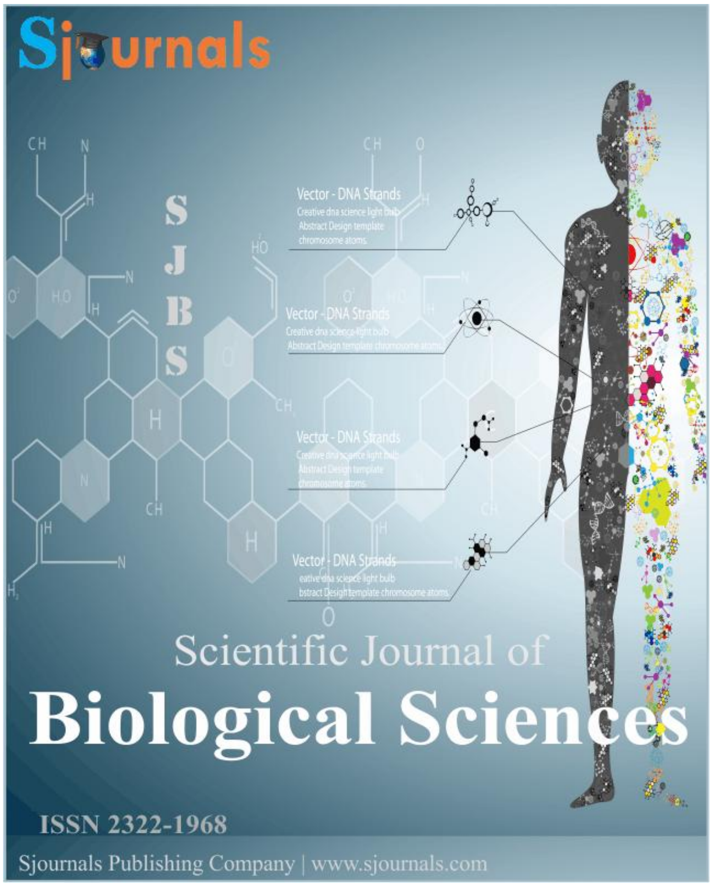
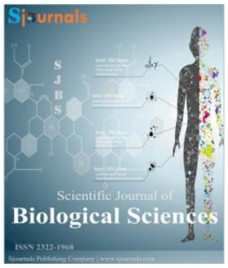

Sjournals
SJBS
Scientific Journal of
Biological Sciences
ISSN 2322-1968
Sjournals Publishing Company | www.sjournals.com

Sjournals
Scientific Journals
Scientific Journal of Biological Sciences (2017) 6(11) 237-241
ISSN 2322-1968
doi: 10.14196/sjbs.v6i11.2510

CODEN (USA): SJBSBH



Contents lists available at Sjournals

Scientific Journal of **Biological Sciences**

Journal homepage: www.sjournals.com

Original article

Stability analysis for grain yield of black cumin (*Nigella sativa* L.) genotypes in Bale, South-East Ethiopia

Mohammed Beriso* **and Getachew Asefa**
Sinana Agricultural Research Center, Oromia Agricultural Research Institute, Ethiopia.

*Corresponding author: mbariis2008@gmail.com

A R T I C L E I N F O

Article history,
Received 10 October 2017
Accepted 11 November 2017
Available online 18 November 2017
iThenticate screening 12 October 2017
English editing 10 November 2017
Quality control 17 November 2017

Keywords,
AMMI
ASV
Yield
Biplot
Genotypes
GxE interaction
PCA

A B S T R A C T

Yield data of 12 black cumin (*Nigella sativa* L.) cultivars tested across 9 rain-fed environments during the 2013-2015 growing season using RCBD in 3 replications. The AMMI analysis tested in nine environments (years) were showed that the yield was significantly affected ($P<0.001$) by genotypes and environment main effects. But non significant for GxE interaction. The model revealed that differences between the environments accounted for about 90% of the treatment sum of squares. The genotypes and the GxE interaction also accounted significantly for 4% and 6% respectively of the treatment SS. The first principal component axis (PCA 1) of the interaction captured 51.32% of the interaction sum of squares. Similarly, the second principal component axis (PCA2) explained a further 18.20% of the GEI sum of squares. The mean squares for the PCA 1 and PCA 2 were significant at P=0.01 and cumulatively contributed to 69.52% of the GxE interaction SS, leaving 30.37% of the variation in the GxE interaction in the residual. The AMMI and AMMI stability value (ASV) identified G10 as the most stable and high yielding genotype.

