

## Principal Coordinates Analysis of Yield Stability Performances of Grain Yield in Durum Wheat Genotypes

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### ABSTRACT

Twenty genotypes of durum wheat were evaluated in five different test locations over three growing seasons and analyzed for stability of yield performance. The combined analysis of variance revealed the presence of significant genotype  $\times$  environment (GE) interaction for grain yield. The GE interaction was examined using multivariate analysis technique as principal coordinate analysis (PCOA). According to grand means of test environments and total mean yield (2504 kg ha<sup>-1</sup>), test environments are grouped to low (seven environments) and high (eight environments) mean yield. Considering scatter point diagrams, plot of minimum spanning tree and values of centroid distances, genotypes G13 with 2592 kg ha<sup>-1</sup> (mean rank=2), and G15 with 2575 kg ha<sup>-1</sup> (mean rank=7), were identified for unfavorable or poor environmental conditions while genotypes G9 with 2566 kg ha<sup>-1</sup> (mean rank=8), and G14 with 2694 kg ha<sup>-1</sup> (mean rank=1), were identified for favorable environments.

**Keywords:** Genotype, Environment Interaction, Principal Coordinate Analysis, *Triticum turgidum* ssp. Durum.

### INTRODUCTION

Stability of grain yield performance is becoming an important requirement for the durum wheat (*Triticum turgidum* ssp. durum) farmers, because of potentially high annual variation in its grain yield, particularly under arid and semiarid conditions. Inconsistent genotypic responses to the different environments from environment to environment are a function of genotype  $\times$  environment (GE) interaction which has been defined as the

failure of genotypes to achieve the same relative performance in different environments (Baker, 1990; Flores et al., 1998). The economic yield stability, as defined by the farmers, is commonly caused by both environment and GE interaction effects. Knowledge of GE interaction nature and yield stability is important issue for improvement genotypes with proper adaptation to the environmental constraints prevailing in the target test environments (Cooper, 1995; Ceccarelli et al., 2006). Information about phenotypic stability is useful for the selection of new genotypes as well as for increasing of breeding programs efficiency.

Some authors found that durum wheat yield performances follow a static concept of stability (Becker and Leon, 1988), meaning that a stable genotype is defined as one having an unchanged performance ignoring of any variation in the test environments (Karimizadeh et al., 2012; Sabaghnia et al., 2012d).

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Development of high yielding and stable durum wheat genotypes is the main objective of its breeding program in the dry-lands. The performance of a genotype is not necessarily the same under different environments and GE interaction is important in the development of genotype because they reduce the stability values (Rharrabti et al., 2003). For plant breeders, stability of yield performances is important in terms of changing ranks of genotypes across test environments and affects selection efficiency whereas for agronomists and farmers, consistency in yield performances of genotypes is very important, regardless of changing genotypes ranks (Becker, 1981; Flores et al., 1998). However, the yield performance usually reacts similar to the other quantitative traits to favorable or unfavorable environmental conditions and a genotype is regarded to be stable if its contribution to the GE interaction is low.

Several statistical models have been suggested for yield stability analysis with the aim of describing the information contained in the GE interaction structure. These models range from univariate, such as linear regression model (Finlay and Wilkinson, 1963), and nonparametric methods (Huehn, 1990), to multivariate methods such as additive main effects and multiplicative interaction (Zobel et al., 1988), which extracts genotype and environment main effects and uses principal component axes (PCA) to explain patterns in the GE interaction or residual matrix (Romagosa and Fox, 1993). Principal components analysis (PCOA) as a generalization of the linear regression model overcomes the general limitations of the common linear regression model (Mohebodini et al., 2012).

It is a method used to visualize similarities of a dataset and assumes that the original variables had a Euclidean space and that their similarities are modeled by Euclidean distance (Westcott, 1987; Sabaghnia, 2012a). The PCOA starts with a similarity or distance

matrix and assigns for each individual, a position in a low dimensional space. Like AMMI, this analysis maintains most of the initial configuration of the dataset in the first axes so some original information is lost (Sabaghnia et al., 2012c). The PCOA can effectively reduce the pattern of a two-way dataset of multi-environment trials' dimensions in a subspace of fewer dimensions (Ibanmez et al., 2001). The limitations of the PCOA as an ordination approach of multivariate methods are similar to AMMI. Eigenvalues of the PCOA are usually from the greatest to the least and the first eigenvalue is often called the leading eigenvalue. The PCOA is according to the sequential accumulation of the test environments according to their rank order, the environments being ranked in ascending order according to their overall means (Crossa et al. 1989; Sabaghnia et al., 2012b). Each analysis produced a two-dimensional plot according to the first two PCOA axes. Using the eigenvectors of the main PCOA axes via the initial distance matrix can be visualized.

Therefore, our objectives in this study were to (1) determine the magnitude of the GE interaction effects, and (2) identify durum wheat genotypes that performed well and remained stable under different test environments.

## MATERIALS AND METHODS

Twenty durum wheat genotypes (Table 1) were used in this study and analyzed by a randomized complete block design with 4 replications. These genotypes were selected due to their yield potential because they were new improved lines from breeding programs of ICARDS (International Center for Agricultural Research in the Dry Areas), CIMMYT (International Maize and Wheat Improvement Center) and Iran. The trials were performed under rain-fed conditions during three growing seasons in five different test locations; Gachsaran, Ilam, Kouhdasht, Gonabad and Moghan.

These test locations vary in latitude, rainfall, soil types, temperature and other agro-climatic factors (Table 2). The rainfall of these test locations ranged from 271.2 (Moghan) to 502.6 mm (Ilam). The rainfall and altitude properties of all test locations were relatively similar except Moghan these stations were the most producing of durum wheat in Iran. The seeds were sown using an experimental drill in  $1.05 \times 7$  m plots consisting of 6 rows with a 17.5 cm row space. The seeding rates were about 230 seeds  $m^{-2}$  for rain-fed conditions. The experiment trials were sown and managed according to local practice where appropriate pesticides were used to control insects, diseases and weeds. The experiment plots were fertilized with 70 kg N  $ha^{-1}$  and 70 kg P<sub>2</sub>O<sub>5</sub>  $ha^{-1}$  at planting. An area of 4.2  $m^2$  (4 rows with 6 m long) was harvested at 14 % humidity to estimate grain per plot and then converted to kg  $ha^{-1}$ .

