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Stability of Chickpea (*Cicer arietinum* L.) Landraces in National Plant Gene Bank of Iran for Drylands

M. Pouresmael[1*], H. Kanouni [2], M. Hajihasani[3], H. Astraki[4], A. Mirakhorli[5], M. Nasrollahi[4], and J. Mozaffari[1]

ABSTRACT

Identification of high performance stable genotypes is an important objective for chickpea production in drylands of Iran. Hence, the stability of 12 chickpea local landraces and three check cultivars were evaluated during three consecutive cropping seasons (2010-2013). The experiments were laid out as a randomized complete block design with four replications in four locations. Combined analysis of variance was performed to verify the existence of differences among genotypes. AMMI analysis was performed to analyze the residual multiplicative interaction. The stability was estimated through ranking of genotypes based on different quantitative stability parameters including *IPCA* score, AMMI Stability Value (ASV), Sustainability Index (SUI), and Genotype Selection Index (GSI). Main effects of year, location, and genotype as well as their two- and three-way interaction effects were significant (P≤ 0.01) for grain yield. Significant effect of genotype, location, and year interaction implied presence of genetic variability which provides an opportunity to identify new superior genotypes for each location. AMMI analysis showed that the three main components accounted for 62% of the total genotype by environment interaction. Based on the results, the landraces G1, G2, G3, G8, and G12 had the highest average performance and stability compared to check cultivars and could be used in breeding programs for the development of new chickpea varieties.

Keywords: AMMI analysis, *Cicer arietinum* L., High yielding, Local genotypes, Rainfed.

INTRODUCTION

Chickpea harvested area in Iran is about 463,000 ha, of which the vast majority is in dryland areas (98.43%) (Agricultural Statistics, 2016). Spring cultivation of chickpea in Iran is common; hence, the plant has to use the moisture stored in the soil profile to complete its life cycle and the grain filling stage usually faces dehydration due to increase in evaporation from the soil and transpiration from the plant. Thus, the national average chickpea yield falls down from 1,392 kg ha^{-1} in irrigated land to 402 kg ha^{-1} in dryland (Agricultural Statistics, 2016).

Chickpea reproductive growth phase is sensitive to water shortage and erratic and inadequate amount of rainfall during this phase is one of the main reasons of yield reduction. Therefore, identification and introduction of appropriate genotypes for dryland farming is one of the major attempts

[1] Department of Genetics and National Plant Gene Bank, Seed and Plant Improvement Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Islamic Republic of Iran.
[*]Corresponding author; email: m.pouresmael@areeo.ac.ir
[2] Agricultural and Natural Resource Research Center (ANRRC) of Kordestan, AREEO, Sanandaj, Islamic Republic of Iran.
[3] ANRRC of West Azarbaijan, AREEO, Urmia, Islamic Republic of Iran.
[4] ANRRC of Lorestan, AREEO, Brojerd, Islamic Republic of Iran.
[5] ANRRC of Kermanshah, AREEO, Kermanshah, Islamic Republic of Iran.

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towards the efficient use of water and soil resources of the country (Ebadi Segherloo *et al*., 2008).

Yield is a complex quantitative trait that is often controlled by several genes and influenced by environmental conditions. The importance of Genotypes by Environment Interaction (GEI) in national cultivar evaluation and breeding programs has been demonstrated in almost all major crops (Najafian *et al*., 2010; Zali *et al*., 2011; Kendal *et al*., 2016; Sayar *et al*., 2013; Kendal and Doğan 2016).

Among the multivariate methods, the Additive Bain effects and Multiplicative Interaction (AMMI) analysis is widely used for GEI investigation. The AMMI model combines ANOVA for the genotype and environment main effects with principal components analysis to analyze the residual multiplicative interaction between genotypes and environments to determine the sum of squares of GEI, with a minimum number of degrees of freedom (Gauch and Zobel, 1996). This method captures a large portion of the GEI sum of squares; it clearly separates main and interaction effects and often provides meaningful interpretation of data (Gauch and Zobel, 1996; Crossa *et al*., 1990). The degree of complexity of AMMI estimation model is dependent on crop species, germplasm diversity and the range of environmental conditions (Malhotra and Singh, 1991; Atta *et al*., 2009; Acikgoz *et al*., 2009; Kilic 2014; Mortazavian *et al*., 2014; Kendal and Tekdal, 2016; Sayar *et al.*, 2013).

