differed at the two locations, suggesting that nonsaline and saline conditions differently affected relative expression of the traits of the 50 wheat genotypes. However, a few genotypes grouped together, suggesting similarity among them. The genotypes collected from the same place did not necessarily group together or within the same botanical group. For example, the four genotypes (#12, #15, #41, and #47) grouping together at Absheron had been collected from three different places (Terter, Oguz, and Absheron) and belonged to two botanical varieties. Similarly, the four genotypes (#4, #15, #38, and #47) grouping together in Ujar had been collected from four different places (Terter, Oguz, Zakatala, and Absheron) and belonged to four different botanical varieties.

There were nine genotypes (#48, #40, #11, #44, #8, #46, #1, #42, and #3) that were superior based on 10 traits under nonsaline conditions at Absheron (Figure 2). These nine superior genotypes belonged to different botanical groups, three to *Graecum* (#1, #3, and #8), one to *Milturum* (#11), and five to *Erythroleucon* (#40, #42, #44, #46, and #48). Five of the above nine genotypes (#11, #44, #1, #48, and #40) were also superior under saline conditions at Ujar. Among these five, one belonged to *Graecum*, one to *Milturum*, and three to *Erythroleucon*. The places of collection of these five genotypes were diverse (Terter, Sheki, Shamakhi, and Gabala). The five genotypes common at both locations could be valuable as parents for wheat breeding programs aiming at developing superior varieties for saline and nonsaline conditions.

As expected, there were wide genotypic variations for each of the 10 traits included in this study (Figure 3). In general, the superior genotypes for individual traits differed at the two locations. However, genotypes #48 and #18 were superior at both locations. Genotype #48 was superior for GWSPK, KPS, and spikelet number at both locations. Genotype #18 was superior for peduncle length at both locations, besides also being superior for spike

length and TKW at Ujar. It was interesting to note that the improved local controls (#49 and #50) were comparatively not superior for any of the 10 traits, suggesting that this set of 48 accessions from the gene bank is valuable for utilization in the wheat breeding program.

There is a need to evaluate wheat genetic resources in order to identify superior materials in varietal improvement, and in particular stress-tolerant germplasm. Soil salinity is a huge problem in Azerbaijan, Central Asia, and many other parts of the world (Aliyev and Abbasov, 2004). Most of the previous studies on identifying salinity-tolerant wheat were primarily conducted under controlled condition using hydroponics or pots in greenhouse (Munns et al., 2003). Our study reports findings from field studies conducted in multiple years. Also, the previous studies reported effects of salinity on a limited number of traits. Our study involved examination of 10 traits important for wheat improvement. This makes the findings of this study directly relevant to wheat breeders.

Overall, the gene bank accessions possessed extensive variation for different morphophysiological traits. The variation was spread across botanical groups and places of collection. This demonstrates that valuable wheat genetic resources are spread over Azerbaijan. We identified wheat accessions superior under both saline and nonsaline conditions for individual and multiple traits. This pool of germplasm contains useful genetic diversity for important agronomic traits. Therefore, agronomic traits could be substantially improved by the use of these gene pools in selective breeding. This largely unexplored collection of wheat accessions in Azerbaijan should provide significant diversity for the improvement of national and international germplasm.

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