Analyses of variance were performed for each test environment. Initial statistical analyses including normality test using the Anderson-Darling normality test and homogeneity test of variances using Levene test. After determination of homogeneity of residuals variance via Bartlett's homogeneity test, a combined ANOVA was performed. To partition out the year (Y), site (S), genotype (G) and their interactions effects,

genotypes and sites were considered as fixed effects while years were considered as random effects. The PCOA was performed for stability analysis with computation of a measure of similarity between two genotypes,  $m$  and  $n$ , in a given test environment as (Westcott, 1987):

$$S_{i(m,n)} = [H_i - (m_i + n_n) / 2] / (H_i - L_i)$$

where  $H_i$  is the highest mean yield of a genotype in test environment  $i$ ;  $L_i$  is the lowest mean yield of a genotype in test environment  $i$ ;  $m_i$  is the mean yield of genotype  $m$  in test environment  $i$  and  $n_i$  is the mean yield of genotype  $n$  in test environment  $i$ . Similarity index between two genotypes ( $m$  and  $n$ ) was measured as the average of  $S_{i(m,n)}$  across test environments when more than one test environment was used. The analysis was based on the sequential accumulation of the test environments according to their rank order, the environments being ranked in ascending order according to their overall means. Each cycle produced a two-dimensional plot based on the first two PCOA scores and the minimum spanning tree plot was drawn for identification the most stable genotypes. All of the mentioned computations and were done by GENSTAT 12.1 software (VSN International, 2009).

**Table 1. The characterization of 20 durum wheat genotypes studied in multi-environmental trials**

No	Code	Name / Pedigree	Origin	Mean yield
1	G1	SRN-1/KILL//2*FOLTA-1	CIMMYT	2478
2	G2	GREEN-14//YAV-10/AUK	CIMMYT	2491
3	G3	GA//2×CHEN/ALTAR84	CIMMYT	2430
4	G4	BCR//MEMO/GOO/3/STJ7	ICARDA	2578
5	G5	SERRATOR-1//SRN-3/AJAIA-15	CIMMYT	2357
6	G6	D68-1-93A-1A//Ruff/Fg/3/Mtl-5/4/Lahn ICD93-0654-C-12AP-0AP-4AP-0AP	ICARDA	2491
7	G7	D68-1-93A-1A//Ruff/Fg/3/Mtl-5/4/Lahn ICD93-0654-C-12AP-0AP-6AP-0AP	ICARDA	2505
8	G8	GREEN-14//YAV-10/AUK	CIMMYT	2590
9	G9	Bisu-1//CHEN-1/TEZ/3/HUI//CIT71/CII	CIMMYT	2566
10	G10	BCR/3/CH1//GTA/STK/4/BCR/LKS4 ICD92-0150-CABL-11AP-0AP-8AP-0TR-4AP-0AP	ICARDA	2582

No	Code	Name / Pedigree	Origin	Mean yield
11	G11	GSB1-1-4/D68/1/93A-1A//RUFF/FG/3/MTL/5 ICD95-1174-C-2AP-0AP-2AP-0AP	ICARDA	2246
12	G12	ALTAR84/STN/WDZ-2 ICD92-MABL-0238-4AP-0AP-5AP-0TR-15AP-0AP	ICARDA	2476
13	G13	DON-MD 81-36	ICARDA	2593
14	G14	STJ3//BCR/LKS4 ICD94-0994-CABL-10AP-0AP-2AP-0AP	ICARDA	2694
15	G15	STJ3//BCR/LKS4 ICD94-0994-CABL-10AP-0AP-6AP-0AP	ICARDA	2575
16	G16	OUASERL-1 ICD96-0758-C-2AP-0AP-5AP-0AP	ICARDA	2532
17	G17	TRE97/4/GDOVZ5512/CIT/RUFF/FG/3/ENTE/MARIO//CA ICD97-1044-C-0AP-6AP-AP-5AP-0AP	ICARDA	2454
18	G18	MARSYR-6 ICD95-1127-T-0AP-9AP-0AP-7AP-0TR-5AP-AP	ICARDA	2313
19	G19	ETH-LRBRI-133/3*ALTER 84 CDSP91B31-A-1H-030Y-030M-3Y-0M-1Y-0B	CIMMYT	2587
20	G20	Seimareh	Iran	2537

Table 2. Agro-climatic properties of the location tested in Iran

Location	Longitude Latitude	Altitude (m)	Soil Texture	Soil Type¶	Rainfall (mm)
Gachsaran	50° 50' E 30° 20' N	710	Silty Clay Loam	Regosols	460.8
Gonabad	55° 12' E 37° 16' N	45	Silty Clay Loam	Regosols	367.5
Kouhdasht	23° 26' E 48° 17' N	1148	Silt-Loam	Regosols	433.1
Ilam	46° 36' E 33° 47' N	975	Clay-Loam	Regosols	502.6
Moghan	48° 03' E 39° 01' N	1100	Sandy-Loam	Cambisols	271.2

¶ Based on the FAO soil classification system (FAO, 1990).

## RESULTS AND DISCUSSION

The mean grain yield of durum wheat genotypes varied from 2246 kg ha<sup>-1</sup> in genotype G11 to 2694 kg ha<sup>-1</sup> in genotype G14, maximum mean yields varied from 1360 kg ha<sup>-1</sup> in genotype G3 grown at Gachsaran in 2009 to 5127 kg ha<sup>-1</sup> at Kouhdasht in genotype G12 grown in 2008 and the minimum grain yield of durum wheat genotypes varied from 459 kg ha<sup>-1</sup> in genotype G2 grown at Gachsaran in 2009 to 3650 kg ha<sup>-1</sup> at Kouhdasht in genotype G11 grown in 2008 (Table 3). Average yield was positively correlated with both maximum and minimum mean yield. The test location

Kouhdasht had the largest mean yield (3429 kg ha<sup>-1</sup>), while the test location Ilam had the lowest mean yield (1891 kg ha<sup>-1</sup>). The favorable genotypes G11 and G14 had good performance in Kouhdasht location but their response to the other test locations was not similar. In other word, there was GE interaction in durum wheat genotypes and the combined analysis of variance verified this phenomenon.