1. Introduction

Plant breeders invariably encounter genotype x environment interactions (GEIs) when testing varieties across a number of environments. Depending on the interactions or the differential genotypic responses to environments, the varietal ranking can differ greatly across environments. In field crop trials, this interaction is often analysed with the aim of determining the stability of the genotypes especially when there is a reasonable genotype by environment interaction (GEI). A combined analysis of variance (ANOVA) can quantify the interactions, and describe the main effects. However, analysis of variance is uninformative for explaining GEI. Various statistical methods (parametric and non-parametric) have been proposed to study Genotype × environment interactions (Mohammadi and Amri, 2008; Mohammadi et al., 2010). The main problem with stability statistics is that they don't provide an accurate picture of the complete response pattern (Hohls, 1995). The reason is that a genotype's response to varying environments is multivariate (Lin et al., 1988) whereas the stability indices are usually univariate (Gauch, 1988; Crossa, 1990).

Since the genotype response to environmental variations is usually multivariate, therefore, a multivariate method of analysing genotype stability across environments will be the best option. One of the multivariate techniques is the AMMI (additive main effects and multiplicative interaction) model. AMMI analysis reveals a highly significant interaction component that has a clear agronomic meaning and it has no specific design requirements, except for a two way data structure. The AMMI analysis is a combination of analysis of variance (ANOVA) and principal component analysis (PCA) in which the sources of variability in genotype by environment interaction are partitioned by PCA. The AMMI is, therefore, also known as interaction PCA (Gauch and Zobel, 1990), and can have several models: AMMI0, which estimates the additive main effect of genotypes and environments, and does not include any principal component axis (IPCA); AMMI1, which combines the additive main effects from AMMI0 with the genotype by environment interaction effects estimated from the first principal component axis (IPCA 1); AMMI2, and so forth, until the full model with all IPCA axis (Gauch, 1988). It has both linear and bilinear component of GEI and hence very useful in visualizing multi-environment data (understanding complex GEI and determining which genotype won which environment) and gaining accuracy (improving cultivar recommendation and accelerating progress) (Gauch, 2006). The additive main effects and multiplicative interactions (AMMI) is defined powerful tool for effective analysis and interpretation of multi-environment data structure in breeding programs (Ebdon and Gauch, 2002a; Samonte et al., 2005H; Yan et al., 2000; Zobel et al., 1988). The objectives were to evaluate, select and verify promising accessions/lines with desirable traits.

2. Materials and methods

Twelve black cumin genotypes were evaluated at three locations (sinana on station, goro and ginniir) for three consecutive years (2013-2015) during *bona* production season following selection method. The trial was laid out in RCB design with three replications. Data was collected from central two rows. Data was subjected to analyses of variance using GENSTAT software program. Duncan's multiple range tests was done for grain yield. The genotype by environment interaction analyses (GxE) and stability analyses were conducted using the AMMI model.

3. Results and discussion

The AMMI analysis tested in nine environments were showed that the yield was significantly affected ($P<0.001$) by genotypes and environment main effects as well as GxE interaction for grain yield. The model revealed that differences between the environments accounted for about 90.46% of the treatment sum of squares. The genotypes and the GxE interaction also accounted significantly for 3.94% and 5.57% respectively of the treatment SS. The first principal component axis (PCA 1) of the interaction captured 51.32% of the interaction sum of squares. Similarly, the second principal component axis (PCA2) explained a further 18.20% of the GEI sum of squares. The mean squares for the PCA 1 and PCA 2 were significant at $P=0.01$ and cumulatively contributed to 69.52% of the GxE interaction SS, leaving 30.37% of the variation in the GxE interaction in the residual (Table 1).

The presence of significant differences for grain yield among genotypes and environments reveals not only the amount of variability that existed among environments, but also the presence of genetic variability among the genotypes. The AMMI model 1 biplot of the varietal trials was demonstrated in Fig. 1. The abscissa shows the main effects while the ordinate shows the first PCA axis. The environments showed much variability in both main effects and interactions. However, the high potential environments were sparsely distributed in quadrant II and III, while the lower potential environments were also sparsely distributed in quadrants I and IV with high IPCA1 values (Fig. 1).

