Selection for High Yield, Combining Ability, and Stability in Smooth Bromegrass

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ABSTRACT

To develop synthetic varieties, not only the estimation of General Combining Ability (GCA) for forage production is required but also the stability of *GCA* for parental genotypes is necessary. Little is known about genetic analysis and selection for high production, combining ability, and stability in grasses. In this study, half-sib families derived from the polycross of 25 smooth bromegrass genotypes were evaluated under 10 environments (combination of five years and two moisture environments, including non-stressed and drought stress conditions). Considerable variation for genetic and Genotype×Environment (G×E) interaction was found among half-sib families. Low broad sense heritability (27%) was found for forage yield indicating that selection based on an index may be more useful for improvement of this trait in recurrent selection programs. On the other hand, since the interactions of genetic by environment are significant, selection of superior genotypes for development of synthetic varieties should be done based on multi-environments trails.

Keywords: Additive effects, *Bromus inermis*, Drought stress, Polycross, Synthetic variety.

INTRODUCTION

Genotype×Environment interaction (G×E) results from the differential responses of genotypes across a range of environments and is an important source of variation in any crop (Ebdon and Gauch, 2002; Dehghani *et al.*, 2015). It reduces the correlation between phenotypic and genotypic values and complicates the selection of superior genotypes (Ebdon and Gauch, 2002; Ahmadi *et al.*, 2012). Drought is one of the important factors that cause G×E interactions and limit the survival and growth of plants in arid and semi-arid regions of the world (Kirigwi *et al.*, 2004). Knowledge about the magnitude of G×E interactions is important to develop cultivars with higher yield and stable performance over a wide range of environments (Amini *et al.*, 2013; Dehghani *et al.*, 2015).

Simple Analysis Of Variation (ANOVA) to more specific analyses of genotype performance has been used to study and interpret G×E interaction. The latter includes univariate linear regression models (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Perkins and Jinks, 1968) and multivariate models such as Additive Main effects and Multiplicative Interactions (AMMI) (Zobel *et al.*, 1988) and Genotype×Genotype-Environment interaction (GGE) biplot (Yan, 2001). Although the regression methods provide information on stability of individual genotypes, the main problem with stability statistics is that a single model cannot provide an accurate picture of the complete response pattern (Bose *et al.*, 2014). The reason is that the genotype's response to varying environments is multivariate (Lin *et al.*, 1986), whereas the stability indices are usually univariate (Gauch, 1988; Crossa, 1990). Among the various statistical procedures developed for the study of G×E interaction, AMMI model

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has been revealed to be efficient because it captures a large portion of the G×E sum of squares (Ebdon and Gauch, 2002) and has been proclaimed as superior to both joint linear regression model and principal component analysis (Crossa *et al.,* 1990). Ahmadi *et al*. (2012) in a study on bread wheat (*Triticum aestivum* L.) reported that application of AMMI and GGE biplots facilitated visual comparison and identification of superior genotypes for each target set of environments. Usually a large number of genotypes are tested across a number of sites, seasons, and years, and it is often difficult to determine the pattern of genotypic response across environments without the help of graphical display of the data (Yan *et al.,* 2001). Therefore, usually, the results of AMMI analysis shown in common graphs are called biplot (Tarakanovas and Ruzgas, 2006).

Developing synthetic varieties is the most prevailing breeding method in cross pollinated grasses (Majidi and Mirlohi, 2010). In these plants, not only the estimation of General Combining Ability (GCA) for forage production is required, but also the stability of *GCA* for parental genotypes (clones) is necessary. This stability shows the amount of interaction between Genetic effects and Environment (GE), which is important for breeder. The genetic variance among HS families is equal to the covariance of HS and one-fourth of the additive genetic variance, assuming there is no additive x additive types of epistatic variance (Nguyen and Sleper, 1983; Amini *et al.,* 2013; Araghi *et al.,* 2014). However, in the case of auto-tetraploids, this covariance includes additive and dominance genetic variance, assuming no epistasis (Nguyen and Sleper, 1983). Polycross progeny tests have been used to measure *GCA* and study of genetic parameters in some forage crops (Araujo *et al.,* 2002; Majidi *et al.,* 2009; Araghi *et al.,* 2014).

