Multi-environment Yield Trials of Grass Pea (*Lathyrus sativus* L.) in Iran Using AMMI and SREG GGE

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ABSTRACT

Grass pea (*Lathyrus sativus* L.) is a crop used for both animal and human consumption. Recently, ICARDA has developed new grass pea lines with the objectives of improving its yield potential and adaptability. The objective of this study was to investigate grain and forage yields stability of several ICARDA released grass pea lines by using additive main effects and multiplicative interactions (AMMI) and site regression genotype plus genotype-by-environment interaction (SREG GGE) model. Fourteen grass pea advanced lines were evaluated at three research stations located in semi-warm regions in Iran, during 2005-08 crop seasons. The combined ANOVA showed that forage and grain yields were significantly affected by environment (E), genotype (G) and interactions of G×E. The partitioning of the sum of squares indicated that E accounted for 85% and 91% of the total (G+E+GEI) variation for forage and grain yields, respectively; whereas, G and GEI accounted for 4 and 11% for forage yield and 2 and 7% for grain yields, respectively. Using AMMI and GGE biplots, the lines identified as stable and high grain yielding were Sel.474, Sel.669, and Sel.686, while for forage yield the lines were Sel.474, Sel.678 and Sel.669. Kermanshah and Gachsaran were selected as favorable test environments for grass pea grain and forage yield ME trials, respectively.

Keywords: AMMI, GEI, GGE, Grass pea, Stability.

INTRODUCTION

Grass pea (*Lathyrus sativus* L.) has been a traditional crop both for animal consumption, as forage and grain, and for human consumption, as a food grain. Three main qualities of this grain legume consist of its sturdiness, drought tolerance, and adaptability to a wide range of soil types, including the marginal ones. Also, high protein content makes this species interesting as a forage crop (Polignano, 2007). With all grass pea advantages, until recently, relatively little effort has been made towards the improvement of this crop. Using a rich collection of *Lathyrus* spp.

germplasm, ICARDA is collaborating with national partners to develop new grass pea lines with the objectives of improving its yield potential and adaptability. Genotype×environment interaction (GEI) due to different responses of genotypes in diverse environments makes choosing the superior genotypes difficult in plant breeding programs. Relatively few reports provide information on the GEI studies in grass pea. Abd El-Moneim and Cocks (1992) compared 16 promising lines of grass pea under rain-fed conditions in Syria. Also Hanbury *et al.* (1999) evaluated a selected number of lines for grain yield in Mediterranean-type environments. Their

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results clearly demonstrate the role of the environment on the performance of lines tested and the importance of GEI studies in grass pea breeding strategies. For this reason, multi-environmental trials (METs) are conducted throughout the world for major crops every year (Ma *et al*., 2004). Numerous parametric and nonparametric methods have been used in trying to understand the pattern of GE interaction (Yan and Hunt, 2001; Crossa *et al*., 2002). Although these methods may differ in overall appropriateness, different methods usually lead to the same or similar conclusions for a given dataset. Recently, Yan *et al*. (2000) proposed a GGE biplot that allows visual examination of the GEI pattern of MET data. GGE biplot clearly shows which cultivar won in which environments, and thus facilitates mega-environment identification (Yan and Rajcan, 2002). A mega environment is defined as a group of locations that consistently share the same best cultivar(s) (Yan and Rajcan, 2002). Another essential requirement for mega-environment differentiation is repeatability of the which-won-where pattern. Therefore, multi-site trials conducted over years are essential for addressing the mega-environment issue (Yan and Hunt, 1998; Yan *et al*., 2000). The additive main effects and multiplicative interaction analysis (AMMI) and GGE biplot methodology have been used to evaluate test environments in soybean (Yan and Rajcan, 2002), cotton (Blanche and Myers, 2006) and common bean (Kang *et al*., 2006), and to characterize end-use quality in wheat (Morris *et al*., 2004; Najafian *et al*., 2010) and to target cultivars

to specific environments in rice (Samonte *et al*., 2005).

Thus, our objective was to investigate grain and forage yield stability of several ICARDA released grass pea advanced lines tested across a number of diverse Iranian rain-fed environments by using AMMI and SREG GGE models. This information will be useful to plant breeders in fine-tuning the testing program by targeting appropriate genotypes to different locations and by identifying representative testing sites.