Table 1

Combined analysis of variance of yield data of 12 black cumin genotypes tested across 9 environments.

Source	df	SS	MS	F	F_prob	% Explaind
Total	323	19824	61.4	*	*	
Treatments	107	16958	158.5	14.54	0	
Genotypes	11	674	61.2	5.62	0	3.97
Environments	8	15340	1917.5	48.79	0	90.46
Block	18	707	39.3	3.6	0	
Interactions	88	945	10.7	0.98	0.52458	5.57
IPCA1	18	485	27	2.47	0.00121	51.32
IPCA2	16	172	10.8	0.99	0.47055	18.20
Residuals	54	287	5.3	0.49	0.99877	30.37
Error	198	2159	10.9	*	*	

Table 2

Environment means and scores.

NE	Environment	Mean	IPCAe[1]	IPCAe[2]
E1	Ginir 2005	7.81	0.90621	0.01188
E2	Ginir 2006	23.01	1.85286	-0.41761
E3	Ginir 2007	22.31	-1.8572	0.48973
E4	Goro 2005	9.49	0.41813	0.34252
E5	Goro 2006	29.28	-0.43716	-0.55783
E6	Goro 2007	11.5	0.81301	1.55743
E7	Sinana 2005	19.44	-0.4313	-2.01592
E8	Sinana 2006	13.88	0.59265	0.10007
E9	Sinana 2007	22.31	-1.8572	0.48973

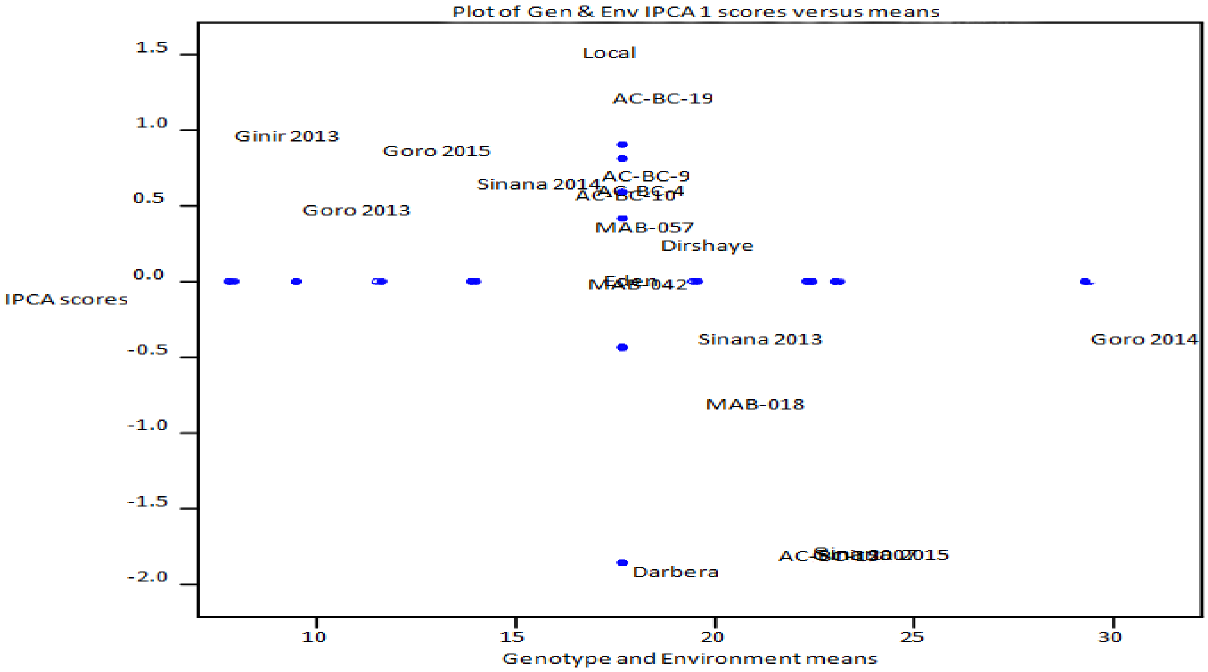


Fig. 1. AMMI model I biplot of the yield of 12 black cumin genotypes evaluated in 9 environments.