Smooth bromegrass (*Bromus inermis* Leyss is a drought tolerant, sod forming, cool season grass species grown mainly for hay production (Casler and Carlson, 1995).

It has a wide distribution in many regions of Iran. To the best of our knowledge, information about genetic and G×E interactions effects using HS families in grasses is rare (Robins *et al*., 2012, 2015). Therefore, the objectives of the present study were to: (i) Interpret genetic main effects and genetic by environment interactions using HS families of smooth bromegrass evaluated across 10 environments; (ii) Estimate general combining ability for forage production in smooth bromegrass genotypes and its stability to select superior parents, and (iii) Identify genotypes that have similar response pattern over all environments as well as high yield using AMMI and regression methods.

MATERIALS AND METHODS

Experimental Site

The experiment was conducted during five years (2010- 2014) on a Typic Haplargid, silty clay loam soil at Isfahan University of Technology Research Farm, Isfahan, Iran (32° 30' N, 51° 20' E). The soil was calcareous, containing 390 g kg^{-1} Ca-carbonate equivalent, 4.0 g kg^{-1} organic C, and 0.77 g kg^{-1} total N, with pH 8.3. The mean annual temperature and precipitation are 14.5 °C and 115 mm, respectively.

Plant Materials

In this study, 25 half-sib families derived from polycross of 25 parental genotypes of smooth bromegrass were evaluated under normal and drought stress conditions for five years. The origin of half-sib families is given in Table 3. The parental genotypes were randomly selected from a large replicated nursery which mainly consisted of natural ecotypes of smooth bromegrass from wide geographical areas of Iran plus some foreign natural ecotypes (Hungary) and polycrossed during 2009.

Evaluation of HS Families

Polycross seeds from the 25 HS families were grown in plastic boxes in a greenhouse during the winter of 2010. Established seedlings were space planted on 1 March, 2010, in the field according to a randomized complete block design with four replications, of which two replications were allocated to each environment (normal and drought stress). Under the full irrigation (normal condition), plants were irrigated when 50% of the total available soil water was depleted from the root zone. Under the deficit irrigation (stress condition), irrigation was carried out when 90% of the total available soil water was depleted from the root zone (Allen *et al.,* 1998). Water stress was alternatively applied during the growing season in each year of the experiment from first of May to the first of October. The irrigation intervals during the growing season and between the two irrigation treatments were variable depending on the weather conditions (for the normal environment 5-8 days and for the stress environment 15-19 days). Soil moisture was measured based on standard gravimetric methods at 3 depths of 0–20, 20–40, and 40–60 cm. The irrigation depth was determined according to the following equation:

$$I = (FC - \theta_{irri}) \times D \times B$$

Where, I is Irrigation depth (cm), FC is soil gravimetric moisture percentage at field capacity, θ_{irri} is soil gravimetric moisture percentage at irrigating time, D is the root-zone depth, and B is the soil Bulk density at root-zone (1.4 g cm^{-3}). Water was delivered from a pumping station *via* polyethylene pipe and the water volumes applied were measured with a volumetric water meter.

When flowering in all plots was completed (about early summer), the grass of all the plots were cut manually from 5 cm above the ground, dried at 75ºC for 48 hours and then weight of forage yield per family was recorded. The second and third cuts were done in mid-summer and early fall of each year, respectively. The average forage weight (g per plant) from the three cuts was used for analysis.

Statistical Analysis

Analysis of Variance, Heritability and General Combining Ability (GCA)

A combination of a single year and moisture environments was considered as the test environment. Thus, 10 test environments were created. The detailed information on test environments is given in Table 1. Combined analysis of variance was performed, considering the effect of genotype (family) and environment as random, to examine differences among the families, and to estimate variance components. As the experiment was conducted for five years in two

Table 1. Information on test environments used to evaluate 25 HS families of smooth bromegrass.

