Genotype x environment interaction and stability of indigenous coriander (*Coriandrum sativum* L.) genotypes for seed yield in different agro-climatic zones of Chhattisgarh

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Abstract

The present study was conducted to find out the stability and yield performances indigenous genotypes of coriander (*Coriandrum sativum* L.) evaluated in different agro-climatic zones of Chhattisgarh. The trials were laid out in a Randomized Block Design (RBD) with three replications at three locations for three years resulting in nine environments (Genotype × year interactions). The genotypes and G × E interactions revealed significant differences at $p < 0.01$ for seed yield indicating varieties and testing environments were distinct from each other. Additive main effects and multiplicative interaction analysis (AMMI-biplot) indicated that the yield performances of indigenous coriander genotypes were highly affected by the environments. The first two principal component axes (PCA 1 and PCA 2) were significant and they explained 67% of the total genotype x environment interaction of which 42.4% and 24.6% were represented by PCA 1 and PCA 2, respectively. A biplot generated using genotypic and environmental scores of the first two AMMI components demonstrated that genotype with larger PCA 1 and lower PCA 2 scores were high yielding and stable genotypes and genotypes with lower PCA 1 and larger PCA 2 scores were low yielding and unstable cultivars in tested locations. The genotype GC 5 C-101 (ICS 4) showed higher grain yields (16.35 q ha^{-1}) over grand mean (13.03 q ha^{-1}) and also had the minimum PCA 1 score, minimum AMMI stability value (ASV) and yield stability index (YSI). Therefore genotype ICS 4 (Chhattisgarh Shri Chandrahasini Dhaniya -2) showed wider stability across different agro climatic environments of Chhattisgarh.

Keywords: adaptability, coriander, G × E × Y interaction, stability

Introduction

Coriandrum sativum L. known for pleasant aroma is a very important seed spice crop consumed for leaf as well as seed purpose. It has diploid chromosome number (2n = 22) and belongs to the family Apiaceae. The seeds of coriander contain minerals such as iron, copper, calcium, potassium, manganese, zinc, magnesium and small amount of phosphorus, thiamine, niacin and carotene. It is cultivated as main crop of rabi season in India for seed purpose and for leaf purpose it is cultivated throughout the year as per availability of water. The major coriander growing states are Rajasthan, Gujarat, Andhra Pradesh, Tamil Nadu, Karnataka, Madhya Pradesh, Chhattisgarh, Uttar Pradesh, Haryana and Bihar (Mishra & Pandey 2017). Among these, Rajasthan ranks first in area and production of coriander followed by Gujarat (NHB 2015). The stable performance of coriander genotypes in different agro climatic environments depends on genotype × environment interactions and genotype × environment × year interactions gives wider adaptable material for respective environments. Graphical approach of AMMI biplot is applied to find out stability of genotype for varying environments. An attempt has been made in the present study to evaluate different coriander genotypes across locations,

in Chhattisgarh to investigate the role of G × E interactions and also to analyze the stability of genotypes for seed yield.

Materials and methods

The experiments were conducted at three locations: College of Agriculture and Research Station (CARS), Raigarh; College of Horticulture and Research Station (CHRS), Jagdalpur and RMD College of Agriculture and Research Station (RMD CARS), Ambikapur representing all the three major agro climatic zones *viz*., CG plain zone, Bastar Plateau and Northern Hills zone of Chhattisgarh, respectively for three years (2015-16 to 2017-18) resulting in nine environments (genotype x year interactions). Thirteen genotypes consisting of 10 local landraces and three checks (two national checks Rajendra Swati and Gujarat 2 and state check Chhattisgarh Dhaniya - 1) were used at all the tested locations (Table 1). The experimental materials were grown in randomized block design (RBD), with three replications. The details of three locations are given in Table 1. Each plot consisted of total 13 rows and twenty four plants in each row in plot size of 4 × 2.4 m. The inter- and intra-row spacing was kept at 30 cm and 10 cm, respectively. The recommended package of cultural practices was followed to