MATERIALS AND METHODS

Fourteen grass pea (*Lathyrus sativus* L.) advanced lines were tested across nine environments, including three semi-warm sites in Kermanshah, Gachsaran and Lorestan (Table 1) during 2005-2008 growing seasons under rain-fed conditions. As the study seasons differed in terms of mean seasonal rainfall, locations in each year were considered as different environments and the combinations of three years and three locations were treated as nine environments. The plant material (fourteen advanced lines developed by ICARDA) in the present study included G1 (Sel.515), G2 (Sel.1326), G3 (Sel.474), G4 (Sel.1329), G5 (Sel.686), G6 (Sel.459), G7 (Sel.669), G8 (Sel.1307), G9 (Sel.554), G10 (Sel.1332), G11 (Sel.678), G12 (Sel.736), G13 (Sel.1327), and G14 (Sel.1321). The experimental layout was a randomized complete block design with three replications. Each plot had four rows of 4.5 m length with spacing of 25 cm between rows. The seeding rate was 150 seeds per m^2. Forage (at 50% flowering stage) and

Table 1. Agro-climatic characteristics and rainfall data of experimental sites in Iran where the experiments were conducted.

Stations	Coordinate		Altitude (m)	Rainfall (mm)		
	Longitude (E)	Latitude (N)		2005-2006	2006-2007	2007-2008
Gachsaran	50.5	30.17	710	560.7	511.2	184.5
Lorastan	48.28	33.39	1125	438.3	557.8	251
Kermanshah	47.07	34.19	1322	505	551	159.2

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grain yields at physiological maturity (kg ha^{-1}) were obtained by converting the yields obtained from the plots to hectares. SAS software was used to perform combined analysis of variance. Total SS were partitioned into proportions due to environments, cultivars, and cultivars×environment interaction. The GGEbiplot software (Yan, 2001) was used to generate graphs showing (i) "which-won-where" pattern, (ii) ranking of cultivars on the basis of yield and stability, (iii) location vectors, and (iv) comparison of genotypes with ideal genotype (Yan and Kang, 2003).

RESULTS

Combined Analysis of Variance

The results of combined analysis of variance for grain and forage yield across locations and years are given in Table 2. Analysis of variance indicated significant GE interaction (P< 0.01 and 0.05) for both forage and grain yield of the genotypes evaluated. Thus, it is important to study adaptation patterns, genotypes response, and their stability in multi-environments trials. The main effect of genotype (G), location (L) and year (Y) were significant at the *P*< 0.01 and 0.05 level for forage and grain yields. The partitioning of the sum of squares indicated that E accounted for 85% of the total (G+E+GEI) variation for forage yield and 91% for grain yield (Table 2), whereas G and GEI, accounted for 4 and 11% for forage yield, 2 and 7% for grain yield, respectively (Table 2). The means for forage and grain yields of the grass pea lines are given in Table 3 and the maximum yield values of each trait are bolded. Overall, the forage yield means of the genotypes varied from 4.776 t ha^{-1} for G10 to 6.177 t ha^{-1} for G3. In the case of grain yield, it varied from 1.269 t ha^{-1} for G10 to 1.548 t ha^{-1} for G3 (Table 3). The environment forage yield means varied from 2.61 t ha^{-1} at Kermanshah2008 to 7.63 t ha^{-1} at Gachsaran2007. Also the environment grain yield means varied from 0.41 t ha^{-1} at Kermanshah2008 to 2.23 t ha^{-1} at Lorestan 2007.

Crossover G×E Interaction Using AMMI Model

Table 2. Combined Analysis of variance for grain and forage yield (t ha^{-1}) of 14 Grass pea advanced lines grown in 9 different rainfed environments of Iran.

Source of Variation	DF^a	MS^b		Explained % of model SS^c	
		Forage yield	Grain yield	FY	GY
Environment (E)	8	144.1**	18.3**	85	91
Location (L)	2	9.94**	19.7**		
Year (Y)	2	554.7**	49.95**		
Year×Location (Y×L)	4	5.86**	1.76**		
Block/Environment (B/E)	18	2.79	0.14		
Genotype (G)	13	4.46**	0.17*	4	2
Genotype×Environment (G×E)	104	1.35**	0.106*	11	7
Genotype×Year (G×Y)	26	1.78**	0.16**		
Genotype×Location (G×L)	26	1.51**	0.07 ^{ns}		
Genotype×Year×Location (G×Y×L)	52	1.05**	0.09 ^{ns}		
Pooled error	234	0.66	0.082		
Total	377				
CV%		15.4	20.8		

**, *: Significant at the 0.01 and 0.05 probability levels; ns: non significant.
^{a} Degree of freedom; ^{b} Mean sum of squares, ^{c} Sum of squares.

