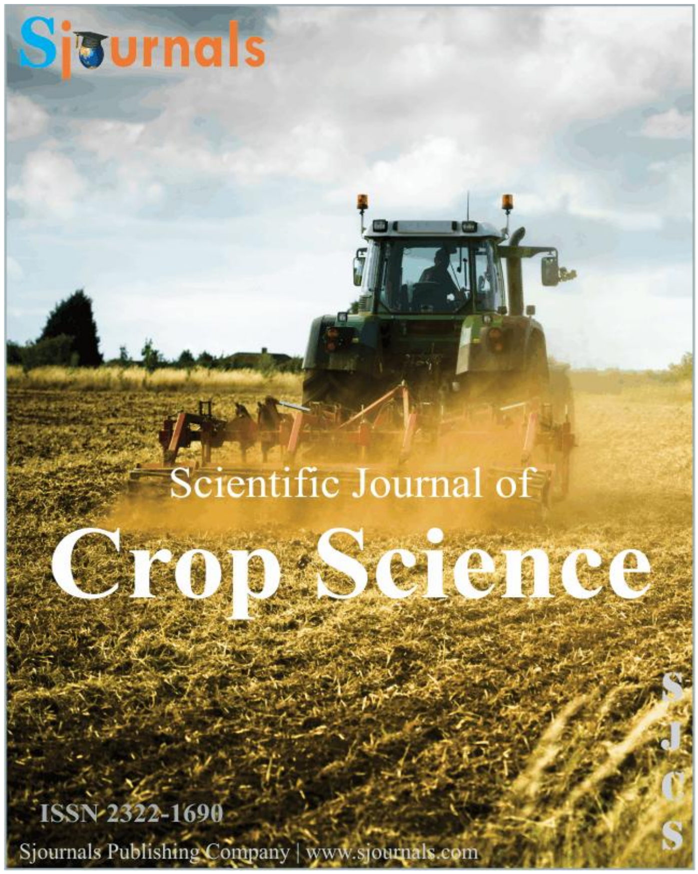
Sjournals
Scientific Journal of
Crop Science
SJCS
ISSN 2322-1690
Sjournals Publishing Company | www.sjournals.com

Scientific Journal of Crop Science (2018) 7(3) 294-298
ISSN 2322-1690
doi: 10.14196/sjcs.v7i3.2509

Contents lists available at Sjournals

Scientific Journal of **Crop Science**

Journal homepage: www.sjournals.com

Original article

Stability analysis for grain yield of coriander (*Coriandrum sativum* L.) genotypes in Bale, South-East Ethiopia

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A R T I C L E I N F O

Article history,
Received 13 February 2018
Accepted 14 March 2018
Available online 21 March 2018
iThenticate screening 15 February 2018
English editing 12 March 2018
Quality control 19 March 2018

Keywords,
AMMI
ASV
Yield
Biplot
Genotypes
GxE interaction
PCA

A B S T R A C T

Yield data of 10 coriander (*Coriandrum sativum* L.) genotypes tested across 9 rain-fed environments during the 2014-2016 growing season using RCBD in 3 replications were analyzed using the AMMI model. 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 as well as GxE interaction. The model revealed that differences between the environments accounted for about 58.16% of the treatment sum of squares. The genotypes and the GxE interaction also accounted significantly for 12.79 % and 29.05% respectively of the treatment SS. The first principal component axis (PCA1) of the interaction captured 41.97% of the interaction sum of squares. Similarly, the second principal component axis (PCA2) explained a further 39.05% of the GEI sum of squares. The mean squares for the PCA1 and PCA2 were significant at P=0.01 and cumulatively contributed to 81.02% of the GxE interaction SS, leaving 18.98% of the variation in the GxE interaction in the residual. The AMMI and AMMI stability value (ASV) identified G8 and G3 as the stable and high yielding genotypes. Therefore, release of these genotypes for production in the mid and lowlands of Bale will result in increased production and productivity of coriander in the country.

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 (IPCA1); 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

Ten coriander genotypes were evaluated at three locations (sinana on station, goro and ginniir) for three consecutive years (2014-2016) 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 test 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 (years) were showed that the yield was significantly affected ($P<0.001$) by genotypes and environment main effects as well as GxE interaction. The model revealed that differences between the environments accounted for about 58.16% of the treatment sum of squares. The genotypes and the GxE interaction also accounted significantly for 12.79% and 29.05% respectively of the treatment SS. The first principal component axis (PCA1) of the interaction captured 41.97% of the interaction sum of squares. Similarly, the second principal component axis (PCA2) explained a further 39.05% of the GEI sum of squares. The mean squares for the PCA1 and PCA2 were significant at $P=0.01$ and cumulatively contributed to 81.02% of the GxE interaction SS, leaving 18.98% 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 coriander genotypes tested across 9 environments.

Source	df	SS	MS	F	F_prob	% Explained
Total	269	14082	52.3	*	*	
Treatments	89	9211	103.5	4.26	0	
Genotypes	9	1178	130.9	5.39	0	12.79
Environments	8	5357	669.6	12.84	0	58.16
Block	18	938	52.1	2.15	0.0064	
Interactions	72	2676	37.2	1.53	0.0139	29.05
IPCA(1)	16	1123	70.2	2.89	0.0003	41.97
IPCA(2)	14	1045	74.7	3.08	0.0003	39.05
Residuals	42	508	12.1	0.5	0.9953	18.98
Error	269	14082	52.3	*	*	

Table 2
Environment means and scores.