Table 1. Description of the test environments

Location	Altitude	Longitude	Latitude	Year	Environment code	Rainfall (mm) (Oct-Feb)	Mean Temp °C (Oct-Feb)	
							Max.	Min.
Raigarh	217 m	83.40	21.90	2015-16	RG	62.8	30.5	13.9
				2016-17	RG	72.1	36.3	17.5
				2017-18	RG	68.6	32.0	14.3
Jagdalpur	564 m	82.03	19.07	2015-16	58.9	58.9	30.6	15.4
				2016-17	182	182	29.1	12.8
				2017-18	237.9	237.9	29.6	12.6
Ambikapur	603 m	83.19	23.11	2015-16	AM	86.2	27.6	12.5
				2016-17	AM	81.4	26.8	11.6
				2017-18	AM	56.3	27.6	13.3

raise a good crop. In each plot, five competitive plants were identified randomly for recording data on seed yield (q ha^{-1}).

Statistical analysis

The data recorded during three years at each location were subjected to stability analysis by estimating analysis of variance (ANOVA) via AMMI model (Gauch 1992). GGE biplot analysis (Yan & Kang 2003) was also employed to examine the genotype, environment, and GEI effects. The yield stability index (YSI) was calculated as per equation: YSI = rASV + rY where, rASV is the rank of AMMI stability value and rY is the rank of mean grain yield of genotypes (rY) across environments. YSI incorporates both mean yield and stability in a single criterion. Low values of this parameter show desirable genotypes with high mean yield and stability. The GGE biplots using genotype plus genotype × environment (G + GE) interaction were studied. To estimate the main and genotype environment interaction effects for seed yield, the GGE biplot approach proposed by Yan (1999) and Yan *et al*. (2000) was used. To achieve this, the total G + GE effect was separated from the observed mean and portioned into multiplicative terms by using singular value decompositions (SVD) for the first (PC1) and second principal components (PC2). All the analyses presented in this study were performed using R statistical software.

Results and discussion

The analysis of variance combined over replications for the genotypes from the three locations evaluated at Raigarh, Ambikapur and Jagdalpur during rabi 2015 to rabi 2017 were subjected to pooled analysis (Table 2). The mean squares due to genotypes (G), environments (E) and G × E interaction were significant indicates that the genotypes differed significantly among themselves and the environments also differed significantly in influencing the performance of genotypes. The significant G × E interaction indicates that the environmental influences on the genotypes was not linear. It is in agreement with Tomar *et al*. (2004), Sastry *et al*. (1989),

Singh & Prasad (2006) in coriander and Jindla *et al*. (1986) in fennel. 56.73% environmental variation observed indicates that all the studied environments were diverse, resulting in large differences among environmental means causing most of the variation in the grain yield. It was followed by 11.24% for genotype and 21.85% variation for G × E (Table 2). The highest variation by environments indicate that environment is major factor on yield performance of coriander in Chhattisgarh.

The AMMI analysis revealed that the first three components accounted for more than 75% of the variation, and among these, the first two accounted for more than 60% variation and hence, the first two components were considered for further interpretations (Table 2). According to Gauch & Zobel (1996) for AMMI biplot analysis only two principal component axes are required while other principal component axes represent non-predictive random variation and did not suit to draw a definite conclusion. The yield responses of 13 coriander genotypes evaluated in the present study are shown in Table 3. The pooled mean data for grain yield of 13 coriander genotypes across the environments and years indicated that genotypes C101 (ICS 4) and C-108 (Rajendra Swati) had the highest (16.35 q ha^{-1}) and the lowest (11.10 q ha^{-1}) seed yield, respectively. Similarly, the environment mean grain yields ranged from 17.02 q ha^{-1} for JD-16 to 8.65 q ha^{-1} for AM 17 and 8.64 q ha^{-1} for JD 15 and grand mean of grain yield over environments and genotypes was 13.03 q ha^{-1}.

