Evaluation of genotype × environment interaction in chickpea genotypes using path analysis

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ABSTRACT

Chickpea (*Cicer arietinum* L.) is one of the most important crops worldwide that is a subject of many plant breeding programs in many countries. In addition, climates are changing all over the world and drought becomes one of the most serious problems versus yield of crops. In order to screen drought tolerant genotype in Chickpea, twenty genotypes were tested under rainfed and irrigated conditions in the experimental field of College of Agriculture, Razi university, Kermanshah, Iran during 2008- 2011 growing seasons. Descriptive diagrams of hundred seed weight (HSW), number of pod per plant (NPPL), number of seed per pod (NSPO) and grain yield (GY) exhibited high GE interaction and variability between the investigated characters indicating possible selection of drought tolerant and stable entries. Analysis of variance revealed highly significant differences (P<0.01) between the genotypes and environments exhibiting genotypic diversity and variability between genotypes and environments. GE interaction was highly significant for HSW and NPPL but non-significant for GY and NSPO. Based on mean comparisons of GY, HSW, NPPL and NSPO, 2, 7, 8 and 3 classes of genotypes were found, respectively. The results extracted from path analysis over environments showed the contributions of NSPO (=0.82), HSW (=0.54) and NPPL (=0.12) on adaptability of grain yield, therefore the most contribution was attributed to number of seed per pod in the phenotypic stability of grain yield.

Key words: Chickpea, Genotype × environment interaction. Path analysis

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is one of the most important crop, belongs to pulse group, in the world (FAO, 2004). The potential yield of chickpea seems to be much higher than 0.78 ton/ha that is average annual yield world-wide for this crop (Singh and Reddt, 1994; Sudupak *et al,* 2002). Having narrow genetic base and sexual incompatibility with other wild species are major reasons for the low performance of cultivated chickpea, so in order to improve this plant in all over the world, germplasm diversity is needed (Robertson *et al*, 1997). Improving the genetic

potential with regard to increase yield is the main goal of many chickpea breeding programs (Robertson *et al,* 1997; Collard *et al,* 2003). Drought is one of the most serious problems versus yield of crops all over the world and different changing climates. Nowadays, scientists are trying to understand and assess of mechanisms that plants use to overcome drought stress by application of several approaches (Reyazul *et al,* 1997; Farshadfar *et al*, 2013). Interaction between genotype (G) and environment (E) often reduce association between genotype and phenotype because of environment interfering. These interactions make some kind of complexity in plant breeding programs so selecting one superior genotype for some climates is a hard issue. To meet this challenge, it is essential to examine genotypes in several environments to determine their genetic potential (Yaghoutipor and Farshadfar, 2007). Both parametric and non-parametric statistical methods are used to study of interaction between G and E (Mohammadi *et al,* 2010). Path analysis is one of the most popular multivariate techniques in statistics science. Path analysis is a form of factor analysis that is similar to principal component method (Darvishzadeh *et al*, 2011; Zobel *et al,* 1988). This model is one of the most effective approaches to analysis of genotype and phenotype correlations lead to understand direct and indirect traits effects on yield as a complex trait. Such a complex characteristic in crop plants is a result of several physiological factors during growth (Grafius and Thomas, 1971). This complexity nature of yield trait is a main reason that we study its components instead of yield (Farshadfar *et al,* 2012). For example, number of heads per plant, kernel per head and kernel weight are components for grain yield so understanding sequential relationship between them and yield is essential to investigate a model to yield trait (Tai, 1975).The objectives of the present investigation were (1) assessment of phenotypic stability of different chickpea genotypes under stress and non-stress conditions and (2) determination of the contribution of yield components in the phenotypic stability of seed yield

MATERIALS AND METHODS

Plants Genetic Materials and Experimental Design

Twenty genotypes of chickpea (*Cicer arietinum* L.) listed in Table 1 were tested in a randomized complete block design with three replications under stress and non-stress conditions during 2008-2011 growing seasons. The experiment was carried out in the Experimental Field of College of Agriculture, Razi university, Kermanshah, Iran (47° 20 N latitude, 34 ° 20 E longitude and 1351.6 m altitude). The location of the experiment is classified as semi-arid climate and the soil of field was clay loam with pH 7.1. The genotypes were planted in 1.5 m rows and at 25×30 cm inter-plant and inter-row, respectively. No fertilizer was used but delta metrin pesticide was used once to control of *Liriomyza huidobrensis* (Blanchard) and Cotton boll worm pests. At harvest time, hundred seed weight (HSW), number of pod per plant (NPPL), number of seed per pod (NSPO) and grain yield (GY) were measured. All traits were recorded from 2 rows of 1 m in length after elimination of border effects.