Table 3. Mean yield data and mean comparisons of 14 grass pea advanced lines and 9 testing environment for grain and forage yields.

Code	Genotype	Forage Yield (t ha⁻¹)		Grain Yield (t ha⁻¹)		Environment	Forage Yield (t ha⁻¹)		Grain Yield (t ha⁻¹)	
G1	Sel.515	5.46	Bc*	1.38	abc	Ker6	5.82	de	1.13	e
G2	Sel.1326	5.1	bcd	1.3	bc	Gac6	6.05	cd	2.02	b
G3	Sel.474	6.18	a	1.55	a	Lor6	5.46	e	2.07	ab
G4	Sel.1329	4.83	cd	1.31	bc	Ker7	7.15	b	1.29	d
G5	Sel.686	5.67	ab	1.45	abc	Gac7	7.63	a	1.69	c
G6	Sel.459	5.26	bcd	1.38	abc	Lor7	6.51	c	2.23	a
G7	Sel.669	5.35	bcd	1.41	abc	Ker8	2.61	g	0.41	h
G8	Sel.1307	4.79	d	1.33	bc	Gac8	3.12	f	0.68	g
G9	Sel.554	5.69	ab	1.48	ab	Lor8	3.22	f	0.86	f
G10	Sel.1332	4.78	d	1.27	c					
G11	Sel.678	5.39	bcd	1.35	bc					
G12	Sel.736	5.49	bc	1.39	abc					
G13	Sel.1327	4.84	cd	1.27	c					
G14	Sel.1321	5.21	bcd	1.36	bc					

Environment is designated as locations first letters (Kermanshah, Gachsaran and Lorestan) followed by 6, 7 or 8 (i.e. 2005-2006, 2006-2007 and 2007-2008) to indicate year.
* Means followed by similar letters are not significantly different at the 0.01 probability level according to Duncan's multiple range test.

An indication of the presence of GE interaction is the differential ranking of genotypes across environments. The performance of the lines was evaluated with nominal yields across environment PC1 scores based on AMMI model (Figures 1-a and -b). Such analysis helps in targeting genotypes onto its growing environments (Samonte *et al*., 2005). Therefore, the adaptation patterns of the genotypes were assessed based on average environment PC1

score, which was 0.055. It is very common for multi-environmental yield trials (MEYTs) data to embody a mixture of crossover and non-crossover types of GEI. In this study, different lines produced the highest grain and forage yields (Figures 1-a and -b) at different environments. Therefore, the differential rankings of genotypes across test environments revealed a plausible existence of crossover GEI. In the case of grain yield (Figure 1-a), G3, G9, and G8
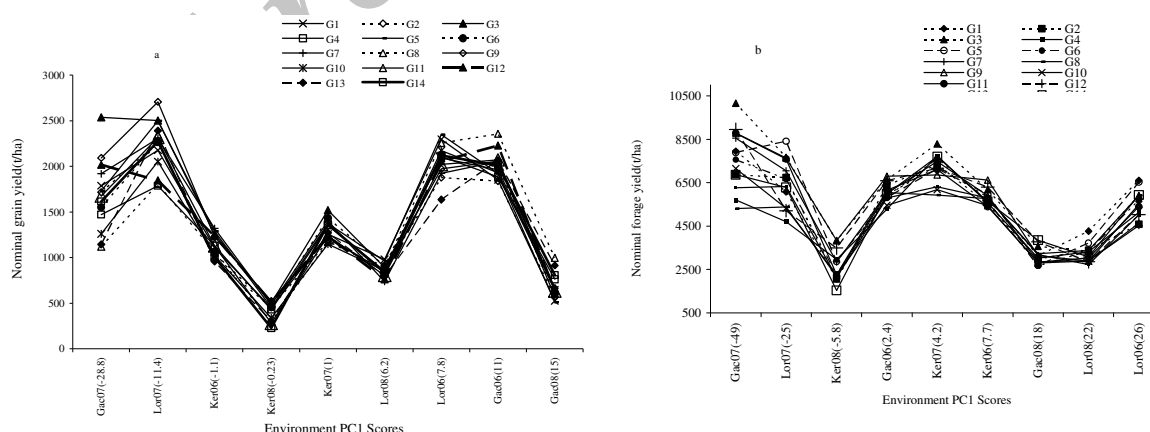
Figure 1. Nominal: (a) Grain yield and (b) Forage yield of 14 grass pea advanced lines based on AMMI model equation without environmental deviation, across environment PC1 score.

were the highest yielding lines at two environments, while G1, G5, and G7 were the highest at one environment. In the case of forage yield (Figure 1-b), G3 was the highest yielding line at three environments, G9 and G1 were the highest yielding lines at two environments, and G5 and G14 were the highest at one environment. Based on the frequency that genotypes were expected to yield highest in an environment, G3 (Sel.474) and G9 (Sel.554) were the best qualified (both for grain and forage yields) for national recommendation for cultivation by growers.