NE	Environment	Mean	IPCAe[1]	IPCAe[2]
E1	Ginir 2014	15.34	-0.29222	0.8799
E2	Ginir 2015	20.85	1.44524	1.30762
E3	Ginir 2016	14.86	-3.72563	0.04384
E4	Goro 2014	14.97	-0.02069	0.53685
E5	Goro 2015	13.66	0.26492	0.82639
E6	Goro 2016	17.87	1.68111	0.388
E7	Sinana 2014	17.53	0.00509	-0.91474
E8	Sinana 2015	19.38	0.62822	-3.71502
E9	Sinana 2016	29.12	0.01397	0.64716

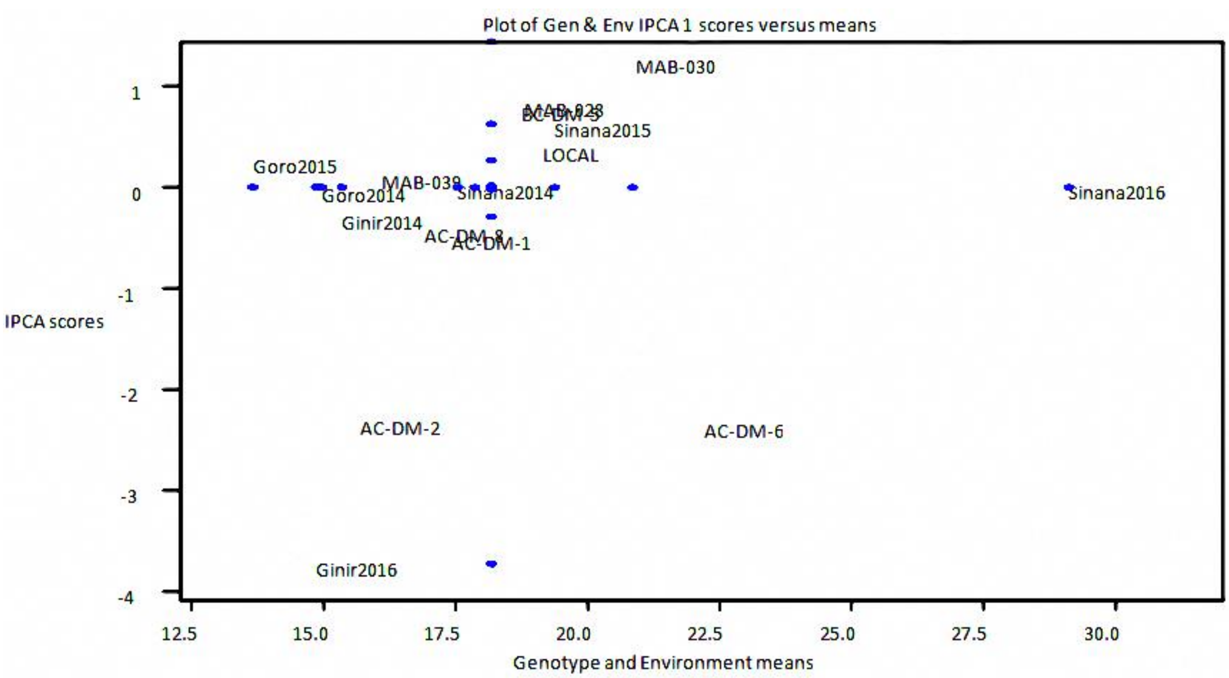

Fig. 1. AMMI model I biplot of the yield of coriander genotypes evaluated in 9 environments.

Table 3
AMMI yield means, AMMI stability values (ASV), and ranking orders of the 10 genotypes tested across 9 environments.

G	Genotype	Yield(Qt/h)	IPCAg[1]	IPCAg[2]	ASV
G1	AC-DM-1	17.41	-0.5	-1.07	1.197336
G2	AC-DM-2	15.7	-2.33	1.99	3.198388
G3	AC-DM-6	22.21	0.82	-0.55	1.038761
G4	AC-DM-8	16.89	-0.42	-0.41	0.609767
G5	BC-DM-5	18.75	0.79	0.49	0.980227
G6	LOCAL	19.16	0.38	-1.43	1.487165
G7	MAB-028	18.8	-2.34	-1.37	2.863637
G8	MAB-030	20.9	1.25	-1.27	1.84861
G9	MAB-039	16.09	0.11	2.43	2.432874
G10	WALTA'I	15.82	2.24	1.19	2.685273

In ASV method, a genotype with least ASV score is the most stable, accordingly genotype G4, followed by G5 were the most stable. But G3 and G8 are 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 coriander in the country.

4. Conclusion

AMMI analyses revealed the stable and high yielding genotypes over ranges of environments. That is genotypes G3 and G8. Therefore, release of these genotypes for production in the mid and lowlands of Bale will result in increased production and productivity of coriander in the country. It can be concluded and recommended from this study that genotypes should be selected for wider adaptations.

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How to cite this article: Beriso, M., Asefa, G., 2018. Stability analysis for grain yield of coriander (*Coriandrum sativum* L.) genotypes in Bale, South-East Ethiopia. Scientific Journal of Crop Science, 7(3), 294-298.