Statistical analaysis

Analysis of variance and comparison of means with Tukey test were performed using SAS (2003) software. The path analysis was done by SPSS software. The model of path analysis is as follows:

$$W_{ij} = \mu_{wi} + V_{1i}R_{1j} + V_{2i}R_{2j} + V_{3i}R_{3j} + e_{ij}$$

Where the observed yield (W_{ij}) is composed of mean genotypic effect (μ_{wi}), genotype environment interaction effects (V_{1i}, V_{2i} and V_{3i}), environmental components (R_{1j}, R_{2j} and R_{3j}) and error deviate (e_{ij}). V_{gi} in this formula is the variance of yields of genotype (Tai, 1975, 1979; Tai *et al*, 1994).

RESULTS AND DISCUSSION

Descriptive diagrams

Descriptive diagrams of the measured traits (Fig. 1) showed GE interaction and high variability for all traits. GY variation was high for genotypes 12 and 17, while low for 8 and 19. Very low GE interaction was found for GY in environment 2 (Fig. 1a) indicating specific adaptation of GY in this environment. Interaction between genotype and environment of HSW was lower than that of GY and almost the same for all genotypes with a little higher in genotypes 1 and 9 (Fig. 1b). The variation and genetic interaction for NPPL trait (Fig. 1c) was higher than HSW but lower than GY. Genotypes 11 and 13 displayed lower variation in comparison to other genotypes, hence they are more stable. Variation of environments 4 and 5 was lower than others and this variation is almost similar in three initial environments. Descriptive diagram for NSPP (Fig. 1d) showed very low variation among genotypes. Only genotypes 6 and 13 showed a little higher variation among others. Farshadfar *et al*, (2012) showed different values of variability and GE interactions Between 14 genotypes of bread wheat (*Triticum aestivum* L.) in six environments for yield and yield components.

Analysis of variance and mean comparisons

Analysis of variance revealed highly significant difference (P< 0.01) for both genotype and environment (Table 3) indicating the presence of variability between genotypes and environments. GE interaction was highly significant for HSW and NPPL, exhibiting the effect of environment in GE interaction, but non-significant for GY and NSPO. As the genotype× environment was significant for two of measured traits, so more estimation of phenotypic stability is possible for these traits (Farshadfar and Sutkla, 2006). But as F-test in the analysis of variance can only detect large differences between the genotypes, therefore non-significancy in the table of analysis of variance does not mean no significant between genotypes for the characters GY and NSPO, therefore mean comparisons classified these traits into different groups (Farshadfar *et al*, 2008). Mean comparisons for all measured traits is illustrated in Table 3. For the grain yield, values ranged from 143.18 g for genotype 19 to 228.18 g for genotype12. Totally 2, 7, 8 and 3 classes of genotypes were found based on mean comparison for GY, HSW, NPPL

and NSPO, respectively. Observed variability among genotypes was higher for HSW and NPPL. Genotypes 1, 9 and 20 occupied first class for HSW, exhibited higher values, and others located in classes 2 to 7. Genotypes 4, 7, 12, 17 and 18 showed maximum value of NPPL locating in the first class with significant differences with other genotypes. There were three classes for NSPO, hence low variability was found in this trait for all 20 genotypes.

Covariance of yield with other characters

Successful application of genotypic and phenotypic variances to study of complex traits such as yield depends on the attitude of researcher (Mehdi, 1986).
Genetic covariance between yield and another trait shows that selection on yield will affect response to selection on the other (Guillaume and Whitlock, 2007). The results revealed higher phenotypic covariance between NPPL and GY with the average of 0.25 followed by HSW (0.033) and NSPO (0.022). Variance, standard deviation and coefficient of variation for each genotype are indicated in Table 4. High values of genetic and/or phenotypic covariance between two traits may represent a high level of variation that can be very useful in plant breeding programs.