G×E Relations as Winning Genotype and Mega-environment

There are numerous ways to look at a GGE biplot, but the polygon view of a biplot is most relevant to the investigation of the mega-environments and visualization of the "which-won-where" pattern of MET data (Yan *et al*., 2000, 2001). The polygon is a succinct summary of the GEI pattern of a MEYT data set. With the present data set, the biplots (Figures 2-a and -b) explained 75.7 and 72.8% of the variations for grain and forage yields in this study, respectively. Crossover-type GEI was evident in the GGE biplots constructed for examination of GE interaction (Figure 2). That is, genotypes are partitioned into distinct sectors of the biplot. For grain yield (Figure 2-a), the genotypes G3, G9, G13, G8 and G12 expressed a highly interactive behavior. Connecting the extreme genotypes on a GGE biplot forms a polygon and the perpendiculars to the sides of the polygon form sectors of genotypes and environments. The genotypes at vertex are the winners in the environments included in that sector. Five rays in Figure 2-a divide the biplot into five sectors and the environments fall into four of them. Five environments, Gac2007, Ker in (2006, 2007 and 2008) and Lor2008 fell into sector 1 and the vertex genotype for this sector was G3 (Sel.474). A single environment, Lor2007, fell into sector 2 and the vertex genotype for this sector was

the G9 (Sel.554). Two environments, namely, Gac2006 and Gac2008, fell into sector 4 and the vertex genotype for this sector was the G8 (Sel.1307). Lor2006 with vertex genotype G12 (Sel.736) fell into sector 5. These four sectors were identified as four mega-environments.

The length of an environmental vector is an estimation of discriminating power of the environment (Yan *et al*., 2007). Gac2006 with longer vector (Figure 2-a) was more discriminating of the genotypes. Kermanshah in all years was relatively closer to biplot origin (Figure 2-a) and, hence, less interactive location and could be a good enough location for selection of genotypes with average adaptation. In Figure 2-b, polygon view for forage yield is presented. Two mega-environments are suggested in Figure 2-b. The first mega-environment contains environments Gac2006, 2007, 2008 and Ker2006, 2007, 2008, with genotype G3 (Sel.474) being the winner. The second mega-environment contains environments Lor2006, 2007, 20008, with genotype G5 (Sel.686) being the winner (Figure 2-b). As expected from Figure 2 (c, d) across three years, Lorestan was different from the other two sites in discriminating among the genotypes; even this difference was large enough for Lorestan to have a different winning cultivar G5. Therefore, it could be a strong case to conclude that Lorestan represents a mega-environment different from the other sites.

