Interpretation of Genotype × Environment Effect on Oil Content in Castor

P.B. Dave[1*], B.N. Patel[2], D.J. Parmar[3] and N.A. Patel[4]

[1]Research Associate, Regional Research Station, AAU, Anand, Gujarat. 388 110

[2]Associate Research Scientist, Agricultural Research Station, AAU, Sansoli, Gujarat. 387 130

[3]Associate Professor, Dept. of Agril. Statistics, AAU, Anand, Gujarat. 388 110

[4]Assistant Research Scientist, Main Vegetable Research Station, AAU, Anand, Gujarat. 388 110

*Corresponding Author. E-mail: pbdsl.259@gmail.com

Abstract: In agricultural experimentation, a large number of genotypes are normally tested over a wide range of environments (locations, years, growing seasons, etc.). Genotypes stability and adaptability was directly effected in different environmental conditions through genotype × environment interaction. In this sense, plant breeders look for genotypes that have general adaptability, or they look for genotypes that have specific adaptability for specific environments. In this regard, a set of 56 genotypes of castor were studied to characterize oil yield stability under four environments. Out of 56 genotypes, genotype G40 and G46 had non-significant unit regression coefficient and deviations from regression could be considered as stable and widely adapted hybrids for all the environments. AMMI analysis showed that castor oil yield was significantly ($p < 0.01$) affected by environments (*E*), genotypes (*G*) and genotype × environment interaction (GEI) indicating the presence of genetic variation and possible selection of stable entries. 7.64% of the total sum of squares was accounted for environmental fluctuations exhibiting that the environments were diverse, with small differences among environmental means causing most of the variation in oil yield. GEI was further partitioned into three principal component axis. The first multiplicative axis (PCA I) explained 43.20 of GEI sum of squares and it was significant. According to AMMI biplot, genotypes G18, G19, G40 and G47 exhibited adaptability and identified as stable genotypes for all the environments.

Key words: AMMI model, biplot, Eberhart and Russell model, genotype × environment interaction.

INTRODUCTION

A phenotype is a result of interplay of genotype and its environment. A particular genotype does not exhibit the same phenotypic characteristics under different environments and different genotype response differently to a particular environment. When interaction between genotype and environment is present, ranking of genotype will be different under different environments. The genotypes are said to be stable when their performance under changing environments are stable. Differences between genotypic values may increase or decrease from one environment to another which might cause genotypes to even rank differently between environments. Environmental factors (non-genetic factors) such as locations, growing seasons, years, rainfall, temperature, etc. may have positive or negative impacts on genotypes.

Genotypes are normally tested over a wide range of diverse environments (*e.g.*, locations, years and growing seasons) and agricultural experiments involving $G \times E$ interactions may involve a large number of genotypes. Genotype × environment interactions are of common occurrence and often creates manifold difficulties in interpreting results and thus hamper the progress of breeding programmes aiming at further genetic improvement in crop plants. Hence, the knowledge of magnitude and nature of genotype × environment interaction is very useful to plant breeder. The present study was carried out for interpretation of $G \times E$ interaction through AMMI analysis and to find stable and adaptable genotypes of castor for oil percentage.

MATERIALS AND METHODS

The experimental materials consisted of 56 castor genotypes which were evaluated in a randomized complete block design with three replication in different four environments which was created by using two categories of date of sowing (timely and late sowing) in different two years (2013 and 2014) at Agricultural Research Station, Anand Agricultural University, Sansoli (Gujarat).

A number of statistical models are available for evaluating the stability of different genotypes. The present study was based on joint regression analysis (Eberhart and Russel model, 1966[1]) and AMMI model with objective to interpret $G \times E$ interaction and to find stable genotypes of castor for oil percentage.

Eberhart and Russel Model

Eberhart and Russel model uses the mean performance of genotypes, regression coefficient (b_i, linear sensitivity) and deviation from regression (S^2_{di}, non-linear sensitivity) as the parameters of the stability and suggested that linear and non-linear functions should be while judging the phenotypic stability of genotypes. They further emphasized that an ideal genotype/variety should have high mean with unit regression coefficient (b_i) and deviation from regression equal to zero ($S^2_{di} = 0$) was stable one.