AMMI biplot 1: variation of the principal additive effects of genotypes and environments

The AMMI biplot analysis grouped in to total four quadrants. Three environments *i.e.* AM-17, RG-17 and AM-16 and four genotypes (C-112 (ICS-3), C-110 (Chhattisgarh Dhaniya -1), C 104 (ICS 2) and C- 111 (ICS 5) were present in the first quadrant of AMMI biplot while only two environments (RG 16 and AM 15) present in II quadrant of AMMI biplot (Fig. 1) have positive interaction because they have the same positive sign of PCA 1 score. Similarly the environments

Table 2. ANOVA for AMMI analysis of genotype environment interaction on yield of indigenous coriander

Source of Variation	DF	SS	MSS	F value	Pr(>F)	% of Variation	G × E (Expl.)%
Env	8	2603.20	325.40	134.22	<.0001	56.73	
Rep (Env)	18	43.64	2.42	1.24	0.2335	0.95	
Genotype	12	515.57	42.96	21.92	<.0001	11.24	
Env* Genotype	96	1002.73	10.45	5.33	<.0001	21.85	
Residuals	216	423.30	1.96				
PC1	19	424.87	22.36	11.41	<.0001	42.4	42.4
PC2	17	247.06	14.53	7.42	<.0001	67.0	24.6
PC3	15	174.79	11.65	5.95	<.0001	84.4	17.4
PC4	13	93.39	7.18	3.67	<.0001	93.8	9.3
PC5	11	39.17	3.56	1.82	0.0521	97.7	3.9
PC6	9	15.50	1.72	0.88	0.5439	99.2	1.5
PC7	7	6.47	0.92	0.47	0.8556	99.9	0.6
PC8	5	1.50	0.30	0.15	0.9799	100.0	0.1
Total	350	4588.44					

Grand mean=13.03; R-squared=0.91; C.V.=10.74%

Table 3. Performance and stability of 13 coriander genotypes based on mean grain yield (q ha^{-1}), PC1, PC2 scores and AMMI stability value (ASV)

Entry No	Genotype	Seed yield q ha^{-1}	PC1	PC2	ASV	Rank ASV	YSI	Rank Y
C-101	ICS-4	16.35	-0.34	0.03	0.58	1	2	1
C-102	RCC-12-6	13.73	-0.63	-0.42	1.16	6	9	3
C-103	ICS-12-7	13.88	-0.79	-0.60	1.48	8	10	2
C-104	ICS-2	13.22	0.50	0.60	1.05	5	10	5
C-105	ICS-12-5	13.46	-0.38	-0.32	0.72	3	7	4
C-106	ICS-5-1	13.02	-0.64	-0.55	1.23	7	13	6
C-107	GUJRAT-2	12.24	-0.36	-0.36	0.72	2	12	10
C-108	RAJENDRA SWATI	11.10	-1.82	1.90	3.66	13	26	13
C-109	ICS-5-2	12.83	-0.06	-1.66	1.66	9	17	8
C-110	ICS-1	11.89	0.97	1.08	1.99	11	23	12
C-111	ICS-5	12.90	1.05	-0.06	1.80	10	17	7
C-112	ICS-3	12.68	0.42	0.01	0.72	4	13	9

RG 15, JD 16 and JD 17 and genotypes C 101 (ICS 4), C 102 (RCC 12-6), C103 (ICS 12-7) and C 105 (ICS 12-5) present in III quadrant of biplot AMMI 1 graph (Fig. 1) have positive interaction because they all have the same negative value of PCA 1 score. In Quadrant IV environments JD 15 with four genotypes C 109 (ICS 5-2), C106 (ICS 5-1), C 107 (Gujarat 2) and C 108 (Rajendra Swati) had negative PCA 1 and positive PCA 2 values indicating below average performance of genotypes over grand mean. Genotypes with PCA 1 scores near zero (either positive or negative) had little interaction across environments and, vice versa for environments (Crossa *et al.* 1991). Genotype and environment mean combinations with PCA 1 scores of the same sign produced positive specific interaction effects, whereas combinations of opposite sign had negative specific interactions. It was observed that the genotypes or environments on the right side of the midpoint of the axis have higher yields than those on the left hand side. The high yielding genotypes with above average mean (13.03 q ha^{-1}) were C-101 (ICS-4), C-102 (RCC 12-6), C-103 (ICS 12-7), C-104 (ICS-2), and C-105 (ICS -12-5), while low yielding genotypes were C-107 (Gujarat-2), C-108 (Rajendra Swati), C-109 (ICs 5-2), C-110 (Chhattisgarh Dhaniya -1), C-111 (ICS-5), C-112 (ICS 3), and C-113 (ICS 5-3). Genotype C-106 (ICS 5-1) yield was at par with average mean (Fig. 1.). Similar results were reported by Jindla *et al.* (1985), Darvhankar *et al.* (2015), and Yadav & Bartholia (2016) for seed yield of coriander.