Combined analysis of variance for grain yield of durum wheat genotypes indicated that the effect of year was significant, the site effect was not significant and their interaction was highly significant (Table 4). Therefore, the

mean of three years were different statistically while the mean of five location were not different significantly. Also, the main effect of genotypes was significant, the genotype year interaction was significant, the genotype site interaction was not significant and three way interactions (GYS) or genotypes  $\times$  environment interaction were highly significant (Table 4). Thus, the mean of twenty durum wheat genotypes were different but the responses of genotype across years as well as the responses of genotype across locations were not significant. Finally the responses of genotypes across years and locations (three way interaction) were completely different. The highly significant differences among genotypes indicating the presence of genetic variation among the 20 durum wheat genotypes, and the significant value of GE interaction revealed that the genotypes interacted with different

environments. Also, it seems that the studied genotypes exhibited both crossover and non-crossover types of GE interaction. The yield performance as a quantitative characteristic is considered as a complex characteristic and this complexity is a result of diverse processes that occur during plant development and its expression is the result of genotype, environment and GE interaction (Sabaghnia et al., 2008). The larger magnitude of GE interaction causes the more dissimilar the genetic systems which control some of the physiological processes conferring adaptation to various environmental conditions (Cooper, 1995). According to Ceccarelli et al. (2006), when genotypes are tested in multi-environment trials in rain-fed conditions, a crossover GE interaction occurs and complicates recommendation issue in breeding programs.

**Table 3. mean yield of twenty durum wheat genotypes across fifteen test environments.**

	Gachsaran			Gonabad			Kouhdasht			Ilam			Moghan		
	Y1	Y2	Y3	Y1	Y2	Y3	Y1	Y2	Y3	Y1	Y2	Y3	Y1	Y2	Y3
G1	2673	2735	1098	2705	3117	1045	3506	4484	2198	2650	1272	1877	2562	3154	2093
G2	2973	2576	459	2450	2968	1030	3646	4607	2162	2540	1191	1965	3513	3273	2018
G3	2298	2465	1360	2579	2808	1168	3331	4713	2054	2278	876	1810	3290	3227	2191
G4	2896	2341	1206	2558	2745	1175	4100	4157	1982	2912	812	2071	3833	3480	2408
G5	2675	2499	650	2254	2638	1495	3700	4177	1925	2367	1156	1924	2772	2988	2133
G6	3019	2559	903	2394	2687	1266	3429	4496	2254	2435	985	1862	3873	3134	2068
G7	2919	2480	981	2464	3185	1188	3142	4594	2306	2839	1281	2011	3301	2694	2191
G8	3244	2961	768	2461	2693	1068	3173	4806	2434	2627	1412	2077	3377	3440	2314
G9	3329	2905	1036	2503	2903	1200	3332	4335	2229	2789	1203	1792	3157	3289	2489
G10	3359	2647	1055	2266	3350	1105	3423	4248	2269	2196	890	2000	3129	3387	3404
G11	2808	2573	1067	1949	2414	810	3242	3650	1902	2326	1120	2059	2595	3281	1888
G12	3090	2676	1203	1905	2479	1000	4002	5127	2460	2720	1283	2034	2996	2724	1437
G13	3306	2723	1299	2450	3362	1415	3419	4606	2269	2767	1143	1941	3111	3037	2041
G14	3443	2769	737	2831	3022	880	3583	4861	2190	3407	1286	2110	3952	3226	2117
G15	2943	2697	1144	2606	2904	815	3188	4988	2123	2771	1377	2329	3413	3116	2218
G16	2810	2725	1265	2460	2951	1315	3790	4850	2215	2194	1013	1849	3653	2971	1915
G17	2866	2496	939	2688	2798	900	4073	4465	2219	2343	1130	1731	2858	3294	2017
G18	3015	2417	460	2651	2484	968	3569	4540	1692	1728	1312	2078	3511	2738	1539
G19	2991	2636	1032	2599	2542	1280	4007	5081	2429	2818	684	2044	3186	3166	2316
G20	3053	2602	920	2601	3192	1398	3864	4067	2073	3009	1032	1714	3063	3283	2178

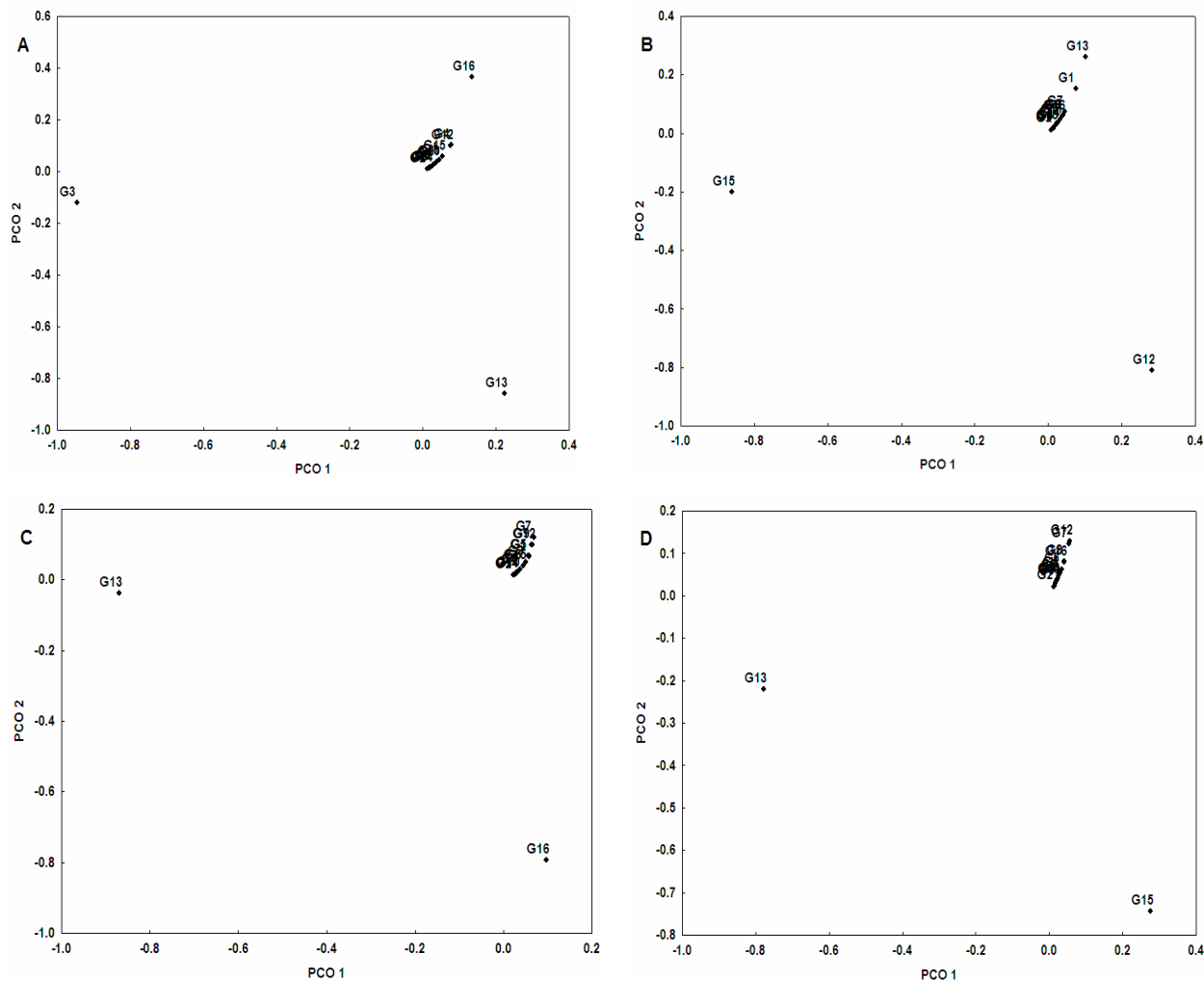
**Table 4. Combined ANOVA of twenty durum wheat genotypes across fifteen test environments.**