The GEI have been studied by different researchers in chickpea and in other important agricultural crops (Arshad *et al*., 2003; Sabaghpour *et al*., 2006; Yaghotipoor and Farshadfar, 2007; Yadav *et al*., 2010; Bakhsh *et al*., 2011; Hamayoon *et al*., 2011; Imtiaz *et al*., 2013, Kendal and Sayar, 2016). Researchers almost describe stable genotypes using different parametric and non-parametric or univariate and multivariate statistical methods. Shafi *et al*. (2012) used stability parameters according to Eberhart and Russel methods to identify genotypes with stable performance across various environments. Mahtabi *et al*. (2014) studied phenotypic stability of chickpea genotypes using univariate parametric statistical methods. Kanouni *et al*. (2015) used AMMI model to analyze for seed yield stability of chickpea genotypes in the western cold zone of Iran. Farshadfar *et al*. (2011) explored the effect of genotype and genotype×environment interaction on grain yield of 17 chickpea genotypes using the GGE Bi-plot method. Wricke's ecovalence analysis and AMMI analysis were used by Tilahun *et al*. (2015) to examine the magnitude of environmental effect on yield of chickpea genotypes in Ethiopia. Rashidi *et al*. (2013) studied phenotypic stability in chickpea genotypes over stress and non-stress environments using AMMI analysis. Johnson *et al*. (2015) used mean performance and regression coefficient and deviation from regression for stability analysis of seed yield and its components in chickpea.

Plant Genetic Resources for Food and Agriculture (PGRFA) are the biological cornerstone of global food security. The agricultural diversity and genetic resources for food crops need to be used efficiently both to maintain current levels of food production and to confront future challenges. Crop production in all countries relies on genetic resources originating from all over the world. Chickpea dryland farming in Iran almost rely on samples received from international research centers such as ICARDA (International Center Agricultural for Dryland Area) and ICRISAT (The International Crops Research Institute for the Semi-Arid Tropics) and there is negligible attention to native landraces. Landraces locally adapted to the environmental conditions of the places where they have traditionally been grown are key component of PGRFA. This wealth of genetic diversity has been preserved during the natural process of domestication and cultivation (Yesmin *et al*., 2014). Today, due to climate change and need for higher genetic diversity to cope with this

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phenomenon, dependency on national landraces is felt necessary. Comprehensive assessments of materials housed in gene banks can compensate risks resulting from climate change (Jarvis *et al*., 2008).

Different studies have demonstrated that the seed yield of chickpea in the Central and West Asia and North Africa region can be substantially increased by changing the planting season from the traditional spring to winter (Imtiaz *et al*., 2013). However, farmers prefer chickpea planting in the spring. Therefore, developing suitable high yielding cultivars is needed for spring sowing or dual season sowing (Imtiaz *et al*., 2013). This way, farmers have a chance to select suitable cultivars for spring or winter sowing depending on their local environmental or agro-climatic conditions (Imtiaz *et al*., 2013).

Iran is one of the countries of origin of chickpea. Chickpea collection of National Plant Gene Bank of Iran (NPGBI) contain 3365 accessions of Desi and 2012 accessions of Kabuli type chickpea, ranked as sixth collection among major chickpea collections in the world (FAO, 2010). The accessions of this collection are very diverse and all imaginable variations in the international descriptor are present in this collection. Hence, evaluation of these valuable resources to find out their undiscovered potential is urgent and will help breeders to work towards the proper utilization of these landraces for parental selection and linkage map construction for discovery of useful alleles (Yesmin *et al*., 2014).

For this purpose, 12 accessions of Kabuli chickpea landraces, which were identified as terminal drought stress tolerant in previous NPGBI projects (Pouresmael *et al*., 2012; Pouresmael *et al*., 2009), were compared with three commercial cultivars for spring sowing in four provinces of Iran. This study aimed to estimate the adaptability and yield stability of chickpea landraces using AMMI analysis to compare national landraces, introduce genotype with high performance and stability for breeding cycle, and to achieve the full potential under variable and unstable conditions of the dryland areas.