Path analysis over environments

Generally, the aim of path analysis is using correlation matrix or covariance of fewer factors for interpretation of variance. Path analysis for different environments is shown in Fig. 2. As it can be seen from this Figure, direct effect of NSPO on GY (0.82) is greater than HSW (0.54) and NPPL (0.12). Falak *et al*, (2003) reported the same results. Indirect effect of NPPL through HSW was higher than direct effect (0.56) but the conditions were different for NSPP by lower indirect effect of (0.59). Among V1, V2 and V3 that are considered as genotypic components for each genotype, V2 showed higher values followed by V3. Therefore relative contribution of number of seed per pod (NSPO) in the phenotypic stability of GY is higher than HSW (V3) and NPPL (V1). Environmental components of genotype × environment interaction exhibited that absolute value of r_1 and r_3 in all environments was higher than r_2 indicating that sensitivity of NPPL and HSW to the environmental variation was higher than NSPL. Therefore high grain yield and stability of chickpea genotypes were because of higher genotypic component V_2 (NSPO) and lower environmental components r_2 (NSPP).

Conclusion

It is common that plant breeders use grain yield to study genotype × environment interaction. As yield is a complex trait with low heritability, therefore it is essential to detect which of the yield components contribute more to the yield stability over environments. The reason is that yield components are simple characters and more heritable with easier performance for manipulation and improvement. Path analysis is a strong statistical technique to discover relative contribution of yield components in the stability of grain yield. Using this method number of seed per pod showed more effective role in the phenotypic stability of grain yield in chickpea.

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Table: List of chickpea genotypes under investigation

Code	Genotype number	Genotypes
1	G_1	X96TH54
2	G_2	FLIP-82-150C
3	G_3	FLIP-00-40C
4	G_4	S96085
5	G_5	Bivanidi
6	G_6	S925274
7	G_7	S91181
8	G_8	S95349
9	G_9	Hashem
10	G_{10}	Arman
11	G_{11}	X95TH12
12	G_{12}	X96TH46
13	G_{13}	FLIP-82-245
14	G_{14}	X95TH154
15	G_{15}	ILC482
16	G_{16}	FLIP-99-26C
17	G_{17}	X96TH41K4
18	G_{18}	X95TH69
19	G_{19}	FLIP-82-115
20	G_{20}	FLIP-00-6C

Table 2: Analysis of variance for yield and yield components.

| Source	df	GY	HSW	NPPL	NSPP
Replication	2	7689.527ns	4.906ns	13.629ns	.071ns
Environment	5	460591.2**	179.272**	3746.125**	0.137**
Genotype	19	9668.1**	148.4**	96.6**	0.047**
Environment × Genotype	95	2987.2ns	12.952**	16.573**	0.012ns
Error	238	2820.961	7.032	10.68	0.015

*, **: Significant at 0.05 and 0.01 level of probability, respectively; ns: non-significant.

**Table 3:** Mean comparison of yield and yield component

Genotypes	GY	HSW	NPPL	NSPP
1	171.94ab	33.1ab	17.97cdefgh	1.19bc
2	149.3b	30.63bc	15.527fgh	1.23abc
3	164.64b	28.291cdef	18.22cdefg	1.25abc
4	191.5ab	26.51f	22.84a	1.25abc
5	169.13ab	30.41bc	16.83cdefgh	1.26abc
6	173.86ab	23.37g	18.86bcdef	1.3ab
7	164.89b	26.97ef	21.9ab	1.28ab
8	151.36b	29.78cde	16.15efgh	1.28ab
9	178.28ab	35.58a	16.24defgh	1.2bc
10	177.34ab	30.81bc	16.25defgh	1.25abc
11	154.419b	26.916ef	14.29h	1.26abc
12	228.16a	28.62cdef	20.15abc	1.29ab
13	167.2ab	27.28ef	14.5gh	1.369a
14	148.43b	30.29cd	17.326cdefgh	1.28ab
15	187.46ab	28.81cdef	18.06cdefg	1.23abc
16	191.47ab	27.425def	17.49cdefgh	1.2bc
17	226.44a	28.202cdef	19.94abcd	1.248abc
18	175.53ab	28.09cdef	19.85abcde	1.27abc
19	143.18b	27.308ef	15.645fgh	1.18bc
20	193.54ab	34.46a	19.29[bcdef]	1.13b