Source	DF	Mean Squares
Year (Y)	2	206213572.0*
Site (S)	4	94220057.1 <sup>ns</sup>
Y × S	8	34610128.9**
Replication/ YS	45	618760.2
Genotype (G)	19	680166.4*
G × S	76	341113.3*
G × Y	38	314535.9 <sup>ns</sup>
G × Y × S	152	248317.9**
R × G / Y S	855	102927.8

\*\* , \* and <sup>ns</sup> significant at the 0.01 and 0.05 probability level, respectively and non-significant.

According to grand means of test environments and total mean yield (2504 kg ha<sup>-1</sup>), test environments are grouped to two main groups as L (low mean yield) and H (high mean yield). There are seven L test environments and eight H test environments which analyzed in the sequential cycles. Grain yield performances are first analyzed for the lowest test environment (cycle L1); the second cycle (L2) involves analyzing the two lowest environments, and so on. Rather than including all seven scatter diagrams, the stability patterns of the durum wheat genotypes are described in the first four cycles in Low test environments (L1 to L4). A typical plot for the cycles is shown in Fig. 1A where the scatter point diagram shows the results of analysis for the first low cycle (L1). Plot of

first two principal coordinates analysis axes in cycle L1 indicated genotypes G3 and G13 were different from the other durum wheat genotypes. Similar plot for cycle L2 (Fig. 1B) showed genotypes G12 and G15, for cycle L3 (Fig. 1C) showed genotypes G13 and G16, and for cycle L4 (Fig. 1D) showed genotypes G13 and G15 were identified as the different ones from the other durum wheat genotypes. Our findings are in good agreement with results of Mohebodini et al. (2012) which used principal coordinates analysis for interpreting GE interaction in grain yield of some lentil genotypes. They conclude that PCOA can explore the structure of GE interaction and identify the most favorable genotypes especially in dry land areas.



**Fig. 1. Plot of the first two principal coordinate analysis axes for 20 durum wheat genotypes in 15 test environments, in (A) the first low cycle L1, (B) the second low cycle L2, (C) the third low cycle L3, and (D) the fourth low cycle L4.**

The scatter diagrams use only first two principal coordinates analysis axes and so ignoring some information of the other principal coordinates axes. For overcoming this problem, the plot of minimum spanning tree could be useful. Rather than including all seven minimum spanning tree plots, the stability patterns of the durum wheat genotypes are described in text and only two plots, corresponding to cycles L1 and L2, are presented. In these plots, the high-yielding genotypes are those which are furthest from the plot centre, and so

genotypes G3, G13 and G16 were detected as the high yielding genotypes in L1 cycle (Fig. 2A), while genotypes G12, G13 and G15 were detected as the high yielding genotypes in L2 cycle (Fig. 2B). The minimum spanning tree plot is represented in only two dimensions ignoring information in the next principal coordinates axis and Flores et al. (1996) proposed using a parameter as centroid distances which are benefits from all of the principal coordinates dimensions. The centroid distances of seven L cycles are presented in Table 5 and ranking