MATERIALS AND METHODS

In order to compare and identify the most stable and high yielding genotypes, multi-environment trials were conducted at the Agricultural and Natural Resources Research Station of Borujerd, Sararod, Sanandaj and Urmia located in four provinces of Iran, respectively, Lorestan, Kermanshah, Kurdistan and West Azerbaijan, during three cropping seasons (2010–2013). In total, 15 genotypes, including 12 Iranian Kabuli chickpea landraces provided by NPGBI (Table 1) and three common commercial cultivars (Hashem, Azad, and Arman) were evaluated and compared to each other for agronomical traits and performance point of view for spring sowing under dryland conditions. Experiments were carried out in a randomized block design with four replications. Each plot was 0.9 m wide and 3 m long, consisting of three rows of a single genotype. The inter-row and interplant spacing were 30 cm and 7 cm, respectively. Planting was done in the second half of March. Total rainfall, seasonal maximum and minimum temperature, and humidity percentage during cropping seasons (March. - July) are shown in Table 2. Standard agricultural practices including fertilizer, weeds and diseases control was done in each location, based on need. Plants were harvested manually, grain yields were determined according to IBPGR (1993) and combined analysis of variance was performed for each environment (year by location integration) to verify the existence of differences among genotypes. AMMI analysis was used to analyze the residual multiplicative interaction between genotypes and environments to determine the sum of squares of the GEI. The sum of squares of the GEI was divided into Interaction Principal Component Axis (IPCA), which

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Table 1. The accession number of used chickpea materials in the study.

Genotype No	Accession number	Genotype No	Accession number	Genotype No	Accession number	Genotype No	Accession number
G1	KC215171	G5	KC215671	G9	KC215995	G13	Arman
G2	KC215296	G6	KC215686	G10	KC216066	G14	Azad
G3	KC215654	G7	KC215767	G11	KC216084	G15	Hashem
G4	KC215664	G8	KC215843	G12	KC216325		

Table 2. Environmental code, soil characteristics and agro climatic information of different locations used in the study.

Location	Geographic information		Soil characteristics			Experiment		Climatic information		
	Longitude and latitude	Altitude (m)	Texture	pH	EC	Growing seasons	Environment code	Growing seasons rainfall (mm)	Max ttemperature (°C)	Min temperature (°C)
Borujerd	48° 55 E 33° 40 N	1476	Loam (Sand 20%, Silt 46%, Clay 25%)	7.8	0.04	2010-11 2011-12 2012-13	E1 E5 E9	51 26.44 39.55	30.56 28 30.44	5.88 4 5.96
Sararod	47° 19 E 34° 20 N	1351	Silty Clay Loam (Sand 9%, Silt 47%, Clay 44%)	7.4	0.78	2010-11 2011-12 2012-13	E2 E6 E10	35.78 17.04 20.86	31.9 31.45 21.74	2.24 -0.2 2.88
Sanandaj	48° 08E 35° 43 N	2120	Loam (Sand 21%, Silt 30% ,Clay 49%)	7.4	0.69	2010-11 2011-12 2012-13	E3 E7 E11	64 25 29.4	32 30.45 32.36	2.72 -0.3 2.28
Urmia	45° 09 E 37° 21 N	1520	Sandy/Loamy Silty (Sand 17%, Silt 44% , Clay39%)	7.4	1.5	2010-11 2011-12 2012-13	E4 E8 E12	51.24 19.04 23.3	27.86 22.65 28.04	2.28 -1.3 0.4

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reflects the standard portion in which each axis corresponded to a particular AMMI model. Combined analysis of variance and mean comparison were performed using SPSS 16.1 and the AMMI analysis was done using GenStat 12.The genotype adaptability was estimated through ranking of genotypes based on different quantitative stability parameters including:

IPCA SCORE

The larger the *IPCA* (Interaction Principal Component Analysis) scores, either negative or positive, indicate the more specific adaptation of a genotype to a certain environments. Smaller *IPCA* scores indicate the lower contribution of the GEI and more genotype stability (Purchase *et al*., 2000).

AMMI Stability Value (ASV)

The AMMI stability value was calculated as described by Purchase *et al*. (2000); the lower *ASV* values indicate greater stability of a genotype.

Sustainability Index (SUI)

The sustainability index for each genotype was calculated as previously described by Babar Manzoor *et al*. (2009):

$$SUI= (Y-\sigma n/YM)\times 100 \quad (1)$$

Where, *Y, σn* and *YM* stand for the average performance, the standard deviation and the best performance of a genotype, respectively. The sustainability index values were arbitrarily divided into three stability groups as follows: low (up to 35%), medium (36 to 70%) and high (71 to 100%).

Genotype Selection Index (GSI)

Genotype Selection Index (GSI), was calculated using the following formula:

$$GSI= RASV+RY \quad (2)$$

Where, *RASV* and *RY* are the rank of AMMI stability value and mean grain yield rank of a genotype, respectively (Farshadfar, 2008).