Environment No.	Location-Irrigation level-Year	Rainfall (mm)	Temperature (°C)	IPCA1 scores[a]
E1	Lavark- Full irrigation- 2010	99.2	19.4	-9.911
E2	Lavark- Deficit irrigation- 2010	99.2	19.4	2.322
E3	Lavark- Full irrigation- 2011	141.6	18.3	-3.330
E4	Lavark- Deficit irrigation- 2011	141.6	18.3	3.190
E5	Lavark- Full irrigation- 2012	216.7	17.8	1.142
E6	Lavark- Deficit irrigation- 2012	216.7	17.8	0.437
E7	Lavark- Full irrigation- 2013	123.1	18.8	1.354
E8	Lavark- Deficit irrigation- 2013	123.1	18.8	1.318
E9	Lavark- Full irrigation- 2014	194.9	18.2	1.957
E10	Lavark- Deficit irrigation- 2014	194.9	18.2	1.521

[a] First Interaction Principal Component Axis (IPCA1) score of environments.

environments, a split-plot in time (year) model was used for the combined analysis proposed by Steel and Torrie (1980) and Nguyen and Sleper (1983). Data were also subjected to ANOVA separately for drought stress and normal environments across five years using a split-plot in time design with genotypes (HS families) as the main plots and years as subplots. Variance components were estimated from mean squares of the ANOVA after being equated to their expected variance components (Nguyen and Sleper, 1983). Broad-sense heritability (h^2_b) on a phenotypic mean basis averaged over replications, years, and environments was estimated as described by Nguyen and Sleper (1983).

Analyses of variance and estimation of variance components were performed using the PROC Mixed of the SAS/STAT program (SAS Institute, 2002). *GCAs* were calculated as the deviation of each HS progeny from the population mean as defined by Majidi *et al*. (2009).

Stability Analysis

Stability analysis was applied to forage yield using the stability parameters proposed by Finlay and Wilkinson (1963) and Eberhart and Russell (1966). These stability parameters were regression coefficients of the family means (b_i) on the environmental indices (average of all families in each environment) and mean squares of deviations from regressions (S^2_{di}) that were calculated as below:

$$b_i = 1 + \frac{\sum_j (X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..})(\bar{X}_{.j} - \bar{X}_{..})}{\sum_j (\bar{X}_{.j} - \bar{X}_{..})^2}$$

$$S^2_{di} = \frac{1}{E-2} \left[\sum_i (X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..})^2 - (b_i - 1)^2 \sum_i (\bar{X}_{.j} - \bar{X}_{..})^2 \right]$$

Where, X_{ij} is the forage yield of genotype i in environment j, $\bar{X}_{i.}$ is the mean forage yield of genotype i, $\bar{X}_{.j}$ is the mean forage yield of the environment j, $\bar{X}_{..}$ is the grand mean and E is the number of Environments.

AMMI Model Analysis

After verifying the existence of interaction, analysis of adaptability and phenotypic stability was conducted by the AMMI model (Zobel *et al.,* 1988), using the following model:

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{n} \lambda_k \, \alpha_{ik} y_{jk} + r_{ij} + \varepsilon_{ijk}$$

Where, Y_{ij} is the mean yield of genotype i in environment j for replicate r; μ is the overall mean; g_i is the main effect of genotype i; e_j is the main effect of environment j; ε_{ij} is the average experimental error; λ_k is the singular value of the kth Interaction Principal Component Analysis (IPCA) (k is the number of axis or Principal Component (PC) retained by the model); α_{ik} is the singular value of the ith genotype in the kth IPCA; y_{jk} is the singular value for the jth environment in the kth IPCA; r_{ij} is the error for the GE interaction or AMMI residue (Noise). In this analysis, the main effect of genotype was considered as fixed and the main effect of environment was considered as random. AMMI analysis for the data collected on forage yield was implemented through the Crop stat 7.2 (Crop stat, 2009). The results of the AMMI model analysis were interpreted on the basis of AMMI1 biplot analysis.