A mega-environment should be defined as part of the growing region of a crop represented by a group of sites among which there are no major repeatable crossover GE interactions. Consequently, for a given mega-environment, there exists a cultivar that performs best at all sites when evaluated over several years. Following this definition, a mega-environment can be simple or complex. A simple mega-environment involves no crossover GEI at all, whereas a complex mega-environment involves crossover GEI's that are not repeatable over years. For a simple mega-environment, one or a few test sites would be sufficient for
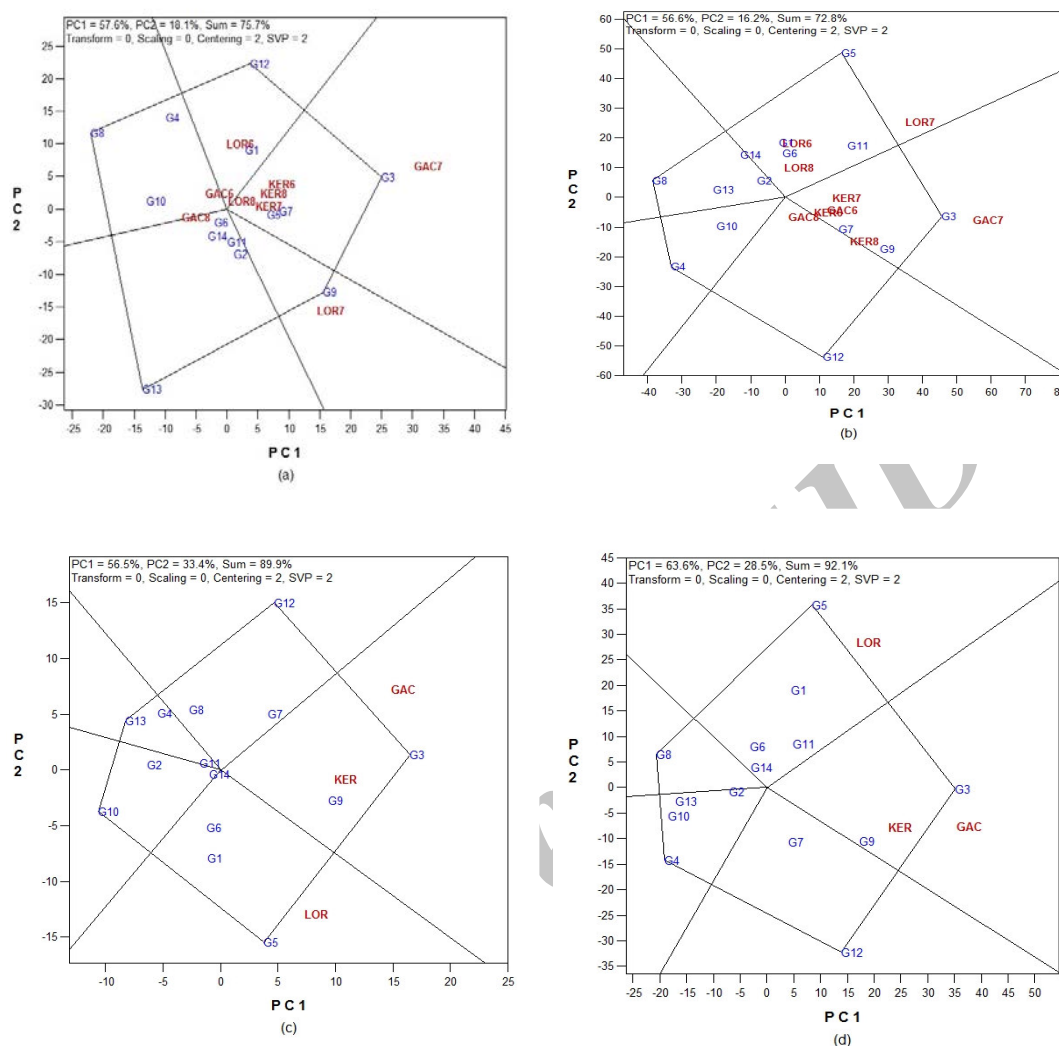
Figure 2. Polygon views based on the: (a, c) Grain yield and (b, d) Forage yield data of 14 grass pea advanced lines. (a, b) The genotype by environment biplot taking each year-site combination as a single environment, (c, d) The genotype by site biplot on the basis of data averaged over years.

effective cultivar evaluation. However, for a complex mega-environment, distinct test sites are required to select cultivars that are superior across the whole region over years. Based on the genotype by environment relations in Figure 2 (c, d), the semi-warm rain-fed zone of Iran seems to be a single complex mega-environment, with Lorestan as a unique test site. On the other hand, Gachsaran always grouped together with Kermanshah, suggesting that it provided no unique information on the genotype performances. Consequently, in future tests, Lorestan should always be used as a test site but Gachsaran or Kermanshah can be removed from the test sites.

Mean Yield and Stability of Genotypes

The mean yield and stability effects of the genotypes were examined by defining an average tester coordinate (ATC). The average (virtual) environment is indicated by

a circle and shows the positive end of the ATC *x* axis (Figure 3). The average yield of the genotypes is approximated by the projections of their markers on the ATC *x* axis. Genotypes with above-average grain means (in order G3> G9> G7> G12> G5> G1) were selected, whereas the rest were discarded (Figure 3-a). G3 (Sel.474) was the most stable genotype as well as high yielding. Conversely, G9 and G12 were the least stable genotype (variable performance) but high yielding. In addition to G3, the performance of genotypes G7 (Sel.669) and G5 (Sel.686) were highly stable. In Figure 3-b, genotypes G3 (Sel.474) and G9 (Sel.554) had the highest and G4 and G8 had the poorest forage mean yield. Genotypes with above-average forage mean yield were in the following order: G3> G9> G5> G11> G7> G12 > G6. The performance of genotypes G3, G11 and G7 were highly stable with high yielding.