Additionally, Biplot graph interpretation based on the additive main effects (genotype and environment) and the effect of the G×E interaction were used for determination of ideal (more stable and high yielding) genotypes. An ideal genotype is a genotype with high yield average and *IPCA* values close to zero. An undesirable genotype is a genotype with low yield average and high *IPCA* values (Kendal *et al*., 2016; Sayar, 2017). Besides, GGE Biplot was employed to analyze the multi environmental trial data.

RESULTS AND DISCUSSION

AMMI for seed yield of 15 chickpea genotypes at 12 environments are presented in Table 3. The analysis revealed that Kabuli chickpea yield were significantly ($P\leq 0.01$) affected by Environments (E), Genotypes (G), and GEI. The main effects of environments and genotypes accounted for 44.23 and 4.8%, respectively. Genotype by environment interaction effect attributed to 28.9% of the total sum of squares. Similarly, Sayar (2017) reported that the most effective factor on yield performance of genotypes was the environmental effect (42.23%). It was followed by GEI effect (36.13%) and genotype effect (21.64%).

Large amount of environment sum of squares imply that environment has created main portion of variations in seed yield in dryland cultivation of Kabuli chickpea in Iran. Similarly, Tilahun *et al*. (2015) reported that the main portion of Kabuli chickpea seed yield variations in Ethiopia was created by environment. The magnitude of the genotype by environment sum of squares was two times more than that for genotypes, indicating that there were considerable differential in genotype responses across environments. Formerly, the presence of significant genotype by environment interactions for chickpea and

[DOR: 20.1001.1.16807073.2018.20.2.13.7]

different crops reported by many agricultural researchers (Singh and Bejiga, 1990; Duzdemir, 2011; Farshadfar *et al*., 2011, 2013; Sayar *et al*., 2013:Tilahun *et al*., 2015; Mortazavian *et al*., 2014; Kanouni *et al*., 2015; Sayar and Han, 2016; Kendal and Sayar, 2016). Significant effect of GEI implied the importance of stability analysis and splitting of GEI to its parts (Najafian *et al*., 2010; Mortazavian *et al*., 2014).

GEI sum of square was significantly ($P \leq 0.01$) affected by five principal components (IPCA 1 to IPCA 5). The IPCA1 and IPCA2 components accounted for 25.6 and 20.8% of the total GEI sum of squares, respectively (Table 3).

Stability Analysis of Genotypes

The first two components coefficients of GEI are the simplest method to select stable genotypes (Annicchiarico, 1997: Grausgruber *et al*., 2000; Purchase *et al*., 2000; Mohammadi *et al*., 2008; Kilic, 2014, Sayar *et al*., 2016). Based on the results, the lowest amount of IPCA 1 belonged to G15, G7, G12 and G14, respectively. Also, low amount of IPCA 2 was specialized to genotypes G10, G7, G13, and G12, respectively (Table 4). Genotypes with low amount of IPCA1 and IPCA2 scores have negligible role in genotype by environment interaction effect and IPCA1 and IPCA2 coefficient closer to zero, indicating genotype stability (Farshadfar *et al*., 2013: Kilic, 2014; Kendal *et al*., 2016; Sayar *et al*., 2016; Sayar, 2017).

AMMI Stability Value (ASV) is also one of parameters that are used to estimate genotypes stability. *ASV*, in fact, is distance of a special genotype from the origin coordinates of IPCA 1 against IPCA 2 two-dimensional scatter plot. Lower amount of *ASV* value shows greater stability of genotypes (Purchase *et al*., 2000). Genotypes G7, G12, G4 and G14, respectively, were the more stable genotypes because of having the lowest amount of *ASV*. Genotypes G2, G5, and G8 with a maximum amount of *ASV* were the less stable genotypes (Table 4). Genotypes G1, G12 and G14, respectively, were the more stable genotype because of having the lowest amount of *GSI* (Table 4). Genotypes G5, G15, G6 and G10 with a maximum amount of *GSI* were the less stable genotypes (Table 4).

Ranking genotypes based on yield mean values and coefficients of the first two GEI components (IPCA 1 and IPCA 2) showed that G14 and G12 genotypes with high yield and low coefficients were the most stable genotypes. Following these two genotypes, genotype G4 with medium yield and high stability was the best genotype (Table 4).

G1 was included in the four superior genotypes in ten environments (Table 5). This genotype had the highest yield average, the medium amount of *ASV* and high interaction coefficients of the first two AMMI components (Table 4). G2 and G8,

Table3. Additive Main effects and Multiplicative Interaction (AMMI) analysis of variance for grain yield (g m^{-2}) of the 15 Kabuli-type genotypes tested across 12 environments.