AMMI Analysis

Statistical model

$$\text{ANOVA} : Y_{ij} = \mu + \alpha_g + \beta_e + \alpha\beta_{ge} + \rho_{ij} + \varepsilon_{ijk}$$

$$\text{PCA} : Y_{ij} = \mu + \Sigma_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ij} + \varepsilon_{ijk}$$

$$\text{AMMI} : Y_{ij} = \mu + \alpha_g + \beta_e + \Sigma_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ij} + \varepsilon_{ijk}$$

Where,

μ = Grand mean

α_g = Deviations of genotypes (G)

β_e = Deviations of environment (E)

λ_n = Singular value for Interacction Principal Component Axis n (IPCA)

γ_{gn} = Genotype eigenvector for axis n

δ_{en} = Environment eigenvector

ρ_{ij} = Residual

ε_{ijk} = Error term

The biplot is a graphical representation from AMMI analysis which is a useful tool to understand more complex specific pattern of genotypes and GEI or both genotypes and environments. The concept of biplot was first developed by Gabriel (1971[2]). It is a scatter plot that graphically displays the genotype (entries) and the environments (testers) of a two-way data and allows visualization of the interrelation among the entries (genotypes) testers (environments).

RESULTS AND DISCUSSION

Castor oil content data of 56 genotypes grown at Agricultural Research Station, AAU, Sansoli in different environments were subjected to analysis of variance for individual environment as well as pooled over environments. The analysis of variance (ANOVA) for individual environment indicated that the source of genotype variance was found significant in all the environments. This suggested that the presence of genetic variability among the genotypes under study (Table 1). On the basis of pooled analysis, the results of mean performance for 56 genotypes indicated that the genotypes G 40 (45.58%), G 56 (44.96%), G 32 (43.85%), G 50 (43.20%) and G 1 (43.17%) had the significantly highest oil content over environments.

The result of combined analysis of variance is presented in Table 2. The variance of genotype and

Table 2
Pooled analysis of variance over four environments for stability of oil character

Source of Variation	df	SS	SS (%)	MS
Repl/Environments	8	4.80	–	0.60
Environments	3	126.12	7.64	42.04**
Genotypes	55	507.65	30.73	9.23**
$G \times E$	165	1018.05	61.63	6.17**
Pooed error	440	422.40	–	0.96
Total	671	2079.02	–	–

**Significant at $P = 0.01$ level of probability.

environments were found highly significant indicating variability in genotypes and environments. The variance of $G \times E$ interaction was significant for oil content indicated the differential response of genotypes towards the environments. Since the interaction was significant, the oil content of different genotypes was subjected to stability analysis. The combined ANOVA revealed that genotypes, environments and $G \times E$ interaction contributed 7.64%, 30.73% and 61.63% of trial variation (Gauch and Zobel, 1997[3]), respectively.

Eberhart and Russell Model

Analysis of variance was carried out over environments as per Eberhart and Russell (1966) and the results are presented in Table 3. The results indicated that

Table 1
Analysis of variance for individual environments

Source of Variation	df	E1	E2	E3	E4
Replication	2	7.87	2.87	0.64	1.28
Genotypes	55	59.16**	44.37**	54.08**	33.33**
Error	110	2.66	2.68	3.30	2.98
Mean of Environment		42.81	41.61	42.05	41.98

Where, E_1, E_2, E_3 and E_4 were different four environments. *,**Significant at $P = 0.05$ and $P = 0.01$ levels of probability, respectively.

Table 3
Analysis of variance for stability model (Eberhart and Russell model, 1966)

Source of Variation	df	SS	MS	%
Genotypes	55	168.85	3.07**	–
Env. + $(G \times E)$	168	381.36	2.27**	100
Environment (Lin.)	1	42.06	42.06**	11.03
$G \times E$ (Lin.)	55	140.80	2.56**	36.92
Pooled Deviation	112	198.24	1.77**	51.98
Pooled error	440	140.80	0.32	–
Total	671	1072.11	–	–

**Significant at $P = 0.01$ level of probability.

the mean square for $G \times E$ interaction (GEI) was found significant. In stability analysis, environment and GEI component were further partitioned into environment (linear), $G \times E$ (linear) and pooled deviations from regression. These three components *i.e.* environments (Lin.), $G \times E$ (Lin.) and pooled deviations were found significant and they accounted for 11.03%, 36.92% and 51.98% of total environment and GEI, respectively.

The stability parameters for oil content of genotypes in different environmental condition were given in Table 4. Out of 56 genotypes, twenty three genotypes had higher mean than overall mean. Out of twenty three genotypes, fifteen genotypes had significant s^2_{di} and hence, they were unstable whereas eight genotypes had non-significant s^2di hence, they were stable. Among the stable genotypes, G 19 and G 25 were found stable and adapted to all environments as b_i were found non-significant. The genotypes G 44 and G 55 were stable and adapted to poor or unfavorable environments ($b_i < 1$). The regression coefficient of genotypes G 10, G 40, G 46 and G 56 were found significant and greater than one thereby, they were stable and adapted to favorable environments.