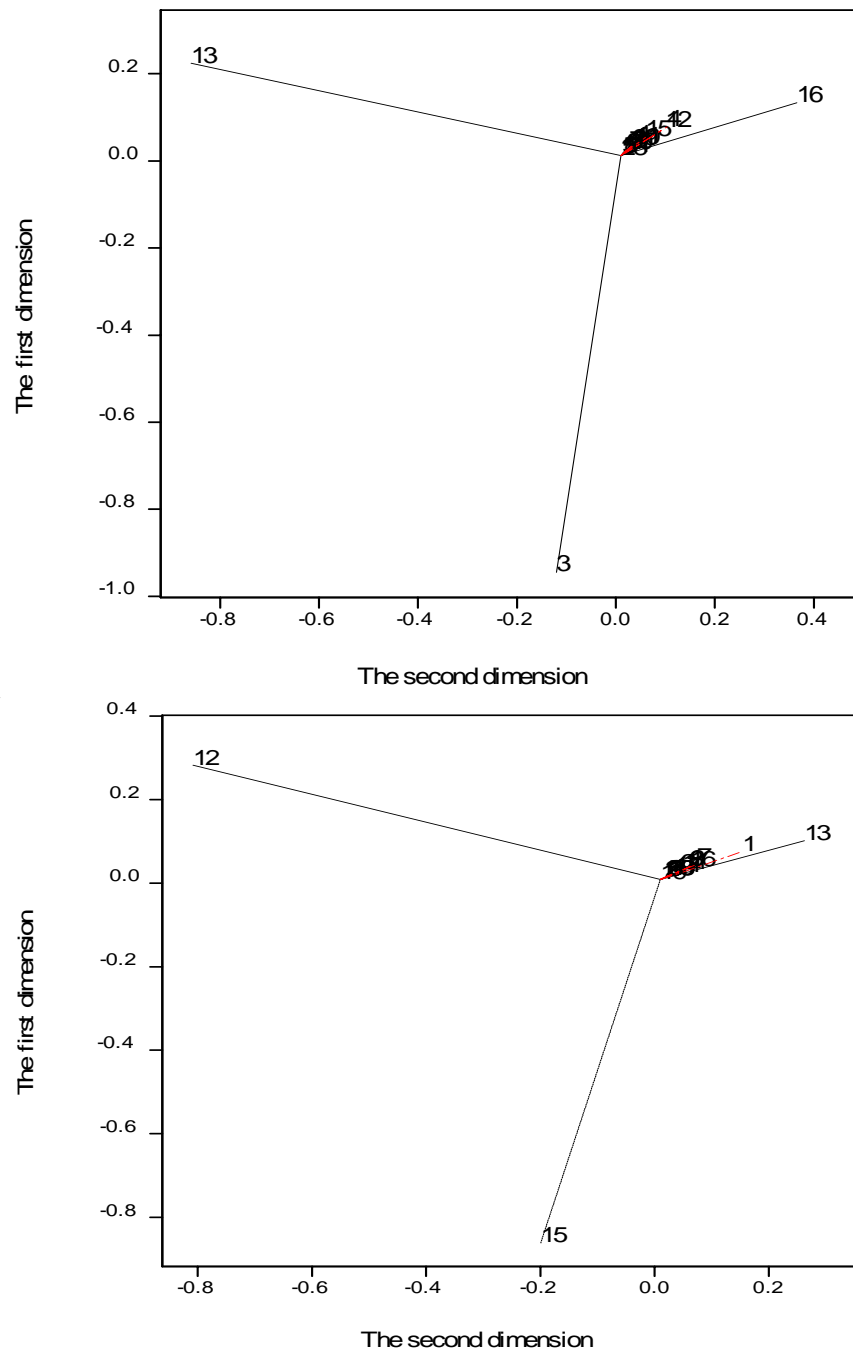
of durum wheat genotypes based on the maximum values of centroid distances for each cycle are given in Table 6. Thus, genotypes G13 and G15 were the most favorable stable ones with seven and five repetitions as the vertex genotypes. Also, genotypes G8, G12 and G16 were located two times and genotypes G1, G3, G5, G7, G10 and G11 were located one time in the vertex

positions. The most stable genotypes are the ones that are consistent over cycles (Westcott, 1987; Flores et al., 1996) and so the identified most stable and high mean yield genotypes had acceptable mean yield; G13 with 2593 kg ha<sup>-1</sup> (mean rank=2), and G15 with 2575 kg ha<sup>-1</sup> (mean rank=7), and therefore could be recommended for unfavorable or poor conditions.

**Table 5. Lengths of the total minimum spanning tree as centroid distances for the seven low cycles of durum wheat genotypes.**

	L1	L2	L3	L4	L5	L6	L7
G1	0.817	0.843	0.765	0.710	0.683	0.702	0.734
G2	0.170	0.585	0.577	0.589	0.578	0.613	0.634
G3	0.964	0.773	0.750	0.680	0.665	0.667	0.693
G4	0.880	0.694	0.699	0.709	0.703	0.689	0.708
G5	0.469	0.645	0.765	0.722	0.696	0.674	0.665
G6	0.687	0.661	0.706	0.658	0.639	0.675	0.680
G7	0.742	0.811	0.765	0.757	0.729	0.754	0.754
G8	0.581	0.796	0.577	0.739	0.721	0.764	0.763
G9	0.778	0.799	0.750	0.698	0.700	0.720	0.729
G10	0.790	0.673	0.699	0.663	0.732	0.751	0.734
G11	0.798	0.776	0.765	0.662	0.629	0.613	0.577
G12	0.878	0.878	0.706	0.759	0.682	0.737	0.685
G13	0.931	0.855	0.872	0.812	0.766	0.779	0.775
G14	0.554	0.735	0.631	0.670	0.652	0.676	0.725
G15	0.845	0.894	0.737	0.798	0.765	0.760	0.773
G16	0.913	0.797	0.808	0.738	0.695	0.714	0.720
G17	0.713	0.738	0.641	0.565	0.559	0.607	0.655
G18	0.173	0.646	0.596	0.636	0.581	0.535	0.595
G19	0.777	0.575	0.651	0.666	0.661	0.713	0.729
G20	0.701	0.700	0.762	0.664	0.650	0.653	0.679





**Fig. 2. The minimum spanning tree of the first two principal coordinate analysis axes of 20 durum wheat genotypes in 15 test environments, in up (A) the first low cycle L1 and down (B) the second low cycle L2.**

Eight H test environments analyzed in the sequential cycles for the highest test environment (cycle H1); the second cycle

(H2) involves analyzing the two highest environments, and so on. Similar to L cycles and rather than including all eight

scatter diagrams, the stability structure of genotypes are explained in the four cycles including H1, H2, H3 and H4. The scatter point diagram for cycle H1 (Fig. 3A) showed genotypes G14, G19 and G20, for cycle H2 (Fig. 3B) showed genotypes G8, G9 and G14, for cycle H3 (Fig. 3C) and for cycle H4 (Fig. 3D) showed genotypes G13 and G14 were identified as the different ones from the other durum wheat genotypes. For using of the plot of minimum spanning tree and rather than including all eight plots, the stability patterns of genotypes are described in text and only two plots, corresponding to cycles H1 and H2, are presented. The high-yielding genotypes G14, G19 and G20 were detected in H1 cycle (Fig. 4A) whereas genotypes G8, G9 and G14 were detected as the high yielding

genotypes in H2 cycle (Fig. 4B). The centroid distances of eight H cycles are presented in Table 7 and ranking of durum wheat genotypes based on the maximum values of centroid distances for each cycle are given in Table 8. Thus, genotypes G9 and G14 were the most favorable stable ones with five and eight repetitions as the vertex genotypes. Also, genotypes G4 and G20 were located two times, genotype G13 was located three times, genotype G8 was located four times, and genotype G9 was located five times in the vertex positions. The identified most stable and high mean yield genotypes had acceptable mean yield; G9 with 2566 kg ha<sup>-1</sup> (mean rank=8), and G14 with 2694 kg ha<sup>-1</sup> (mean rank=1), and therefore could be recommended for favorable or rich conditions.

