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Full Research Article

Mega Environment Analysis and Cultivar Selection for Resource Optimization

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Abstract

Coriander crop improvement is vested with several issues like lack of unified protocol, delineation of suitable test environments and difficulties in the selection of a genotype over a wide range of environments. A study was taken up with three fold objectives viz. genotype evaluation in a mega environment consisting of diverse sub-environments, test environment discrimination and selection, suitability and superiority of superior genotype in a specific set of environments. Thirteen genotypes were evaluated in eleven diverse agro-climatic zones for three years (2009−2012). The graphical tool GGE (genotype main effect [G] and genotype and environment interaction [GE]) biplot was used to analyze the multi-environment data obtained. The biplot explained the 75% (53 and 22% by PC1 and PC2, respectively) of the total G+GE and adequately represented the environment-centered data.The evaluation of test environments revealed the nature of mega-environment and ideal test environments among the environments evaluated. Based on this, the test sites could be grouped into two diverse sub-mega-environments. The best performing and candidate genotypes were identified for each sub-mega-environment. Among the eleven test environments, three sites were the most discriminative of the genotypes, hence to evaluate a large number of genotypes in India these three ideal test environments can be deployed thus saving time, resources and energy. The results revealed that GGEbiplot is very useful in discriminating coriander genotypes and test environments in traditional coriander growing areas of India.

1. Introduction

Coriander (*Coriandrum sativum* L.) is grown widely as a '*grain* or *seed'* spice. Though the spice is used worldwide, its production is limited to some Mediterranean, African and Asian countries. India, Mexico, China, Syria, Iran, Bulgaria, Morocco, Egypt, Tunisia, Afghanistan, Russian Federation, Turkey, Canada, Peru and Ukrain are the major producers of the spices (FAOSTAT, 2015). It is grown mainly in two farming situations-irrigated light soils and rainfed vertisols. The majority of the crop improvement programs mainly aim at developing long duration varieties suitable for irrigated light soils (Bhandari and Gupta, 1993), sodic wastelands (Singh et al., 2005) and special traits (Lopez et al., 2007). However, yield performance of a genotype varies significantly when it is subjected to diverse environments. The variation in yield performance over environments is a product of genotype-by-environment (GE) interaction (Allard and Bradshow, 1964). The GE interaction necessitates the selection of widely adapted and stable genotype across a wide range of environments. It is also possible to select a genotype that best adapts to the particular environment, thus taking the advantage of the environment (Ceccarelli, 1989). Grain yield being a quantitative trait and a product of genotype, environment and their interactions depicts cultivar response to environmental influences (Akcura et al., 2011; Flis et al., 2014). Various methods are used to analyze the GE interaction. Regression models were widely used and are popular among the plant breeders for discrimination of genotypes or cultivars across a wide array of environments (Eberhart and Russell, 1966; Finlay and Wilkinson, 1963; Perkins and Jinks, 1968). Other methods such as the stability variance (Shukla, 1972), coefficient of determination (Pinthus, 1973) and coefficient of variation (Francis and Kannenberg, 1978) are also used but are less popular. Additive main effects and multiplicative interaction (AMMI) was subsequently introduced as a powerful tool (Gauch, 1992) and its application was widely appreciated (Gauch, 2013). All these approaches paved the way for robust selection of genotypes and help the farmers to realize higher yields (Annicchiarico, 2002; Gauch et al., 2008).

However, development of improved cultivars is hampered by the lack of information about delineation of mega-environments and issues related site specific adaptability of the genotypes. It is very crucial to analyze, understand and exploit the nature of environment and genotype interactions for facilitating identification of array of test environments and identification of suitable, promising genotypes for such environments. Discrimination of test environments, the relation of test environments to the whole mega environment and the analysis of genotype performance from the perspective of mega environment, strengthen the efforts to maximize grain yields (Gauch and Robel, 1997; Yan, 2002). GGEbiplot analysis was proposed by Yan (2001); Yan and Kang (2002); Yan and Tinker (2006) as an intuitive tool to zoom in the various perspectives of mega environment, genotype and stability. Alwala et al. (2010) compared the robustness, reliability and accuracy of the GGEbiplot model with Eberhart and Russell joint regression and reported the superiority of GGEbiplot even with one year data.