Ideal Genotype

An ideal genotype is defined as one that is the highest yielding across test environments and is absolutely stable in performance (Yan and Kang, 2003). Generally, a genotype is more desirable if it is located closer to the ideal genotype. Thus, using the ideal genotype as the center, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype. When the ideal genotype view for grain yield was drawn (Figure 4a), the G3 (Sel.474) in the center of the concentric circles represented the ideal genotype. G7 (Sel.669) and G9 (Sel.554) (in the second concentric circle) were the closest to the ideal genotypes and could be regarded as desirable genotypes. Ranking of other genotypes based on the ideal genotype is presented in Figure 4-a, while the ideal genotype view for forage yield is shown in Figure 4b. Similar to grain yield, G3 (Sel.474) was selected as the ideal genotype for forage yield and G9 (Sel.554), G11
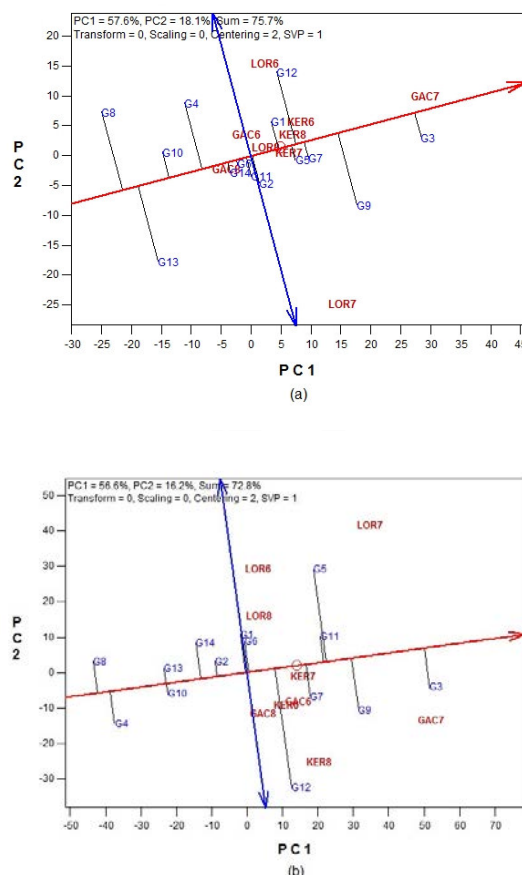

Figure 3. GGE biplot obtained from sites regression (SREG) analysis showing: (a) Grain and (b) Forage yield mean and stability of 14 grass pea advanced lines.

(Sel.678) and G7 (Sel.669) were regarded as the desirable genotypes for forage yield.