**Table 6. The ranks of durum wheat genotypes based on centroid distances for the seven low cycles.**

	L1	L2	L3	L4	L5	L6	L7	VG*
G1	7	4	4.5	8	10	10	5.5	1
G2	20	19	19.5	19	19	17.5	18	0
G3	1	10	8.5	11	12	15	12	1
G4	4	14	13.5	9	6	11	11	0
G5	18	18	4.5	7	8	14	16	1
G6	15	16	11.5	17	16	13	14	0
G7	12	5	4.5	4	4	4	4	1
G8	16	8	19.5	5	5	2	3	2
G9	10	6	8.5	10	7	7	7.5	0
G10	9	15	13.5	15	3	5	5.5	1
G11	8	9	4.5	16	17	17.5	20	1
G12	5	2	11.5	3	11	6	13	2
G13	2	3	1	1	1	1	1	7
G14	17	12	17	12	14	12	9	0
G15	6	1	10	2	2	3	2	5
G16	3	7	2	6	9	8	10	2
G17	13	11	16	20	20	19	17	0
G18	19	17	18	18	18	20	19	0
G19	11	20	15	13	13	9	7.5	0
G20	14	13	7	14	15	16	15	0

\*The number of vertex genotypes

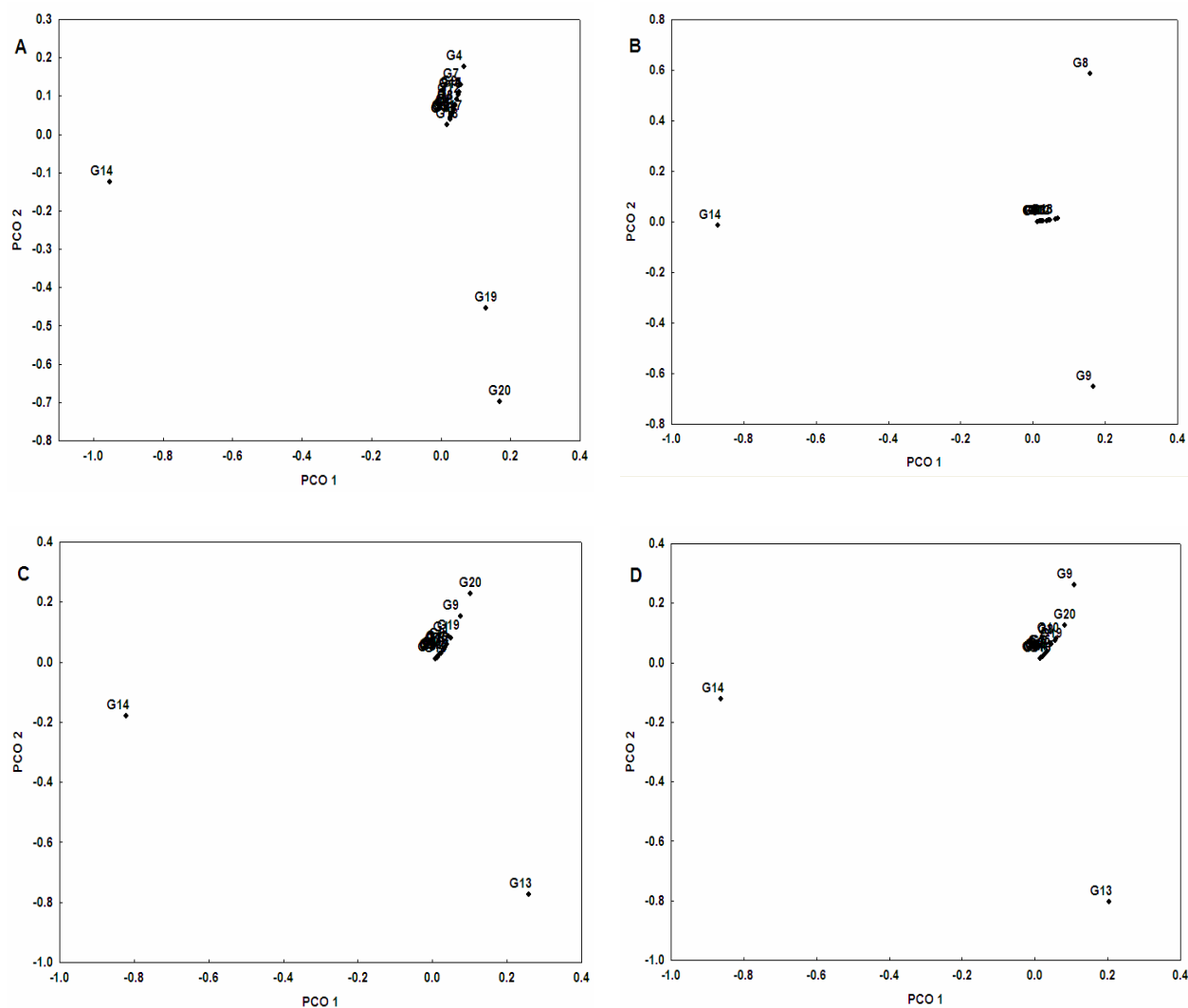
**Table 7. Lengths of the total minimum spanning tree as centroid distances for the eight high cycles of durum wheat genotypes.**