RESULTS

Genetic Analysis

The results of combined analysis of variance indicated that all the main effects and all of the interactions were significant (Table 2). Significant variation among HS families indicates the presence of considerable genotypic variation for forage yield. The significant GE interaction shows the different response of genotypes to environmental variations. The lowest proportion of phenotypic variance belonged

Table 2. Results of analysis of variation and estimates of variance components for forage yield of 25 HS families of smooth bromegrass evaluated at 10 environments (five years and two moisture conditions).

Source of variation[a]	Degree of freedom	Mean squares	Variance components
Environment	1	36047.94***	189.09[b]
Rep (E)	2	186.20	-
Family	24	756.95***	10.47
F×E	24	520.55**	8.11
F×R/(E)	48	259.88ns	-
Year	4	71679.74***	-
E×Y	4	2333.37***	-
F×Y	96	395.69*	6.75
F×E×Y	96	368.70*	89.81
Error	192	189.09	-

[a] F= Family; E=Environment, Y= Year. [b] Only variance components of family and its interaction with environments (E and Y) are shown. *** Significant at 0.001 probability level; ** Significant at 0.01 probability level, ns: Not significant.

to the interaction of Family×Year (FY effects), while the interaction of Family×Environment×Year (FEY) had the highest portion of phenotypic variance (Table 2). The broad-sense heritability level based on family mean was 27%. According to the results of mean data (obtained over years) forage yield was decreased by 21% under drought stress conditions (Table 3). The mean values of families for forage yield ranged between 65 and 100 g plant^{-1} and 53 and 86 g plant^{-1} at normal and drought stress conditions, respectively. At normal condition, among the 25 HS families, F1 (from Hamedan), F4 (from Semirom), F6 (from Isfahan) and F15 (from Hungary) had the highest forage yield, while the lowest value belonged to all other families, except for F2 and F7 (from Isfahan), F8 (from Hamedan), F10 (from Kordestan) and F13 (from Hungary) (Table 3). The highest *GCA* belonged to the parental genotypes F3 and F6 (from Isfahan) and F4 (from Semirom) (Table 3). Therefore, these genotypes are good combiners for forage yield in developing synthetic varieties. Parental genotypes F5 and F24 (from Isfahan), F9 (from Semirom) and F12 (from Hungary) had relatively low *GCA* for forage yield and, therefore, are not good combiners. Under stress condition, the highest yield was observed for F3 and F6 (from Isfahan) and F4 (from Semirom), and the lowest value was observed for all other

families, except for F14 (from Hungary) (Table 3).

Stability Analysis

Application of AMMI model for partitioning of GEI (Table 4) revealed that the first three terms of AMMI were significant using an approximate *F*-statistic. The partitioning of GE interaction through the AMMI3 model analysis justified 72.76% of GE interaction, in which IPCA1 to IPCA3 were highly significant factors that explained 43.14, 16.10, and 13.52% of GE sum of squares, respectively (Table 4). Results of AMMI1 analysis (Table 4) showed that environments, genotypes, and GE interaction effects had significant variations. The model showed that environmental effects accounted for 76.1% of the total sum of squares; only 4.2% of variations were attributable to genotypic effects, and 19.7% to GEI effects (Table 4).

In Figure 1, IPCA1 scores of both families and environments are plotted against the main effects (genotype mean and environment mean) as a biplot (AMMI1 biplot). The pattern clearly indicated that most of the families gathered in a specified area of biplot, mainly around the overall mean of forage yield. Regardless of IPCA1 scores direction, among these families, a group of them

Table 3. Names, origin, mean forage yield and stability parameters of 25 HS families of smooth bromegrass evaluated in five years at two moisture conditions.