Source	df	SS	MS	F	Prob level	Explained (%)
Genotypes (G)	14	27499	1964	9.00	0.000	4.83
Environments (E)	11	251989	22908	32.88	0.000	44.24
G*E	154	164771	1070	4.90	0.000	28.93
IPCA1	24	42232	1760	8.06	0.000	25.6
IPCA2	22	34265	1558	7.13	0.000	20.8
IPCA3	20	26033	1302	5.96	0.00	15.8
IPCA4	18	21978	1221	5.59	0.00	13.3
IPCA5	16	17003	1063	4.87	0.00	10.3
Residual G×E	54	23259	431	1.97	0.0001	14.1
Total	719	569611	792			

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Table 4: Grain yield mean (g m^{-2}), first and second Interaction Principal Components Analysis (IPCA), AMMI Stability Value (ASV) and Genotype Stability Index (GSI) of 15 chickpea genotypes over 12 environments.

Genotype	Grain yield mean	Rank grain yield	IPCA 1	Rank IPCA 1	IPCA 2	Rank IPCA 2	ASV	Rank ASV	GSI
G1	71.43	1	-2.66448	10	-2.04563	12	3.594013	7	8
G2	69.68	2	-4.60291	14	-0.727	5	5.156381	13	15
G3	63.81	4	-1.074	6	3.77919	13	3.962455	9	13
G4	58.25	9	0.51973	5	-1.40511	7	1.518743	3	12
G5	49.53	15	4.82565	15	-1.58415	8	5.581435	14	29
G6	55.96	11	4.55317	13	-0.83637	6	5.118504	12	23
G7	52.86	14	0.20587	2	0.56694	2	0.611189	1	15
G8	66.44	3	-1.35833	9	-6.05899	15	6.243459	15	18
G9	56.08	10	-1.29478	7	1.78842	10	2.293575	5	15
G10	54.25	12	-3.55412	12	0.43979	1	3.966168	10	22
G11	58.55	8	1.32486	8	1.93439	11	2.429162	6	14
G12	58.68	7	-0.27542	3	0.60718	4	0.679684	2	9
G13	62.88	5	3.29323	11	0.57413	3	3.697218	8	13
G14	62.36	6	0.28715	4	-1.60492	9	1.636211	4	10
G15	53.01	13	-0.18562	1	4.57211	14	4.576742	11	24

Table 5. Yield total average, four high performances AMMI recommended genotypes and yield improvement amount through planting of these genotypes in each environment.

Environment	Yield total average (g m^{-2})	Four AMMI recommended genotypes	Yield (g m^{-2})	Yield improvement (g m^{-2})	Environment	Yield total average (g m^{-2})	Four AMMI recommended genotypes	Yield (g m^{-2})	Yield improvement (g m^{-2})
E1	72.86	G2	117.72	44.86	E7	56.9	G8	72.53	15.63
		G8	88.78	15.92			G1	70.57	13.67
		G1	104.49	31.63			G2	65.75	8.85
		G10	94.58	21.72			G14	62.33	5.43
E2	61.74	G8	104.6	42.86	E8	45.42	G3	64.34	18.92
		G13	65.92	4.18			G6	52.97	7.55
		G1	82.75	21.01			G15	60.34	14.92
		G14	74.93	13.19			G11	58.17	12.75
E3	37.95	G1	54.35	16.4	E9	50.47	G2	72.91	22.44
		G2	53.17	15.22			G1	68.27	17.8
		G14	42.02	4.07			G3	60.47	10
		G8	52.04	14.09			G8	56.69	6.22
E4	67.25	G13	81.71	14.46	E10	38.1	G13	48.62	10.52
		G3	77.87	10.62			G6	43.98	5.88
		G11	75.01	7.76			G1	43.61	5.51
		G6	74.94	7.69			G3	41.17	3.07
E5	43.07	G8	60.9	17.83	E11	54.93	G13	63.62	8.69
		G1	56.29	13.22			G1	63.13	8.2
		G2	49.81	6.74			G8	62.26	7.33
		G14	49.43	6.36			G6	59.52	4.59
E6	102.91	G3	123.8	20.89	E12	83.42	G14	88.07	4.65
		G2	121	18.09			G2	91.57	8.15
		G15	113.9	10.99			G1	95.86	12.44
		G1	113.3	10.39			G13	88.05	4.63

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which showed high average for performance after G1, were superior in seven environments (Table 5). G3, G13, and G14 were superior in five environments and were categorized as the best genotypes, too (Table 5).