Table 3
AMMI yield means, AMMI stability values (ASV), and ranking orders of the 12 genotypes tested across 9 environments.

G	Genotype	Yield (Qt/ha) Means	Rank	IPCAg[1]	IPCAg[2]	ASV
G1	AC-BC-10	16.36	12	0.5208	-0.7164	1.633964
G2	AC-BC-15	21.45	1	-1.8675	-0.1519	5.268135
G3	AC-BC-19	17.29	5	1.16046	1.36488	3.545472
G4	AC-BC-4	16.91	8	0.54727	0.16003	1.55145
G5	AC-BC-9	17.02	7	0.6429	0.59056	1.906596
G6	Darbera	17.77	4	-1.9732	-0.3405	5.574433
G7	Dirshaye	18.53	3	0.18516	-0.2937	0.599037
G8	Eden	17.06	6	-0.0502	-1.2911	1.298861
G9	Local	16.53	11	1.45818	-1.0376	4.24063
G10	MAB-018	19.6	2	-0.8614	1.23067	2.722903
G11	MAB-042	16.67	10	-0.0706	0.58209	0.615191
G12	MAB-057	16.84	9	0.30811	-0.0969	0.87419

In ASV method, a genotype with least ASV score is the most stable, accordingly genotype G7, followed by G11 were the most stable. But G10 is high yielder and medium ASV. Therefore, release of this genotype for production in the mid and lowlands of Bale will result in increased production and productivity of black cumin in the country.

4. Conclusion

AMMI analyses revealed the most stable and high yielding genotypes over ranges of environments. That is genotypes G10. Therefore, release of this genotypes for production in the mid and lowlands of Bale will result in increased production and productivity of black cumin in the country. It can be concluded and recommended from this study that genotypes should be selected for wider adaptations.

Acknowledgments

The authors would like to express profound gratitude to Oromia Agricultural Research Institute (OARI) and Sinana Agricultural Research Center (SARC) for financial support and facilitating this work.

References

Crossa, J., 1990. Statistical analysis of multilocation trials. Adv. Agron., 44, 55-85.

Ebdon, J.S., Gauch, H.G., 2002a. Additive main effect and multiplicative interaction analysis of national turfgrass performance trials: I. Interpretation of genotype x environment interaction. Crop. Sci., 42, 489-496.

Gauch, H.G., 1988. Model selection and validation for yield trials with interaction. Biometrics, 44, 705-715.

Gauch, H.G., 2006. Statistical analysis of yield trials by AMMI and GGE. Crop. Sci., 46, 1488-1500.

Gauch, H.G., Zobel, R.W., 1990. Imputing missing yield trial data. Theor. Appl. Genet., 79, 753-761.

Holhs, T., 1995. Analysis of genotype environment interactions. S. Afr. J. Sci., 91, 121-124.

Lin, C.S., Binns, M.R., 1988b. A method of analyzing cultivar × location 10 year experiments: A new stability parameter. Theor. Appl. Genet., 76, 425-430.

Mohammadi, R., Amri, A., 2008. Comparison of parametric and non-parametric methods for selecting stable and adapted durum wheat genotypes in variable environments. Euphytica, 159, 419-432.

Mohammadi, R., Roostaei, M., Ansari, Y., Amri, A., 2010. Relationships of phenotypic stability measures for genotypes of three cereal crops. Can. J. Plant Sci., 90, 819-830.

Samonte, S.O.P.B., Wilson, L.T., McClung, A.M., Medley, J.C., 2005. Targeting cultivars onto rice growing environments using AMMI and SREG GGE biplot analysis. Crop. Sci., 45, 2414-2424.

Yan, W., Hunt, L.A., Sheng, Q., Szlavnics, Z., 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop. Sci., 40, 597-605.

Zobel, R.W., Wright, M.S., Gauch, H.G., 1988. Statistical analysis of a yield trial. Agron. J., 80, 388-393.

How to cite this article: Beriso, M., Asefa, G., 2017. Stability analysis for grain yield of black cumin (*Nigella sativa* L.) genotypes in Bale, South-East Ethiopia. Scientific Journal of Biological Sciences, 6(11), 237-241.