	H1	H2	H3	H4	H5	H6	H7	H8
G1	0.721	0.747	0.776	0.730	0.733	0.673	0.663	0.618
G2	0.679	0.643	0.677	0.696	0.725	0.738	0.734	0.700
G3	0.566	0.512	0.554	0.488	0.564	0.590	0.572	0.537
G4	0.813	0.585	0.584	0.617	0.700	0.742	0.777	0.719
G5	0.607	0.557	0.535	0.544	0.557	0.534	0.568	0.488
G6	0.637	0.610	0.585	0.637	0.657	0.711	0.689	0.646
G7	0.789	0.651	0.731	0.728	0.656	0.665	0.619	0.578
G8	0.713	0.846	0.757	0.790	0.822	0.809	0.755	0.734
G9	0.771	0.848	0.801	0.832	0.834	0.805	0.765	0.716
G10	0.526	0.610	0.743	0.794	0.818	0.789	0.759	0.705
G11	0.589	0.594	0.493	0.539	0.610	0.564	0.538	0.399
G12	0.747	0.731	0.620	0.672	0.611	0.602	0.656	0.654
G13	0.764	0.762	0.834	0.853	0.816	0.786	0.756	0.723
G14	0.962	0.886	0.851	0.881	0.865	0.882	0.854	0.839
G15	0.765	0.750	0.734	0.734	0.730	0.735	0.688	0.677
G16	0.525	0.655	0.681	0.675	0.659	0.696	0.711	0.692
G17	0.596	0.550	0.575	0.606	0.661	0.633	0.687	0.642
G18	0.162	0.283	0.289	0.460	0.430	0.511	0.533	0.480
G19	0.772	0.722	0.627	0.661	0.682	0.675	0.710	0.701
G20	0.836	0.740	0.786	0.786	0.797	0.765	0.772	0.703

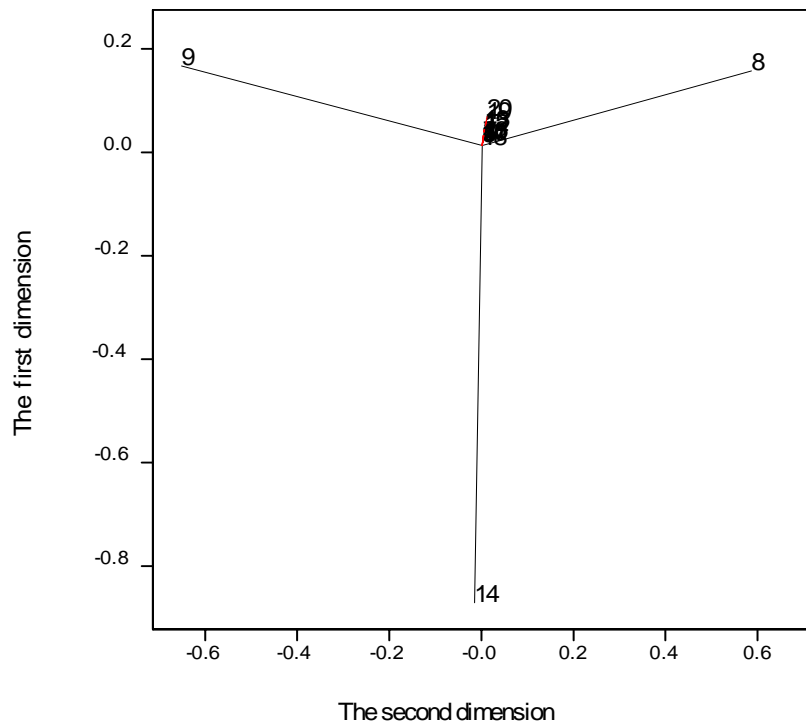
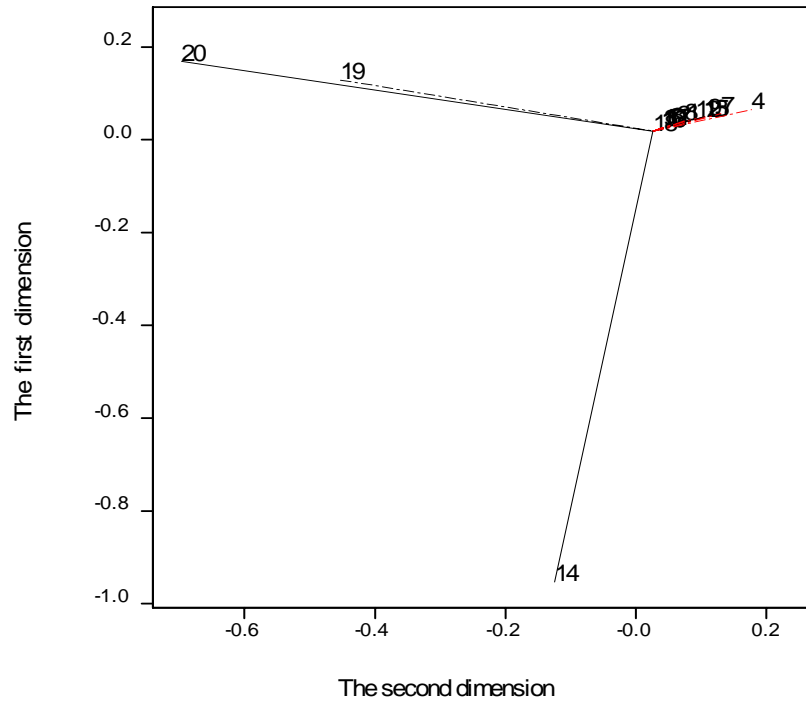
**Table 8. The ranks of durum wheat genotypes based on centroid distances for the eight high cycles.**

	H1	H2	H3	H4	H5	H6	H7	H8	VG*
G1	10	6	5	8	7	13	14	15	0
G2	12	12	11	10	9	8	8	9	0
G3	17	19	17	19	18	17	17	17	0
G4	3	16	15	15	10	7	2	4	2
G5	14	17	18	17	19	19	18	18	0
G6	13	13.5	14	14	14	10	11	13	0
G7	4	11	9	9	15	14	16	16	0
G8	11	3	6	5	3	2	7	2	4
G9	6	2	3	3	2	3	4	5	5
G10	18	13.5	7	4	4	4	5	6	0
G11	16	15	19	18	17	18	19	20	0
G12	9	8	13	12	16	16	15	12	0
G13	8	4	2	2	5	5	6	3	3
G14	1	1	1	1	1	1	1	1	8
G15	7	5	8	7	8	9	12	11	0
G16	19	10	10	11	13	11	9	10	0

	H1	H2	H3	H4	H5	H6	H7	H8	VG*
G17	15	18	16	16	12	15	13	14	0
G18	20	20	20	20	20	20	20	19	0
G19	5	9	12	13	11	12	10	8	0
G20	2	7	4	6	6	6	3	7	2



**Fig. 3.** Plot of the first two principal coordinate analysis axes for 20 durum wheat genotypes in 15 test environments, in (A) the first high cycle H1, (B) the second high cycle H2, (C) the third high cycle H3, and (D) the fourth high cycle H4.