Ideal Environment, Discriminating Ability, and Representativeness

An ideal environment should have more power to discriminate genotypes in terms of the genotypic main effect (large PC1 scores) and at the same time more representative of the overall environments (small absolute PC2 scores). Although such an ideal environment may not exist in reality, it can be used as a reference for genotype selection in the MEYTs. An environment is more
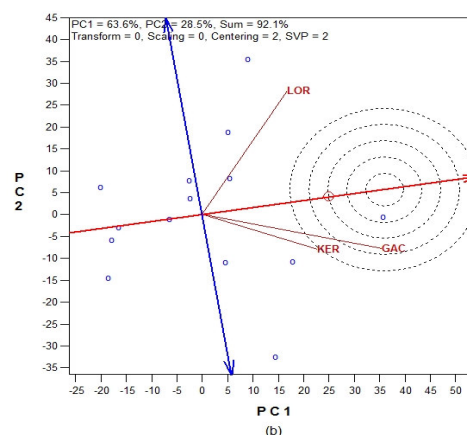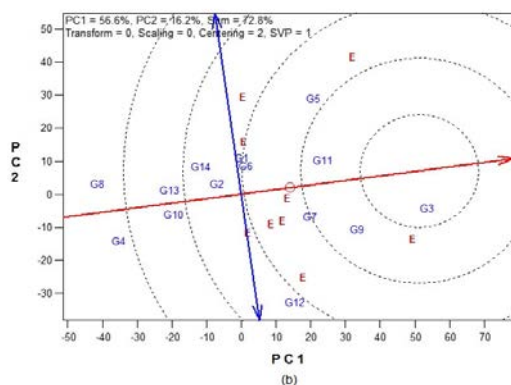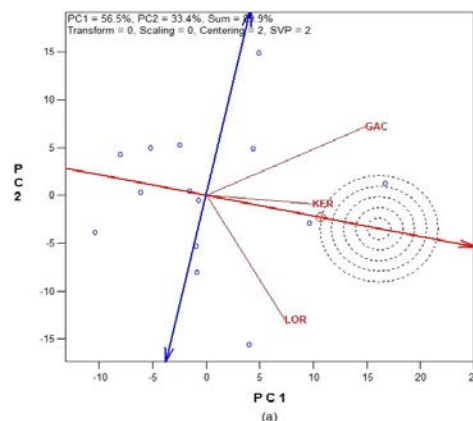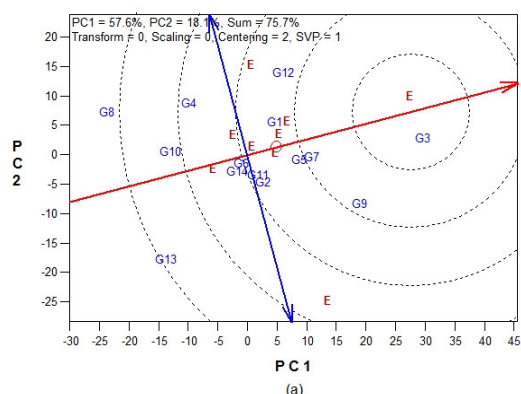
Figure 4. Comparison of 14 grass pea advanced lines against the 'ideal' genotype for: (a) Grain and (b) Forage yield and stability of performance across environments.

Figure 5. Comparison of three experimental locations against the 'ideal' environment for: (a) Grain and (b) Forage yield trails based on discriminating ability and representativeness.

desirable if it is located closer to the ideal environment. Thus, using the ideal environment as the center, concentric circles were drawn to help visualize the distance between each environment and the ideal environment (Yan *et al*., 2000; Yan and Rajcan, 2002). In Figure 5 (a, b), the locations (averaged across three years for grain and forage yields) were ranked based on both discriminating ability and representativeness. Thus, Kermanshah was selected as a favorable test environment for grass pea grain yield ME trials (Figure 5-a), whereas Gachsaran was the favorable test environment for grass pea forage yield ME trials (Figure 5-b). Overall, the poorest test

site relative to the ideal environment was Lorastan, both for grain and forage yields.

DISCUSSION

Stability analysis is an important and efficient tool for the plant breeders and agronomists. It helps to identify and select the most stable, high performing genotypes/varieties that are best suitable under a given set of environmental conditions. The magnitude of genotype×environment interaction (GEI) for grain and forage yields of grass pea

genotypes tested across nine rain-fed environments sampled from the west and southwest of Iranian Plateau was larger than that of the genotype main effect, but smaller than that of environment main effect. Gauch and Zobel (1997) reported that, in normal MEYTs, E accounts for about 80% of the total variation, while G and GE each account for about 10%. The large yield variation due to E, which is irrelevant to genotype evaluation and mega-environment investigation (Gauch and Zobel, 1997; Yan *et al*., 2000), justified the selection of SREG (site regression) as the model and GGE biplot as the appropriate method for analyzing the MET data (Yan *et al*., 2000). The genotypes studied exhibited both crossover and non-crossover types of GEI. The crossover GEI led to differential rankings of genotypes across test environments, thereby making genotypic selection difficult for the rain-fed conditions of Iran. Estimates of genotype nominal grain yield at different environments assisted in the identification of the genotype that yielded the highest at specific environmental IPCA1 ranges or mega-environments, and in the identification of the appropriate genotypes for all locations or for specific locations (Samonte *et al*., 2005). The GGE model aided in determination of the relative performance of genotypes at a specific environment, comparison of the performance of genotypes at different environments, and identification of genotypes suitable for groups of environments. It is clear that the GGEbiplot software is an excellent tool for visual MET data analysis. Compared with the conventional methods of the MET data analysis, the GGEbiplot approach has some advantages (Yan and Hunt, 2001; Yan *et al*., 2007). The visualizing graphic of genotype means and their stability showed different genotype groups and could be classified in four groups. Group one, with high yield and high stability, was greatly desirable and included G5, G12, G1 and G6 for grain yield, and G5, G12 and G1 for forage yield. The second group, which had high yield but