The genotypes with specific adaptation to particular environment have high PCA 1 score with PCA 1 values of the same sign. Genotypes having high PCA 1 score were C-102 (RCC 12-6), C-106 (ICS 5-1), C-103 (ICS 12-7), C-110 (Chhattisgarh Dhaniya -1), C-108 (Rajendra Swati) and C-113 (ICS 5-3) while the environments (JD 17, JD 16, AM 16, RG 17, and AM17) having high PCA 1 score exhibited high interaction (Fig. 1). The genotypes with large negative PCA 1 values have specific adaptation to particular environment; these genotypes were C-108 (Rajendra Swati, and C-106 (ICS 5-1) with specific adaptation to JD 17 environment while

C-102 (RCC 12-6) and C-103 (ICS 12-7) were having specific adaptation to JD 16 environment due to presence of large negative PCA 1 score and C-108 to JD 15 environment. Genotypes having large positive PCA 1 score were C-101 (ICS 4) to JD 16, C-104 (ICS-2) to AM -16, RG -16, have above average mean yield and had wider adaptability to environments. The environments had differences in both main effects and interactions (Fig. 1). Total environments were grouped in to three, *i.e.* above average mean (stable and high yielding environments), below average mean (unstable and low yielding environments) and poor yielding and unstable environments on the basis of yield performance.

Environments with above average mean seed yield: It includes JD 16 (17.02), RG 16 (15.47), AM 15 (15.24), JD 17 (13.88) and RG 15 (13.35). These were productive and recorded above average mean yield across the season and year.

Environments with below average and at par with mean yield: In this environment AM 16 (12.84) and RG 17 (12.21) recorded seed yield at par with grand mean, which indicates that these also have potential for stable genotypes.

Poor yielding unstable environments: In this environment, AM 17 (8.65) and JD 15 (8.64) were present where, seed yield of almost all genotypes fluctuated due to environmental variation.

Coriander genotypes showed variation for seed yield at all the testing environments during 2015–16 to 2017–18. The positive interaction exhibited by genotypes and environments which have similar either positive or negative sign while positive or negative and vice versa sign of PCA 1 score showed negative specific interactions. From the present AMMI biplot analysis a total of five genotype units (GU) were categorised which are explained below (Fig. 1). GU1 consisted of only one genotype C-104 (ICS-2) that was located on quadrant I and had mean yield of 13.22 q ha^{-1}which was greater than total average yield (13.03 q ha^{-1}). It had both positive PCA 1 and PCA 2 with wider ASV value. The
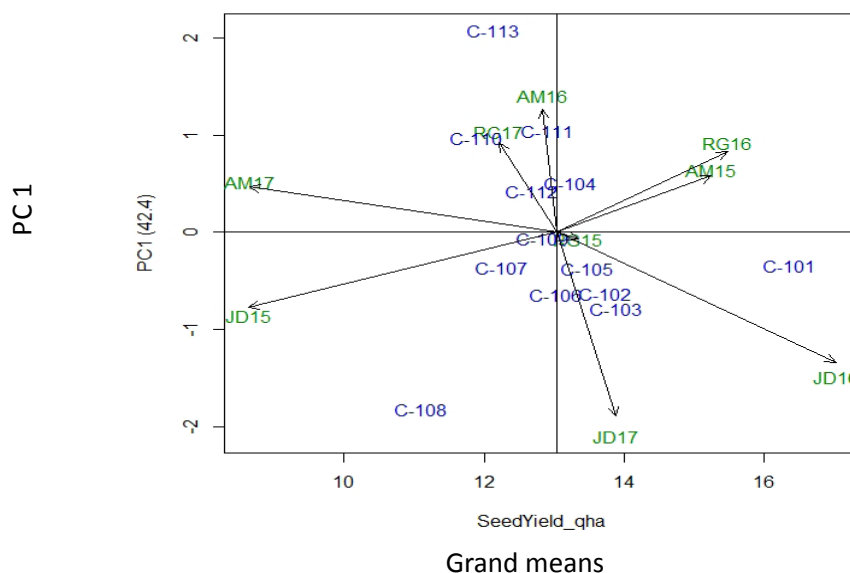
Fig. 1. PCA 1 scores versus grand means. Plot of genotype and environment PCA 1 scores versus grand mean. C-101 to C-113 represent genotypes while environments are represented by two letters followed by numbers. The details of the genotypes and environments are presented in Tables 3 & 4.