Sustainability index values, the average performance, the standard deviation, and the best performance of different genotypes are shown in Table 6. Genotypes divided into two categories based on *SUI*. Genotypes G1, G4, G6, G8, G13, and G14 with *SUI* more than 35% were categorized in medium stability group. All other genotypes had *SUI* less than 35% and were categorized in low stability group (Table 6). None of the genotypes were in the high stability group.

Differences in genotype stability and adaptability to environment can be considered through depicting a two-dimensional Biplot (Figure 1), of which the *x*-coordinate indicates the main effects (environment and genotype means) and the *y*-coordinate indicates the effects of the interaction, IPCA 1 or IPCA 2, (Vita *et al*., 2010, Kendal and Tekdal, 2016).

It is clear from Figure 1 that the points for environment are more scattered than the points for genotypes, indicating that variability due to environments is higher than that due to genotypes. This result is in complete agreement of ANOVA (Table 3). Values closer to the origin of *y*-coordinate provide a smaller contribution to the interaction and either direction away from the Biplot origin indicates greater genotype by environment interaction and reduced adaptability (Gauch, 1992).

Based on Figure 1, some of the environments (E3, E4, E6, E8, and E10 and E12) and some of the genotypes (G2, G5, G6, G10 and G13) stood out with a high contribution to the interaction. Only in environments E1, E2, E4, E6, and E12, averages were recorded above the overall averages, indicating that these environments were favorable to obtain high mean performance for chickpea production

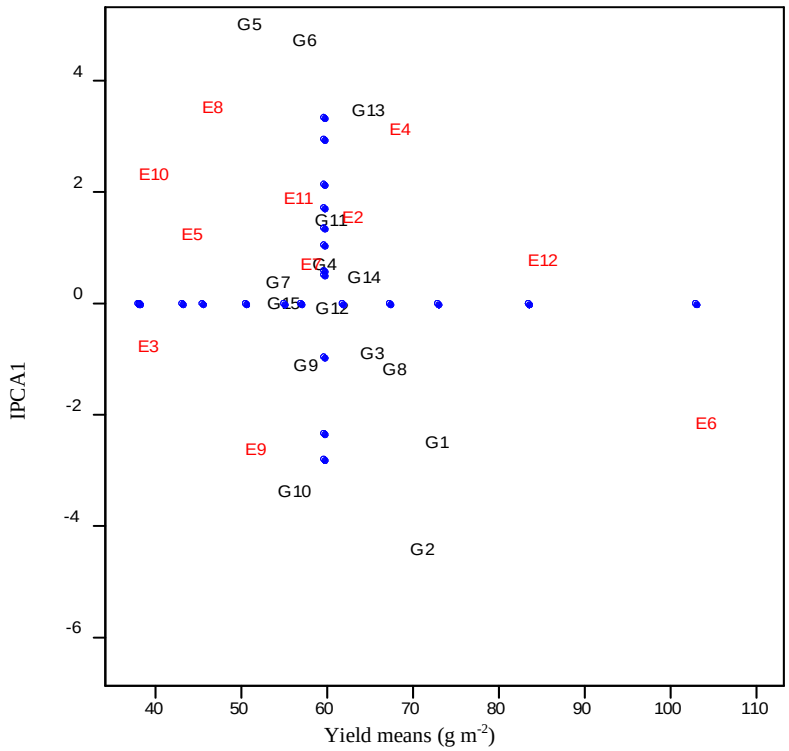

Figure 1. Bi-plot of the first Interaction Principal Component (IPCA 1) versus yield means of different environments and genotypes.

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Table 6. Mean, Maximum, Minimum, standard deviation of yield (g m^{-2}) and Sustainability Index (SUI %) of 15 chickpea genotypes over 12 environments.

Genotype	Mean	Max	Min	SD	SUI (%)	Stability
G1	71.43	113.3	38.46	23.47	39.07	Medium
G2	69.68	121	36.62	27.66	32.06	Low
G3	63.81	123.8	38.43	25.39	28.64	Low
G4	58.25	95.1	37.46	18.62	38.48	Medium
G5	49.53	77.9	24.82	19.42	35.68	Low
G6	55.96	85.5	30.78	19.15	39.74	Medium
G7	52.86	97.8	30.48	19.72	31.28	Low
G8	66.44	104.6	18.43	25.05	36.52	Medium
G9	56.08	109.1	32.36	22.81	28.14	Low
G10	54.25	107.5	25.28	25.76	24.46	Low
G11	58.55	106	33.75	20.41	33.21	Low
G12	58.68	104.9	36.72	20.27	33.79	Low
G13	62.88	100.7	37.52	18.92	40.30	Medium
G14	62.36	99	41	18.85	40.57	Medium
G15	53.01	113.9	26.35	25.88	21.98	Low

(Figure 1).