Genotype	Origin	Forage yield (g plant^{-1})		*GCA*	b_i	S^2_{di}	IPCA1 scores[a]
		Normal	Stress				
F1	Iran, Hamedan	89.77	53.70	1.21	1.39	414.84	-5.569
F2	Iran, Isfahan	81.21	61.71	0.93	1.06	94.14	-1.814
F3	Iran, Isfahan	69.17	86.37	7.24	0.54	543.00	5.637
F4	Iran, Semirom	100.32	74.83	17.04	1.56	280.70	-5.081
F5	Iran, Isfahan	69.46	54.82	-8.39	0.77	122.50	1.705
F6	Iran, Isfahan	94.50	72.34	12.89	1.42	147.96	-2.080
F7	Iran, Isfahan	82.62	59.86	0.71	1.01	74.45	0.149
F8	Iran, Hamedan	84.42	66.86	5.11	1.00	308.57	1.305
F9	Iran, Semnan	69.60	53.65	-8.90	0.87	208.40	0.753
F10	Iran, Kordestan	80.77	61.48	0.59	1.05	16.99	0.214
F11	Iran, Isfahan	77.96	54.41	-4.34	0.99	163.34	-0.474
F12	Hungary	72.31	57.81	-5.47	0.87	88.74	0.346
F13	Hungary	83.31	60.53	1.39	1.10	91.75	-2.123
F14	Hungary	78.50	69.32	3.38	1.33	229.34	0.283
F15	Hungary	89.81	57.02	2.88	0.99	130.26	-1.411
F16	Hungary	79.69	66.34	2.48	0.83	61.93	1.034
F17	Hungary	78.26	59.09	-1.86	1.04	80.69	-0.890
F18	Hungary	77.80	54.88	-4.19	0.97	133.86	0.130
F19	Hungary	78.62	65.85	1.71	0.98	145.22	1.556
F20	Hungary	75.45	59.70	-2.96	0.93	159.12	-1.859
F21	Iran, Isfahan	70.17	60.60	-5.15	0.97	270.19	2.501
F22	Iran, Isfahan	78.05	54.56	-4.22	0.90	58.23	0.648
F23	Iran, Isfahan	76.36	59.52	-2.59	0.90	49.91	0.077
F24	Iran, Isfahan	65.42	60.65	-7.50	0.81	212.15	1.793
F25	Iran, Isfahan	72.00	65.11	-1.98	0.73	255.70	3.170
LSD 0.05		14.52	15.19	11.74			

[a] First Interaction Principal Component Axis (IPCA1) score of families.

Table 4. Additive Main effects and Multiplicative Interaction (AMMI) analysis of variance for forage yield (g plant^{-1}) of 25 smooth bromegrass half sib families across 10 environments.

Source of variation	*df*	*SS*	*MS*	Total variation (%)
Total	499	514092.960	1030.246	
Genotype (G)	24	18166.517	756.938***	4.17%
Environment (E)	9	332096.919	36899.658***	76.14 %
G × E	216	85877.333	397.580*	19.69%
IPCA1	32	37047.383	1157.731***	43.14%
IPCA2	30	13821.44	460.717***	16.10%
IPCA3	28	11613.57	414.770***	13.52%
IPCA4	26	6726.994	258.731[n.s]	
Residual	100	16668.43	166.684	27.24%
Error	250	77952.190	311.809	