Genotype C 109 (ICS 5-2) was more near to origin indicating its stable performance for seed yield. Similarly other stable genotypes were C 105 and C-112. GU2 categorised genotypes (C-113 (ICS 5-3), C-111 (ICS 5), C 110 (Chhattisgarh Dhaniya -1) and C-112 (ICS-3) were best suited to environment AM 16 and RG 17 and were present in quadrant I and had lower yield than grand mean (Table 4). Its PCA 1 values ranged from 0.42 to 2.08 while minimum PCA 2 value of -0.06 and maximum PCA 2 value of 1.08 were recorded. This unit has large ASV values hence not accepted. GU3 included four genotypes *viz.*, C-108 (Rajendra Swati), C-107 (Gujarat 2), C-106 (ICS 5-1) and C-109 (ICS 5-2) in quadrant IV with average yield of 12.31 q ha^{-1}, which is below the grand mean (13.03 q ha^{-1}). GU 3 category exhibited negative values of PCA 1 score (-0.06 to -1.82) and PCA 2 score (-0.36 to -1.90) with average ASV values. It indicates presence of high G × E interactions and were highly unstable across the environments and years. GU 3 categories of genotypes performed well at low yielding environments. GU4 category had three genotypes C 103 (ICS 12-7), C102 (RCC 12-6), and C 105 (RCC 12-5), in quadrant III with average seed yield of 13.69 q ha^{-1} which was higher than grand mean (13.03 q ha^{-1}). Both

PCA 1 (-0.38 to –0.79) and PCA 2 (-0.32 to -0.60) scores were negative, while 0.72 to 1.48 positive ASV values and indicating specific adaptability to above average mean yielding environment (JD 17). GU5 had high yielding (16.35 q ha^{-1}) genotype C-101 (ICS 4) than the grand mean (13.03 q ha^{-1}). It has negative PCA 1 (-0.34) score and positive PCA 2 (0.03) scores. It has recorded minimum ASV value (0.58) indicating its less interaction to environments and showed wider adaptability to different environment.

Representation of AMMI stability value (ASV)

The stable genotype will have minimum ASV value. In the present study, the genotype C-101 (ICS 4) and C-105 (ICS 12-5) recorded minimum ASV value (0.58 and 0.72 respectively) and registered stable higher seed yield (16.35 q ha^{-1} and 13.46 q ha^{-1}) over average yield. Darvhankar *et al.* (2015) reported stable performance of high yielding genotypes of coriander across the environments. Least yielding genotypes C-107 (Gujarat 2) and C-112 (ICS-3) were stable for low yielding environments. Yan & Kang (2003) reported that stable performance of genotypes in low yielding environments is the basis for selection of genotypes.

Table 4. Performance and stability of nine test environments based on mean grain yield (q ha^{-1}), PC1, PC2 scores and AMMI stability value (ASV) of indigenous coriander

Env. code	Environment	Seed yield q ha^{-1}	PC1	PC2	ASV	Rank ASV	Rank Y	YSI
AM15	Ambikapur_2015	15.24	0.64	-1.85	2.15	5	3	8
AM16	Ambikapur_2016	12.84	1.41	-0.64	2.50	6	6	12
AM17	Ambikapur_2017	8.65	0.52	1.08	1.39	2	8	10
JD15	Jagdalpur_2015	8.64	-0.86	0.24	1.49	3	9	12
JD16	Jagdalpur_2016	17.02	-1.49	0.15	2.56	8	1	9
JD17	Jagdalpur_2017	13.88	-2.10	-0.35	3.62	9	4	13
RG15	Raigarh_2015	13.35	-0.08	0.22	0.26	1	5	6
RG16	Raigarh_2016	15.47	0.92	-0.69	1.73	4	2	6
RG17	Raigarh_2017	12.21	1.03	1.84	2.55	7	7	14