The genotypes which are characterized by means greater than grand mean and the *IPCA* score nearly zero are considered as generally adaptable to all environment (Rashidi *et al*., 2013). However, the genotypes with high mean performance and with large value of *IPCA* score are consider as having specific adaptability to the environments. Therefore, on the Biplot, the points for the generally adapted genotypes would be at right hand side of the grand mean levels (this suggests high mean performance) and close to the line showing *IPCA* equal to zero (this suggests negligible or no genotype by environment interaction).

It appears from Figure 1 that the majority of genotypes occupied an intermediate position, relatively similar to the check cultivars Azad (G14) and Hashem (G15). Genotypes G12 and G15 were the most stable genotypes, as indicated by values near the origin of the IPCA 1 axis, which is indicative of a smaller contribution to the

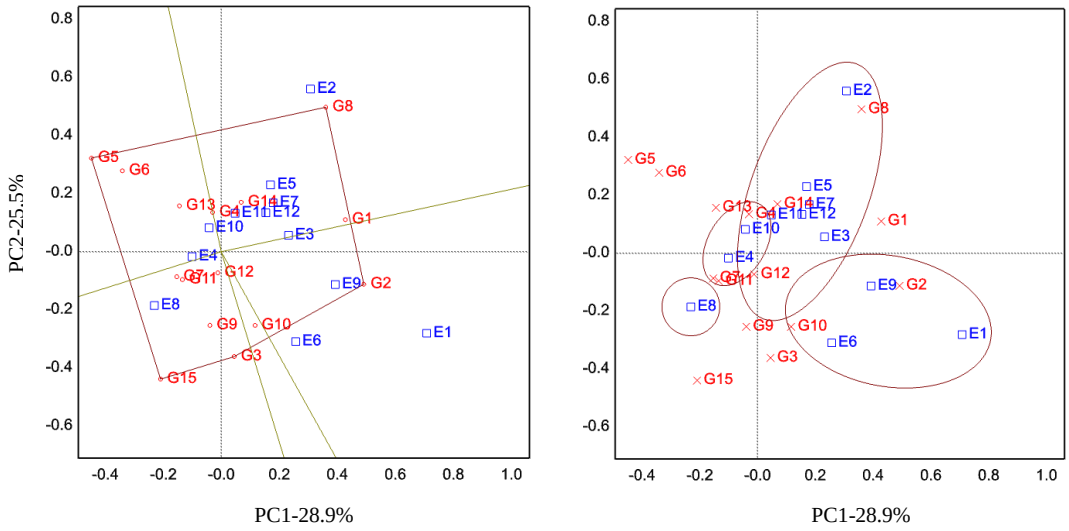

Figure 2. Polygon view of GGE Biplot (A) and the mega environments division (B) for the which-won- where pattern of 15 chickpea genotypes in 12 environments.

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GEI. Following these two genotypes, genotypes G3, G4, G7, G8, G9, G11 and G14 showed greater stability and smaller contribution to the GEI. However, the yield mean of G7, G9, and G15 genotypes were less than the average, therefore, these genotypes could not be recommended. On the other hand, genotypes G3 and G8 were stable and their yield mean were more than overall average (Figure 1). Range of yield improvement through planting of G3 and G8 genotypes were estimated from 10 to 20.89 and from 6.22 to 42.86 g m^{-2} in different environment, respectively (Table 5).

The genotypes G4, G11, G12 and G14 were stable, and their performance was close to the overall average (Figure 1). Therefore, these genotypes could be recommended as stable genotypes. On the other hand, G1, G2, G5, G6, G10 and G13 were the most unstable genotypes because they were more distant from the Bi-plot origin.

In order to observe the pattern of interaction between genotype and environment and interpret the results, Bi-plot polygons were used (Yan and Kang, 2003). This polygonal view graphically addresses important concepts such as crossover GE, mega environment differentiation and specific adaptation and have been used in several research (Yan and Tinker, 2006; Farshadfar *et al*., 2011; Imtiaz *et al*., 2013; Mortazavian *et al*.,2014; Kanouni *et al*., 2015). Polygonal display of current study consisting of 15 genotypes in 12 environments is shown in Figure 2-A. In this figure, a polygon was made through connecting genotypes with highest distance to the origin of biplot. Genotypes located on the vertices of the polygon performed either the best or the poorest genotype in one or more locations. Genotypes G2, G3, G5, G8, and G15, which formed vertices of the polygon, had the longest distance from plot origin. G8, G2, and G3 were the best genotypes in their environment. G5 and G15 were the worst genotypes in their environment. Genotypes, G9, G12 and G4, which were close to the origin of coordinate, produced average yield in all experimental environments.