The AMMI analysis of 56 castor genotypes tested in 4 environments showed that castor oil yield was significantly ($P < 0.01$) affected by environments (E), genotypes (G) and genotype × environment interaction (GEI) indicating the presence of genetic variation and possible selection of stable entries (Table 5). Only 7.64% of the total sum of squares was justified by environmental fluctuations exhibiting that the environments were diverse, with small differences among environmental means causing most of the variation in oil yield. A portion with 30.73% of the total sum of squares was attributed to genotypic effects. GEI significantly explained 61.63% variation in oil yield. The magnitude of the GEI sum of squares was about 2 times larger than that of genotypes, indicating sizeable differences in

genotypic response across environments. As GEI was significant therefore we can further proceed and calculate phenotypic stability (Farshadfar, 2008[4]). The analysis of AMMI showed that the best fit model was AMMI1 in this experiment as only one interaction of Principal Component Analysis (IPCA1) was found highly significant ($P < 0.01$), while the subsequent ones were non-significant. The IPCA1 explained 43.20% variation of $G \times E$ interaction sum of square.

The result of AMMI analysis can also be easily comprehended with the help of AMMI biplot as depicted in Figure 1. The mean performance of genotype and environment *vs.* IPCA I score were used to construct the biplot (Table 4). The IPCA scores of genotypes in the AMMI analysis are an indication of stability or adaptability over environments (Gauch and Zobel, 1997). The greater the IPCA scores, the genotypes was adopted to specific environment. The IPCA scores approximate to zero, the more stable or adapted the genotypes over all the environments.

Biplot of Figure 1 was divided into 4 sections by doing vertical line at overall mean and horizontal line at IPCA I = 0. The points for genotypes were low scattered indicating that variability due to environments was higher than that due to genotypes. On the Biplot, the points for the generally adapted genotypes would be at right hand side of grand mean levels (high mean performance) and close to the line showing IPCA = 0 and this suggested negligible or no $G \times E$ Interaction. According to AMMI model, the genotypes, which had means greater than grand mean and the IPCA I score nearly zero, were considered as stable and adaptable to all the environments. However, the genotypes with high mean performance and with large value of IPCA I score were considered as having specific adaptability to the environments. Genotypes (G 18, G 19, G 40 and G 47), whereas remaining genotypes present in

Table 4
Stability parameters of 56 genotypes of castor
(Eberhart and Russell model, 1966)

Genotypes	Pooled mean performance	b_i value	S^2_{di}	IPCA I	IPCA II
G1	43.17	0.88	1.23*	−0.29	−0.07
G2	41.13	−0.96	0.90	−0.61	−0.19
G3	41.77	−0.58+	0.04	−0.20	0.39
G4	41.40	0.46	2.22**	−0.45	−0.44
G5	42.58	1.00	1.29*	0.29	0.21
G6	42.50	3.73*	2.11**	0.51	−0.85
G7	42.61	2.97	1.61**	0.54	−0.49
G8	41.91	−1.64+	0.49	−0.71	−0.01
G9	41.69	0.86	2.01**	0.10	0.66
G10	42.89	3.63**+	0.95	0.76	−0.07
G11	42.86	−2.08	2.01**	−0.87	−0.32
G12	41.17	2.02*	0.26	0.37	0.10
G13	41.27	−0.95	1.85**	−0.57	0.46
G14	41.46	1.96	2.39**	−0.01	−0.79
G15	41.78	0.56	0.50	−0.27	0.05
G16	42.15	0.76	1.34*	−0.19	−0.53
G17	41.42	−1.15*++	−0.16	−0.41	0.05
G18	42.49	0.39	6.51**	0.03	1.14
G19	42.52	0.31+	−0.23	−0.06	0.11
G20	42.42	0.33	6.88**	−0.73	−0.70
G21	42.36	1.18	3.01**	0.26	−0.39
G22	42.49	0.62	1.62**	−0.39	−0.31
G23	41.17	−0.92**++	−0.25	−0.33	0.13
G24	41.55	2.62*	0.85	0.54	−0.09
G25	42.08	−0.64	0.28	−0.14	0.21
G26	42.91	6.39**++	1.63**	1.35	−0.24
G27	41.02	0.27	2.45**	−0.51	−0.09
G28	41.67	0.17	1.38*	−0.46	−0.21
G29	41.81	−1.07++	−0.06	−0.49	−0.02
G30	42.47	−1.45	2.14**	−0.74	0.39
G31	41.85	0.11	0.11	−0.32	0.02
G32	43.85	2.45	5.66**	0.81	0.04
G33	41.19	1.63**	−0.14	0.22	0.04
G34	41.75	2.82	4.22**	0.75	0.65
G35	41.88	0.53	1.18*	−0.30	0.15
G36	41.76	3.27*	1.68**	0.17	−0.76
G37	41.22	3.53**++	0.33	0.65	0.05
G38	41.83	1.94	1.17*	0.25	−0.47
G39	41.83	1.69*	0.24	0.27	−0.11
G40	45.58	1.71**	−0.17	0.12	−0.22
G41	41.03	−1.64*++	0.17	−0.55	−0.05
G42	41.81	2.83**	0.35	0.45	0.18
G43	42.04	2.38	5.04**	0.54	0.87
G44	42.66	−0.88*++	−0.22	−0.43	0.14
G45	41.32	0.72	0.22	0.11	0.13
G46	42.21	2.94*	0.85	0.61	0.14
G47	42.68	2.50	1.50**	−0.02	−0.44
G48	41.99	0.74	6.02**	0.10	1.07
G49	41.59	3.12	2.05**	0.75	−0.04
G50	43.20	−3.36*++	1.17*	−0.65	0.21
G51	41.93	2.11	0.76	0.45	0.12
G52	41.59	2.70**++	−0.06	0.24	−0.36
G53	41.24	−0.38	1.14*	−0.37	0.46
G54	41.85	−0.51	0.36	−0.36	0.36
G55	42.79	−0.68+	0.01	−0.21	0.11
G56	44.96	3.88**++	0.33	0.37	−0.39
Population Mean	42.11				