low stability, was desirable for specific selection and included G3, G9 and G7 for grain yield, and G3, G9, G11 and G7 for forage yield. The third group, which had low yield and low stability, included G8, G13, G10, and G4 for grain yield and G8, G4, and G14 for forage yield. This group was considered suitable for special breeding purposes such as drought resistance selection. Finally, the most undesirable group had low yield but high stability and included G11, G14 and G2 for grain yield, and G6, G2, G10 and G13 for forage yield. Notably, GGE biplots not only showed different genotype groups, but also showed their favorite environments. In spite of the fact that improving a rain-fed crop such as grass pea variety is a persistent challenge, among the genotypes studied there were desirable ones in terms of both stability and high yield. As for the test environments, there existed two possible rain-fed MEs i.e. Kermanshah and Gachsaran (ME1) and Lorestan (ME2) in the west and southwest of Iran. Kermanshah was selected as favorable test environment for grass pea grain yield ME trials, whereas Gachsaran was the favorable test environment for grass pea forage yield ME trials. Overall, the poorest test environment relative to the ideal environment was Lorastan, both for grain and forage yields. The results obtained in this study demonstrated the efficiency of GGE biplot technique for selecting cultivars that are stable, high yielding, and responsive. The GGE biplot analysis identified superior lines for grain and forage yields. The most stable and high yielding lines were G3 (Sel.474), G7 (Sel.669) and G5 (Sel.686) for grain yield; and G3 (Sel.474), G11 (Sel.678) and G7 (Sel.669) for forage yield. Overall, the lines G3 (Sel.474) and G7 (Sel.669) were recorded as the best genotypes in terms of both grain and forage yields. The use of these lines by farmers would result in stable performance over the studied environments. These lines could also be used in breeding programs to develop new cultivars with consistent performance. The relative contributions of

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stability and yield to the identification of desirable genotype found in this study by the ideal genotype procedure of the GGEbiplot are similar to those found in other crop stability studies such as rice (Samonte *et al*., 2005), wheat (Kaya *et al*., 2006), barley (Dehghani *et al*., 2006) and maize (Fan *et al*., 2007).

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آزمایشات ناحیه‌ای عملکرد خلر (.Lathyrus sativus L) در ایران با استفاده از روشهای AMMI و SREG GGE

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چکیده

گیاه خلر محصولی دو منظوره هم برای مصارف حیوانی و هم برای مصارف انسانی می‌باشد. طی سال‌های اخیر موسسه ایکاردا لاینهای جدیدی از گیاه علوفه‌ای خلر بر مبنای بهبود پتانسیل عملکرد و پایداری معرفی کرده است. هدف این تحقیق بررسی پایداری عملکرد دانه و علوفه ۱۴ لاین پیشرفته گیاه خلر آزاد شده از ایکاردا با استفاده از مدل های AMMI و SREG GGE بود. بنابراین ۱۴ لاین پیشرفته انتخاب شده در سه مکان (کرمانشاه، لرستان و گچساران) از مناطق نیمه گرمسیری ایران طی سه سال زراعی ۲۰۰۶ تا ۲۰۰۸ تحت شرایط دیم ارزیابی شدند. تجزیه واریانس مرکب نشان داد که عملکرد دانه و علوفه بطور معنی‌داری تحت تاثیر محیط، ژنوتیپ و اثر متقابل ژنوتیپ در محیط قرار گرفته‌اند. تفکیک مجموع مربعات (SS) نشان داد که محیط به ترتیب ۸۵ و ۹۱ درصد تنوع کل عملکرد دانه و علوفه را توجیه می کند. در حالی که سهم ژنوتیپ و اثر متقابل GE به ترتیب ۴ و ۱۱ درصد برای عملکرد علوفه و ۲ و ۷ درصد برای عملکرد دانه بود. با استفاده از نمودار هایAMMI و SREG GGE لاینهای Sel. 474، Sel. 669 و Sel. 686 برای عملکرد دانه و لاینهای Sel. 474، Sel. 678 و Sel. 669 برای عملکرد علوفه به عنوان لاینهای با عملکرد بالا و پایدار شناسائی شدند. همچنین کرمانشاه به عنوان ایستگاه آزمایشی مطلوب برای آزمایشات ناحیه‌ای عملکرد دانه و گچساران به عنوان ایستگاه آزمایشی مطلوب برای آزمایشات ناحیه ای عملکرد علوفه خلر انتخاب شدند.