Five lines divided the Bi plot to the five sections and environments fell in four sections, 3 of which were mega environment (Figure 2-B). Vertex genotype(s) for each sector has higher yield than the others in all environments that fall in the sector. The first mega environments consist of seven environments including E2, E5, E7, E3, E10, E11, and E12. G8 was the more stable and high yielding genotype of this sector. Similarly, E1, E6, and E9 were located in the second mega environment. G2 was the best genotype in the second sector. E8 alone was placed in an environmental group and G15 was the vertex genotype in this location. G5 was the vertex genotype in E4 and E10 environments (Figure 2).

Totally based on Figure 2, among 12 studied local landraces, yield of genotypes G1, G2, G3, G8, and G10 were more than the overall average. Genotypes G8, G5, and G6 were the more stable genotypes. Genotype G12 with lowest amount of both *IPCA* and yield near the overall average was also a remarkable genotype with general adaptation to all of the experimental environments. G12 was also a remarkable genotype from stability analysis indices like IPCA1 and IPCA2, and *ASV* point of view. Therefore, these genotypes could be recommended as new superior and more stable genotypes.

CONCLUSIONS

Results of the study showed that environmental effect is the most effective factor on grain yield of Kabuli type chickpea genotypes in Iran's dryland conditions. And, with high grain yield averages, Kermanshah and Urmia locations were found as favorable environments for chickpea cultivation. The grain yield performance and stability status of G1, G2, G3, G8, and G12 landraces were found to be higher and better than that of the chickpea varieties used as check. Consequently, the superior chickpea landraces found in this study should be improved for grain production in Iran conditions.

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شناسایی ژنوتیپ های پر پتانسیل و پایدار نخود بانک ژن گیاهی ملی ایران برای کشت در مناطق دیم

م. پوراسماعیل، ه. کانونی، م. حاج حسنی، ح. آسترکی، ع. میرآخورلی، م. نصرالهی و ج. مظفری

چکیده

شناسایی ژنوتیپ‌های پایدار و دارای عملکرد بالا از اهداف مهم تولید نخود در مناطق خشک ایران است. با این هدف، پایداری عملکرد دوازده ژنوتیپ بومی نخود تیپ کابلی همراه با سه رقم شاهددر قالب طرح بلوک کامل تصادفی با چهار تکرار طی سه سال زراعی متوالی (۹۲-۱۳۹۰) در چهار استان مختلف مورد مقایسه قرار گرفت. تجزیه واریانس مرکب به منظور بررسی وجود تفاوت بین ژنوتیپ‌ها و

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تجزیه مدل اثرات اصلی افزایشی و ضرب پذیر(AMMI) به منظور تحلیل اثرات متقابل مورد استفاده قرار گرفت. پایداری ژنوتیپ ها از طریق رتبه بندی آنها بر اساس پارامترهای مختلف نظیر ضرایب مولفه های اصلی، آماره پایداری AMMI (ASV) ، شاخص پایداری و شاخص انتخاب ژنوتیپ(GSI) برآورد شد. اثرات ساده و اثرات متقابل عوامل مختلف به جز صفت ارتفاع کانوپی بر روی کلیه صفات از لحاظ آماری معنی دار بود($P\leq0.05$). معنی دار بودن اثرات عوامل مختلف نشان دهنده وجود تنوع بین ژنوتیپ‌های مورد مطالعه است که فرصتی را برای شناسایی ژنوتیپ جدید برتر برای هر مکان فراهم می کند. تجزیه و تحلیل AMMI نشان داد سه مولفه اصلی ۶۲ درصد از تغییرات اثر متقابل ژنوتیپ × محیط را توجیه می نمایند. بر اساس نتایج به دست آمده، ژنوتیپ‌هایG1، G2، G3، G8و G12 بالاترین میانگین عملکرد را داشته و از نظر پایداری عملکرد مشابه ارقام شاهد بودند. از اینرو می توان در برنامه های اصلاحی برای توسعه ارقام جدید از این منابع ارزشمند استفاده نمود.

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