Contd. Table 4

*,**Significant at 0.05 and 0.01 per cent levels of probability respectively when Ho: $b_i = 0$

+,++Significant at 0.05 and 0.01 per cent levels of probability respectively when Ho: $b_i = 1$

section 2 and 3 exhibited specific adaptability high oil yielding environments (Zobel *et al.*, 1988[5]; Crossa *et al.*, 1990[6] and Naroui Rad *et al.*, 2013[7]).

CONCLUSION

Genotypes showed the variability over environments and also $G \times E$ interaction was found significant. Genotypes G 40 and G 56 gave significantly higher oil yield. Genotypes G 19 and G 25 were found stable and adapted to all environments. Genotype G 44 and G 55 were stable and adapted to poor environments

P.B. Dave, B.N. Patel, D.J. Parmar and N.A. Patel

Table 5
Analysis of variance (ANOVA) according to AMMI model for castor genotypes

Source of Variation	df	SS	MS	F Ratio	Probability	% SS
Trails	223	550.55	2.47	1.20	0.11	–
Genotypes	55	169.19	3.08	1.50*	0.03	30.73
Environments	3	42.05	14.02	6.82**	0.00	7.64
$G \times E$ Interaction	165	339.31	2.06	–	–	61.63
PCA I	57	176.55	3.10	2.36**	0.00	43.20
PCA II	55	93.33	1.70	1.30[ns]	0.17	22.84
PCA III	53	69.40	1.31	1.00[ns]	0.50	16.98
Pooled residual	53	69.43	1.31	–	–	–
Pooled error	440	–	–	–	–	–