*** Significant at 0.001 probability level; * Significant at 0.05 probability level, [ns]: Not significant.
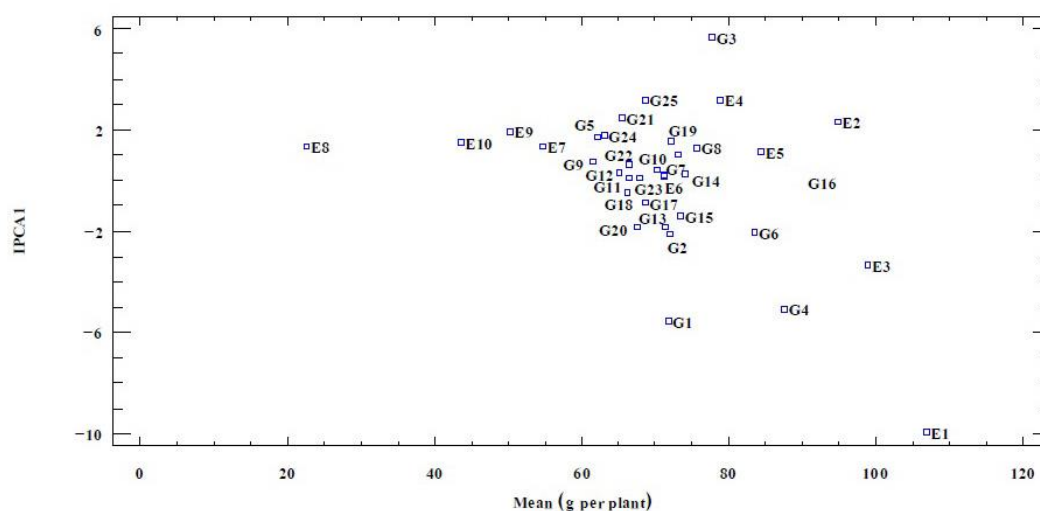
Figure 1. AMMI 1 biplot with the main effects vs. first principal component axis of interaction (IPCA1) for forage yield of 25 smooth bromegrass half sib families at 10 environments.

including F7, F8, F10, F14, F15, F16, and F19 were generally high yielding with IPCA1 scores nearly close to zero (Figure 1). Therefore, these families were generally stable and were hardly affected by the GE interaction. As the genetic materials of this study were HS families, the parental genotypes of these families had high stability for *GCA*. Three families, namely, F1, F3, and F4 had a forage yield above the grand mean and the largest IPCA1 scores (Figure 1). Hence, these families were the most unstable families, but they were identified as specially adapted families to the given environments.

Among the environments used in this study, with regard to IPCA1 scores, E1 mostly contributed to GE interaction, because it attained the highest IPCA1 score and was positioned far from the origin in AMMI1 biplot. On the other hand, E6 gave the lowest score and had low contribution to the GE interaction; therefore, this

environment was recorded as the most stable environment. This indicated that all the families performed well in this environment (Figure 1).

Figure 2 presents the AMMI-2 biplot, with the IPCA1 and IPCA2 for forage yield. The biplot of IPCA1 against IPCA2 compares relative magnitude and sign of the GE interaction controlled by each genotype and each environment. In this graphical representation, genotypes located close to the origin are considered as the most stable, which means that they contributed little to the GE interaction and those distant from the origins are sensitive and have large interaction. In the present study, F1, F3, F4, and F9 were more responsive since they were far from the origin, whereas the families F7, F10, F14, F15, F16, and F19 were close to the origin and hence they were non sensitive to environmental interactive forces.
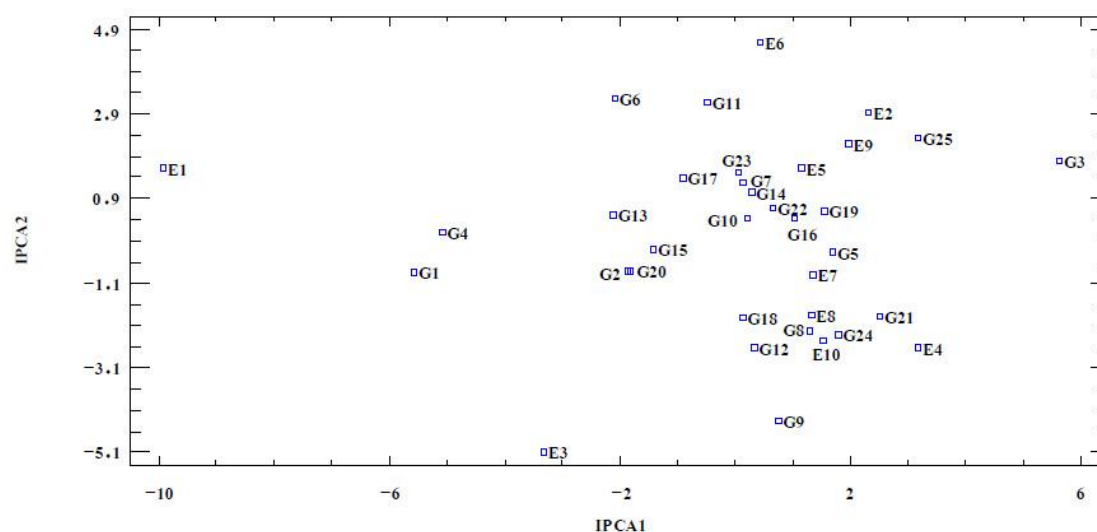
Figure 2. AMMI 2 biplot (IPCA1 *vs.* IPCA2) for forage yield of 25 smooth bromegrass half sib families evaluated at 10 environments.