Representation of G × E interactions from AMMI2 biplot analysis

Genotypes C-111 (ICS 5), C 108 (Rajendra Swati), C 110 (Chhattisgarh Dhaniya -1), C-113 (ICS 5-3) and environments AM 16, AM 15, JD 17, RG 17 were distant from the origin indicating less interactive genotypes and environments. It was observed that C-109 (ICS 5-2), has less distance from the origin followed by C-105 (ICS 12-5), C-107 (Gujarat 2), C 112 (ICS-3), and C 101 (ICS 4) and were judged as non responding to environmental interaction. The presence of genotypes C 103 (ICS 12-7), and C 102 (RCC 12-6) in environmental axis RG 15 to JD 17, were the most adapted to environment JD 17 while C 105 (RCC 12-5), and C 109 (ICS 5-2) were more stable and adapted to RG 15. In quadrant III, JD 17 environment was suitable for high yield performance and is a stable environment for seed yield of genotypes (Fig 1). AMMI2 biplot analysis also showed stability of genotypes in JD 17 environment. Genotypes C 101 (ICS 4), from segment C 109 to C 103 were most adapted to environments JD 17, JD 16, JD 15 and RG 15. Genotype C- 104 (ICS 2) was adapted to environment AM 17 while C 113 (ICS 5-3) was adapted to RG 17 and AM 16. C 111 (ICS-5) and C 112 (ICS-3) were most adapted to environments AM 16 and RG 16.

Selective nature of the environment can be

Table 5. Mean response of five genotype categories (GC) to eight environments (E), range of PCA 1 and PCA 2 scores