**Table 4:** Variance, standard deviation , coefficient of variation and covariance of yield and yield components

| Genotypes	Variance	GY standard deviation	coefficient of variation	Covariance of yield with yield components HSW	NPPL	NSPO
1	0.1	0.32	0.06	-0.02	0.11	0.02
2	0.2	0.48	0.10	0.05	0.25	-0.02
3	0.3	0.58	0.12	0.04	0.39	0.03
4	0.3	0.55	0.11	0.03	0.30	0.00
5	0.2	0.45	0.09	0.03	0.19	-0.01
6	0.3	0.58	0.12	0.02	0.32	0.09
7	0.2	0.45	0.09	-0.01	0.25	0.01
8	0.2	0.48	0.10	0.07	0.22	0.03
9	0.1	0.37	0.07	0.06	0.20	0.02
10	0.2	0.39	0.08	0.03	0.14	0.02
11	0.2	0.46	0.09	0.02	0.19	0.03
12	0.3	0.59	0.11	0.07	0.31	0.04
13	0.3	0.58	0.12	0.05	0.24	0.03
14	0.3	0.57	0.12	0.07	0.30	0.05
15	0.4	0.63	0.12	0.01	0.26	0.03
16	0.3	0.51	0.10	0.03	0.28	0.01
17	0.4	0.63	0.12	0.03	0.32	0.01
18	0.3	0.59	0.12	0.01	0.36	0.00
19	0.4	0.61	0.13	0.03	0.29	0.01
20	0.3	0.56	0.11	0.03	0.27	0.02
Mean				0.031	0.258	0.022
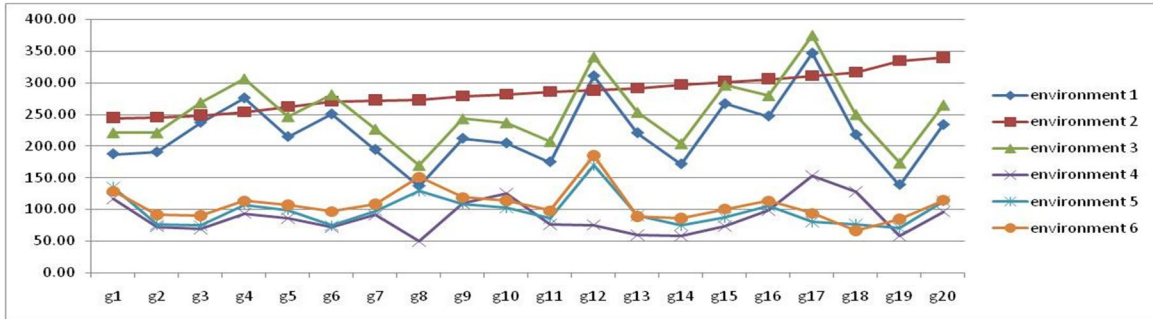
(a)
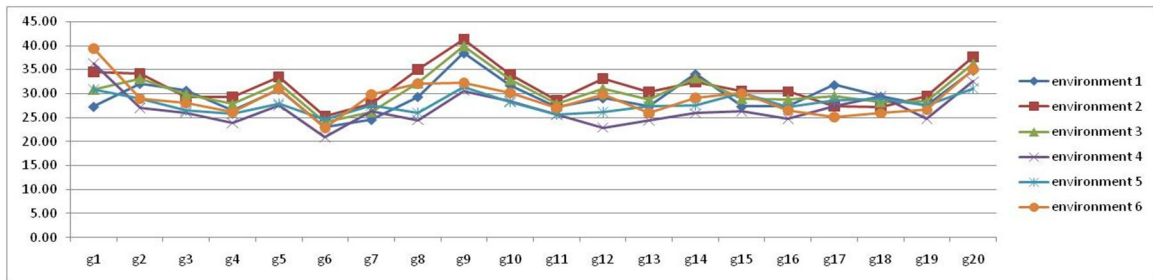
(b)
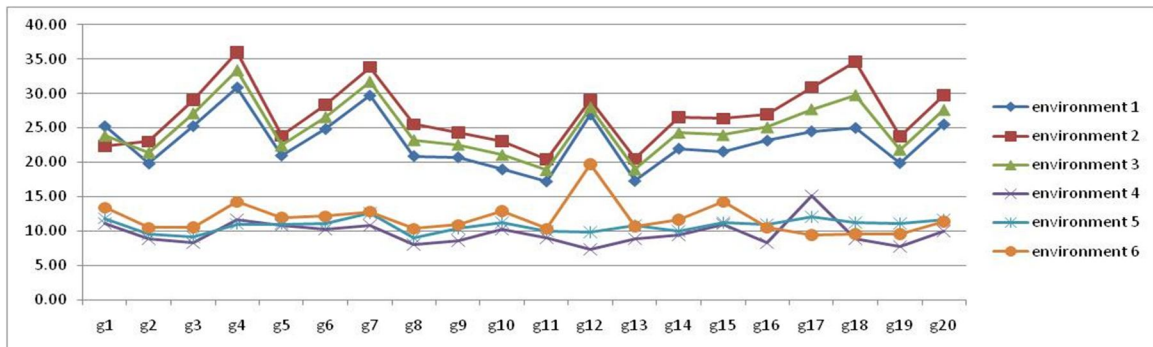
(c)
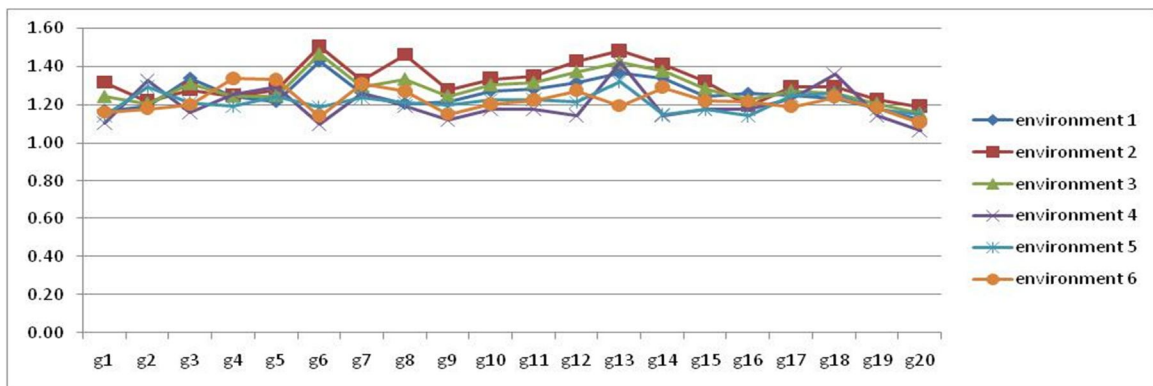
(d)