Stability parameters (b_i, S^2_{di}) of forage yield evaluated in the 25 HS families are given in Table 3. Results showed that the studied families varied in their stability. The b-value of families ranged from 0.54 to 1.42 (F3 and F6, respectively). In respect to Standard deviation of regression (S^2_{di}), families have shown wider ranges, so that S^2_{di} ranged from 16.99 to 543 (F10 and F3, respectively). In some families, the regression coefficients were unity or close to it. For example, F7, F10, F16, and F17 had regression coefficients of nearly 1.0. Also, the S_{di}^2 values of these families were among the lowest (Table 3) and could be considered as having high adaptability to different environments.

DISCUSSION

Self incompatibility, resulting in cross-pollination, mandates breeding efforts to generally focus at the development of superior synthetic cultivars and improved heterogeneous populations in smooth bromegrass (Majidi *et al.,* 2015). In order to select clones for a synthetic variety, data on the individual *GCA* is desired and is usually derived from the analysis of Half-Sib (HS) progenies. In this process, not only the estimation of *GCA* for forage production is necessary, but also the stability of *GCA* for parental genotypes (clones) is required. In the study of half sib mating, this stability also shows the amount of interaction between Genetic effects and Environment (GE). In the study of HS families, the estimated family variance and family×environment interaction variances can be translated into additive genetic variance and additive genetic interaction variances. However, in the case of auto-tetraploids, this covariance includes additive and dominance genetic variance, assuming no epistasis (Nguyen and Sleper, 1983). Considerable variations for stability and forage production were observed among HS families indicating the facility to selection of parental genotypes with variable stability and yield. Both two- and three-way family by environment interactions, i.e. *FE, FY and FEY*, were significant, showing the necessity of extension of analysis in multi-environment trails for estimating *GCA* of parental genotypes.

Broad sense heritability estimates of traits in forage crops provide information related to the value of the genetic variance available to the plant breeders for selection in cross-

pollinated populations (Kearsey and Pooni, 1996). In smooth bromegrass, different ranges of heritability have been reported for forage yield (0–0.46). In this study, h^2_b (27%) was lower than the ones reported for smooth bromegrass and some other perennial forage grasses (Araujo, 2001; Araujo *et al.,* 2002; Araghi *et al.,* 2014). Majidi *et al.* (2015) stated that the estimates of heritabilities based on combined analysis were lower than those for individual environments. The estimate of broad-sense heritability (h^2_b) in normal condition (31%) was greater than drought stress condition (25%), indicating that drought stress may increase the effect of environment and environmental interaction effects. This increase results in a lower contribution of the genetic variability to the phenotypic variation. The utility of the AMMI for the investigation of multi-environment trial data have been clearly demonstrated (Pecetti *et al.,* 2011). However, this potential tool has not yet been used to analyze the multi-environment data in smooth bromegrass. In this study, the AMMI model demonstrated the presence of GE interactions, and this has been partitioned among the IPCAs and noise. Three IPCAs explained 72.76% of variation of the total GEI sum of squares, due to AE interaction, leaving the 27.24% of the variation in the residual, which is in agreement with Gauch (1993) and Purchase *et al.* (2000). On the other hand, this contradicted the findings of Gauch and Zobel (1996) and Yan and Rajcan (2002) who recommended that the most accurate model for AMMI could be predicted by using the first two IPCAs. Differences in stability and adaptability to environments can be qualitatively assessed using the biplot graphical representation that scatters the genotypes according to their principal component values (Vita *et al.,* 2010). Moreover, The AMMI1 biplot can be used to diagnose the GE interaction pattern. Using pattern analysis in AMMI model, genotype and environment of the same response will be grouped (Pourdad and Mohammadi, 2008). In this study, pattern