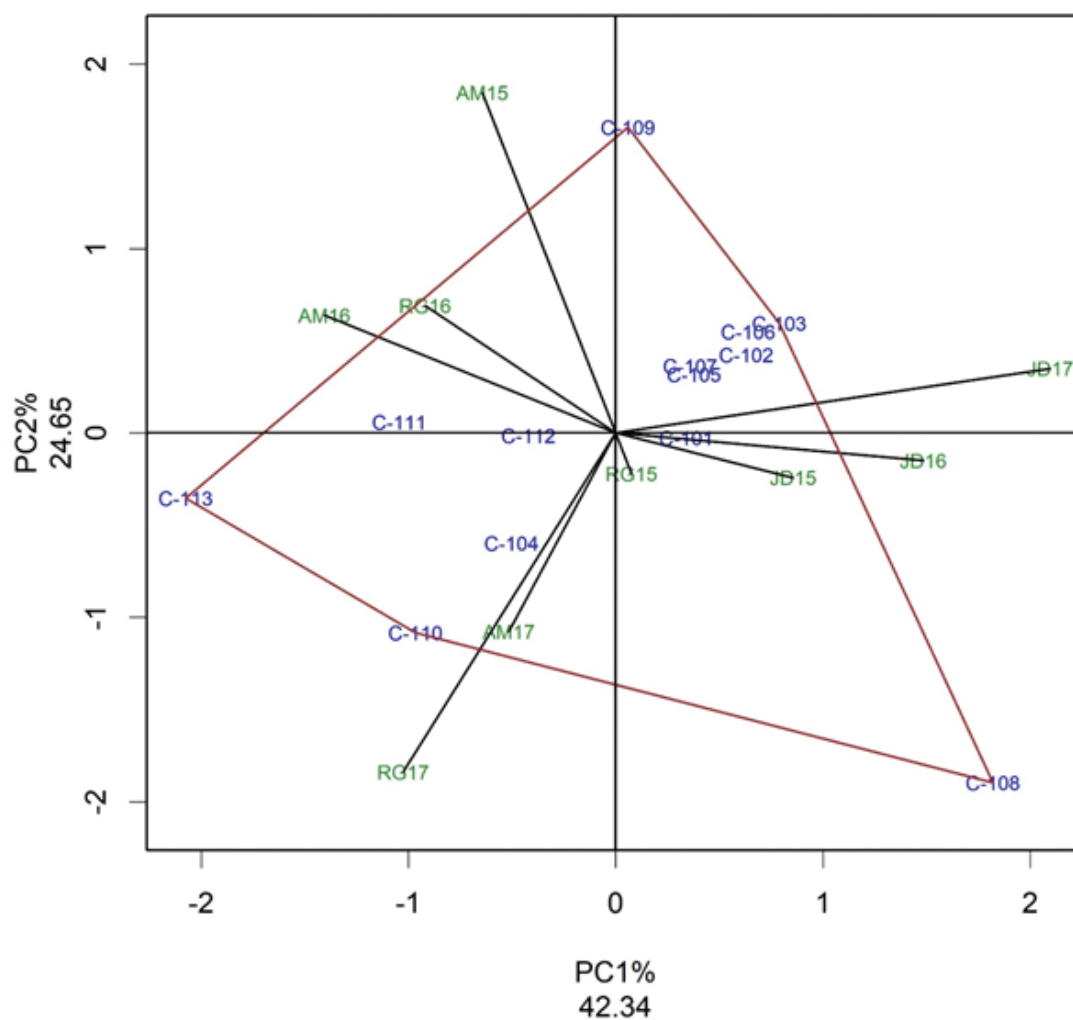| GC	Entry_No	Genotypes	Mean (q ha^{-1})	ASV range	PCA 1 range	PCA 2 range
GC1	C-104	ICS 2	13.22	1.05	0.5	0.6
GC 2	C 113, C 111, C 110, C 112	ICS 5-3, ICS-5, ICS-1, ICS-3	13.73	0.72 to 3.59	0.42 to 2.08	-0.06 to 1.08
GC 3	C 108, C107, C 106, C 109	Rajendra Swati, Gujarat 2, ICS 5-1, ICS 5-2	12.31	0.72 to 3.66	-0.06 to -1.82	-0.36 to 1.90
GC 4	C 103, C 102, C 105,	ICS-2, RCC 12-6, ICS 12-5	13.69	0.72 to 1.48	-0.38 to -0.79	-0.32 to -0.60
GC 5	C 101	ICS 4	16.35	0.58	-0.34	0.03

Fig. 2. Biplot of IPCA1 versus IPCA2 scores of coriander genotypes tested at three locations

determined by its scores from AMMI model. Environments with large IPCA scores are more discriminative of genotypes, while environments with IPCA scores near zero exhibit little interaction across genotypes and less discrimination among genotypes. In this regard, AM 16, AM 15, JD 17, JD 16, and RG 17 were most discriminative as indicated by long distance from the origin of the biplot graph (Fig. 2). Genotypes with positive PCA 1 scores respond positively (adaptable) to the environments. Those that respond negatively to the environments (less adapted) have negative PCA 1 scores (Samonte *et al*. 2005). The biplot revealed that the genotypes C 104 (ICS-2), C 110 (Chhattisgarh Dhaniya -1), C 111 (ICS-5), C 112 (ICS-3), and C 113 (ICS 5-3) with positive PCA 1 scores responded positively to the environments AM 17, AM 15, RG 16, RG 17 and AM 16 and hence are adaptable to these environments. Similarly, genotypes C 101 (ICS 4), C 102 (RCC 12-6), C 103 (ICS 12-7), C 105 (ICS 12-5), C 106 (ICS 5-1), C 107 (Gujarat 2), C 108 (Rajendra swati), and C 109 (ICS 5-2), with negative PCA-1 scores are adapted to the environments RG 15, JD 15, JD 16 and JD 17.

In the present study, AMMI biplot analysis model was used to identify stable coriander genotypes and their genotype × environment interaction over major agro climatic zones of Chhattisgarh. The genotype C-101 (ICS 4) (Chhattisgarh Shri Chandrahasini Dhaniya -2) was found to be high yielding genotype and had wider stability.

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