**Fig. 4.** The minimum spanning tree of the first two principal coordinate analysis axes of 20 durum wheat genotypes in 15 test environments, in up (A) the first high cycle H1 and down (B) the second high cycle H2.

In this investigation, interpretation of the GE interaction was based on PCOA as multivariate analysis. In spite of the certain deficiencies of conventional methods of stability analysis such as linear regression model for determining GE interaction which explain a small part of some of squares of GE interaction, the PCOA appeared to be able to extract a large part of the GE interaction and is thus more efficient in analyzing GE interaction structure, as demonstrated by Ibanmez et al. (2001). This finding was encountered in this and other similar investigations (Flores et al., 1996; Medina et al. 1999) because multivariate methods such as PCOA explore multi-dimension property of GE interaction while univariate methods attempt to define the GE interaction by one or two parameter but the multiplicative GE interaction is far too complex to be summarized by one or two stability parameter. Also, Crossa (1990) concluded that regression analysis should be used with caution when one of the environments is atypical. Medina et al. (1999) found that PCOA might be more straightforward than AMMI model. It should be noted at this point that genetic differences in durum wheat genotypes, in addition to differences in environmental conditions, could have had an influence on the results obtained. The most favorable genotypes selected according to stability of yield performance in our investigation verified the possibility of combining both stable and high mean yielding. However, plant breeders must be aware of the difficulties and problems in selection process. As reported by Sabaghnia et al. (2012d), it seems that an integrated selection system designed to maximize the probability of producing stable durum wheat genotypes with a high level of performance should be developed.

For the durum wheat genotypes analyzed in this investigation, the PCOA could necessary explain adequately the GE interaction and extract a large portion of

the GE interaction. This method was more efficient in analyzing GE interaction in different crops, as demonstrated by Flores et al. (1996), Medina et al. (1999), Ibanmez et al. (2001) and Mohebodini et al. (2012). Using the PCOA for interpreting GE interaction of durum wheat genotypes identified the most favorable genotypes. Also, the identified most favorable genotypes in both high and low cycles or condition (favorable versus unfavorable) are relatively the most high yielding genotypes and so it seems that this strategy can select the most stable genotypes based on the dynamic stability concept (Becker and Leon, 1988; Sabaghnia et al., 2012c). However in the semi-arid regions and rain fed condition, where fluctuations in growing conditions are unpredictable, additional investigations are needed to obtain an integration of GE interaction analysis with environmental factors. Mohebodini et al. (2012) declared that the PCOA is a good strategy for GE interaction studies in arid and semi arid areas of Middle East conditions. The PCOA provided a better description of GE interaction than univariate (Mohebodini et al., 2012)) stability methods, which was ineffective in describing GE interaction. For genotypic stability, showed high stability for grain yield and proved to be the best within the pool of the studied durum wheat genotypes.

## CONCLUSIONS

Genotypes G13 (2593 kg ha<sup>-1</sup>) and G15 (2575 kg ha<sup>-1</sup>) for unfavorable or poor environments and genotypes G9 (2566 kg ha<sup>-1</sup>) and G14 (2694 kg ha<sup>-1</sup>), for favorable environments and therefore could be recommended as commercial cultivars for release in semiarid areas of Iran by Dry-land Agricultural Research Institute.

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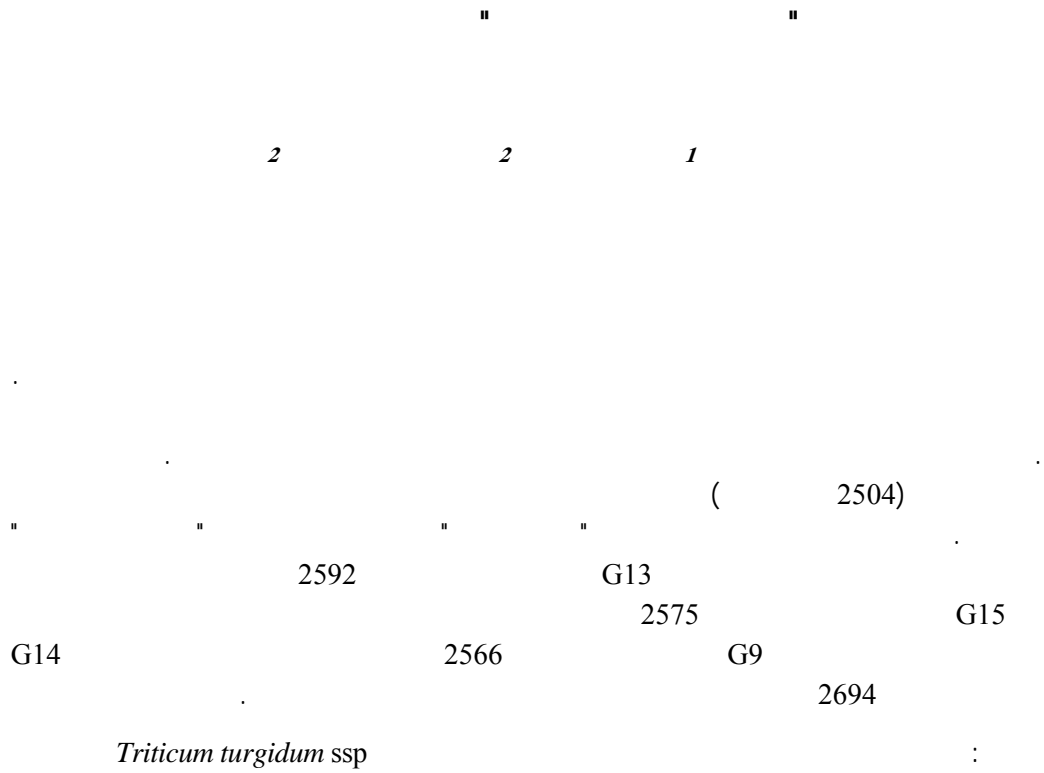
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