analysis of families and environments based on the first IPCA and forage yield showed three groups of families. In the first group, seven families were found with moderately high yield and stability, therefore, these families had high stability for *GCA*. The second group included eight families which had high yield but low stability, and the third group consisted of ten families which had moderate yield and moderate to low stability. These results indicated that it is possible to find the most desirable parental genotypes for developing synthetic varieties with high stability and yield using AMMI model. Distribution of family points in the AMMI II biplot also verified the results of AMMI1 biplot and revealed that the families, F7, F10, F14, F15, F16, and F19 scattered close to the origin, indicating minimal interaction of these families with environments. In this study, according to the method of Eberhart and Russell, the regression coefficient of families F7, F10, F16, and F17 was near unity and had relatively small deviation from regression; therefore, they should be stable in different environments and have stable *GCAs*, too. As these genotypes were identified as the most stable families based on the results of AMMI biplots, considerable concurrence was found among the two methods.

In general, environments with scores near zero have little interaction across genotypes and provide low discrimination among them (Anandan *et al.,* 2009). In this study, this pattern was observed for E6 as it attained the lowest score and had low contribution to the GE interaction.

In conclusion, significant differences for GE interaction among half-sib families indicated that it is possible to find the most desirable parental genotypes for developing synthetic varieties with high stability and yield using AMMI model. From analysis of HS families, superior parents for developing synthetic varieties were identified. Because of the moderately low broad-sense heritability for forage yield, both genetic and non-genetic effects played a role in the genetic control of this trait. Therefore,

selection based on an index may be more useful for improvement of forage yield in recurrent selection programs. On the other hand, since the interactions of G×E are significant, selection of superior genotypes for development of synthetic varieties should be done based on multi-environments trails.

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انتخاب برای عملکرد بالا، ترکیب پذیری عمومی و پایداری در بروموگراس نرم

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چکیده

ایجاد ارقام ساختگی نه تنها به قابلیت ترکیب‌پذیری عمومی بالا برای عملکرد در والدین وابسته است، بلکه پایداری ترکیب پذیری عمومی والدین رقم ساختگی در محیط‌های مختلف نیز ضروری است. اطلاعات اندکی در زمینه‌ی تجزیه ژنتیکی و انتخاب همزمان برای تولید بالا، ترکیب‌پذیری و پایداری در گراس‌ها در دسترس است. در این مطالعه فامیل‌های نیمه خواهری حاصل از پلی کراس ۲۵ ژنوتیپ بروموگراس نرم در ۱۰ محیط (ترکیبی از ۵ سال و دو محیط رطوبتی تنش خشکی و عدم تنش) ارزیابی شدند. تنوع بالایی برای اثر ژنتیک و اثر متقابل ژنتیک و محیط مشاهده گردید. وراثت‌پذیری پایینی برای عملکرد علوفه حاصل شد که نشان می‌دهد انتخاب بر اساس یک شاخص انتخاب برای بهبود عملکرد می‌تواند در برنامه‌های انتخاب دوره‌ای موثرتر از انتخاب مستقیم باشد. معنی‌دار بودن اثر متقابل افزایشی ژن‌ها با محیط نشان می‌دهد که انتخاب ژنوتیپ‌های برتر برای ایجاد ارقام ترکیبی بایستی بر اساس آزمایش‌های چند محیطی صورت پذیرد.