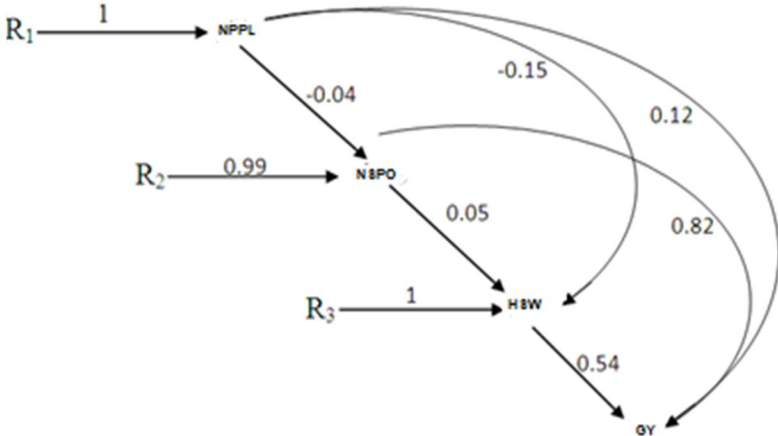**Figure 1:** Descriptive diagrams of GE interaction for GY (a), HSW (b), NPPL (c) and NSPP (d).

Figure 2: Path analysis of yield and yield components over environments