*,**significant at 0.05 and 0.01 per cent levels of probability; *ns* = non-significant.
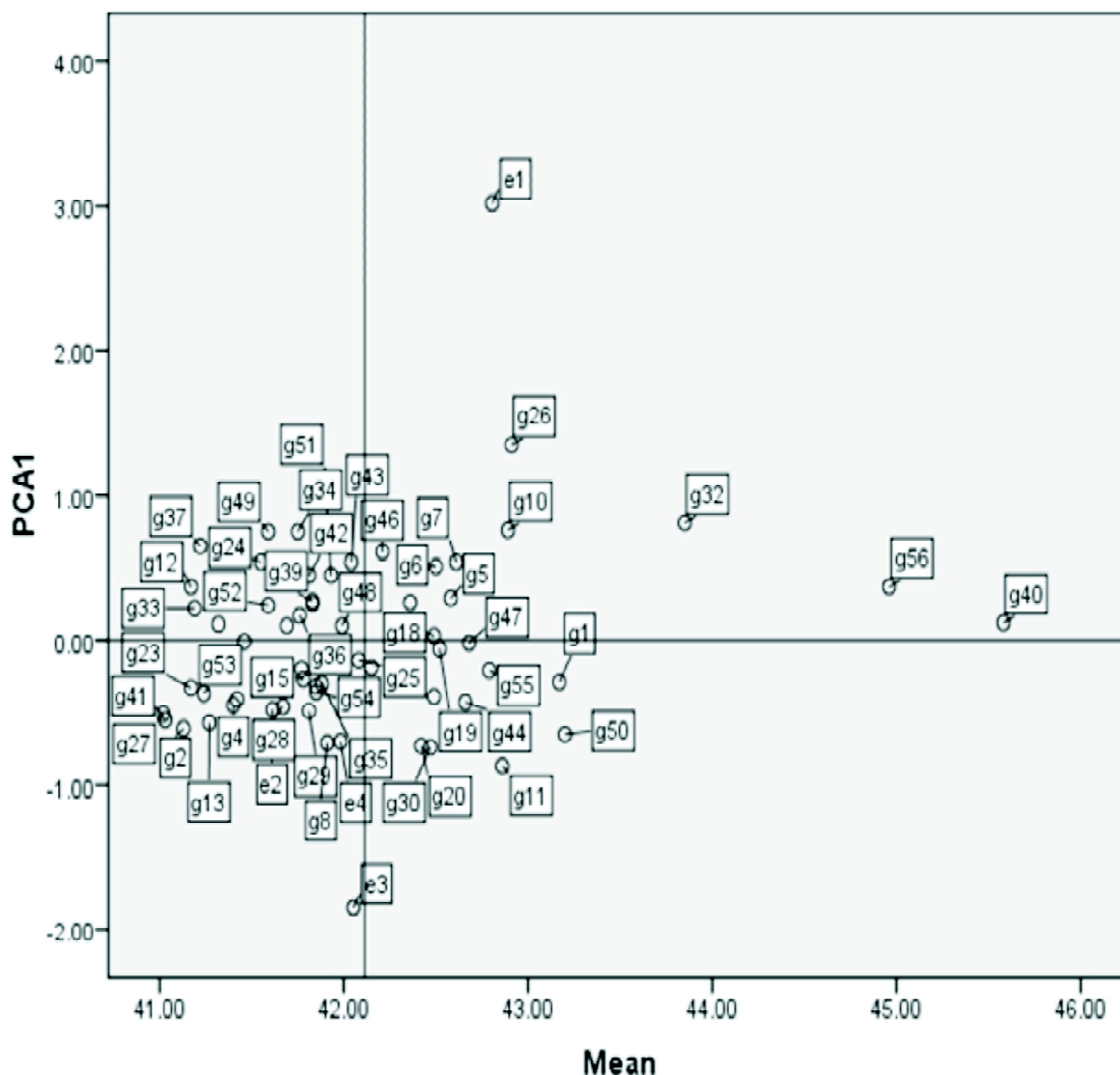

Figure 1: AMMI 1 biplot for castor genotypes and environments

whereas, genotypes *G* 40, *G* 46 and *G* 56 were suitable for favorable environments. AMMI analysis interpreted underline pattern of GEI and genotype *G* 18, *G* 19, *G* 40 and *G* 47 were identified as stable genotypes and adapted to all environments which partial agreement with Eberhart and Russell models because IPCA I explained only about 43.20% variation of GEI.

ACKNOWLGEMENT

REFERENCES

Crossa J.; Fox P. N.; Pfeiffer W. H.; Rajaram S. and Gauch H. *G.* (1990), AMMI adjustment for statistical analysis of an international wheat yield trial. *Theor. Appl. Genet.*, **81**: 27-37.

Eberhart S.A. and Russel W.A. (1966), Stability parameters for comparing the varieties. *Crop Sci.*, **6**: 36-40.

Farshadfar *E.* (2008), Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat. *Pak. J. Biol Sci.*, **11**(14): 1791-1796.

Gabriel K. R. (1971), The biplot graphic display of matrices with application to principal component analysis. *Biometrika*, **58**(3): 453-467.

Gauch H. *G.* and Zobel R. W. (1997), Identifying mega-environments and targeting genotypes. *Crop Sci.*, **37**: 311-326.

Naroui Rad M. R.; Abdul Kadir M.; Rafii M. Y.; Jaafar Hawa Z. *E.*; Naghavi M. R. and Ahmadi F. (2013), Genotype × environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (*Triticum aestivum*) under normal and drought stress conditions. *Aust. J. Crop. Sci.*, **7**(7): 956-961.

Zobel R. W.; Wright M. J. and Gauch H. *G.* (1988), Statistical analysis of yield trial. *Agron. J.*, **80**: 388-393.