The G×E interaction (GEI) was analyzed to study the performance of genotypes under different environments via numerous methods which lead to the development of various statistical analytical methods of GEI, to envisage the phenotypic response to varying environments, and to assess the performance of genotypes in those environments (Akcura et al., 2011; Shojaei et al., 2011). Such procedures differed in the parameters used in the biometric analysis (Fritsche-Neto et al., 2010). These efforts to unveil the patterns of GEI include the ones such as joint regression (Eberhart and Russell, 1966; Finlay and Wilkinson, 1963; Perkins and Jinks, 1968) additive main effects and multiplicative interaction (AMMI) (Gauch, 1992), type B genetic correlation (Burdon, 1977; Yamada, 1962), sites regression (SREG) (Yan et al., 2000) and FGGE (Garbuglio and Ferreira, 2015). Yan et al. (2001, 2007) effectively used a graphical display using Sites regression (SREG), widely known as GGE (G+GE interaction) biplot that evaluated cultivars by graphical representation to display the GGE of METs data. The scheme uses multivariate analysis by separation of GEI data in to PCA components and GGEbiplot based on singular value decomposition environmental-centered or intra-environment standardized GE data. The technique is overwhelmingly and critically deployed to understand GEI data in agriculture and horticulture(Akcura et al., 2011; Badu-Apraku et al., 2011; Francisco et al., 2011; Fritsche-Neto et al., 2010; Hamayoon et al., 2011; Jandong et al., 2011; Mohammadi et al., 2010; Mujahid et al., 2011; Shojaei et al., 2011; Tonk et al., 2011). The GGEbiplot was found very useful utility in several crops across the world which helped in selecting the genotypes in varied environments. Coriander genotypes (subspecies *microcarpum*) show remarkable plasticity in physiological characteristics (time of flower initiation, time of whole-rosette senescence and heat resistance) across seasons thus putting differential bio-mass and vegetable yield (Bashtanova et al., 2013; Diederichsen, 1996). In this context, the present study was initiated to study the multi environment performance of thirteen promising coriander genotypes across eleven diverse environments for three years. The data was subjected to GGEbiplot analysis for evaluating mega environments as well as the performance of the genotypes. The present study was taken up to analyze the MET data by GGEbiplot to evaluate the efficacy of test sites and to determine the performance of different coriander cultivars at eleven locations in India.

2. Materials and Methods

The present investigation was conducted at under the aegis of “All India Coordinated Research Project on Spices (AICRPS)” project, Indian Institute of Spices Research, Kozhikode, India. The experiment was conducted during the winter seasons of 2009, 2010 and 2011.

2.1. Test environments and experimental conditions

The three year testing was conducted (2009–10, 2010–11 and 2011–12) across eleven locations. The geographical location of the experimental stations is presented in Figure 1 and Table 1. The field experiment was laid out in the randomized control block design (RCBD) in 4×2.4 m^2 plots containing eight rows. Sowing was taken up by dibbling at 30×10 cm^2 spacing. At 20 DAS, the seedlings were thinned to maintain optimum plant population. Crop and nutrient management were applied as per recommendations for the specific test environment.

2.2. Genotypes

Thirteen genotypes of diverse geographical origin, which were found promising in three year Station Yield Trials at respective test centers, were included in the study. The genotypes included in the study were ACor-1 from Ajmer, RKD-13 and RKD-18 from Kota, Rajasthan, UD-475 and UD-801 from Jobner, Rajasthan, LCC-236 and LCC-237 from Lam, Andhra Pradesh, DH-220 and DH-233 from Hisar, Haryana and NDCor-30 and NDCor-49 from Kumargunj, Uttar Pradesh. Hisar Anand from Hisar, Haryana was used as national checks. Local variety of the test centrewas used as a random check. The genotypes included in the study were coded every year and evaluated. After three years of evaluation, the genotypes were decoded and their yield performance was assessed. Yield was recorded on net plots and converted to ha^{-1} yield for use as an indicator to the stability of the genotype over the locations.

2.3. Statistical analysis

The data set thus generated, composed of yield data of thirteen genotypes across eleven environments was subjected to GGEbiplot analysis using GGEbiplot GUI package of R-statistical software (Frutos et al., 2014) to disintegrate the G×E interactions. The first two principalcomponents (PC1 and PC2) used in the construction of GGEbiplot were derived from subjecting environment-centered grain yield means for eachlocation, averaged over the three seasons, to singular value disintegration. The data were not transformed but standardized, and were environment-centered. The yield analysis using "which-won-where" graphs, ranking of genotypes on the basis of both yield mean and stability and interrelationship among the genotypes was taken up.

3. Results and Disucssion

The three years mean of the genotypes and environments is presented in Table 2. The means of either the genotypes or the

Figure 1: Eleven test centers in eight states along with two unique (sub) mega environments

Table 1: Geographical location, soil and agro-climatic details of the test environments

Test environment		Latitude	Longi-tude	Altitude (amsl)	Soil		Agro-climatic NARPZone of India
Location	State				pH	Texture	
Ajmer	Rajasthan	26.45° N	74.64° E	486	8.5	Sandy loam	RJ-5: Semi-arid eastern plain zone
Dholi	Bihar	25.59° N	85.35° E	400	7.5	Sandy loam	BI-1: North West alluvial plains
Guntur	Andhra Pradesh	16.18° N	80.29° E	032	7.8	Vertisols	AP-1 Krishna zone
Hisar	Haryana	29.08° N	75 43° E	215	7.7	Sandy loam	HR-2: Western zone
Jabalpur	Madhya Pradesh	23.10° N	79 57° E	411	7.2	Clayey	MP-1: Kymore plateau and Satpura hill zone
Jagudan	Gujarat	23.31° N	72 24° E	70	7.9	Sandy loam	GJ-4: North Gujarat zone
Jobner	Rajasthan	26.58° N	75 23° E	427	8.1	Loamy sand	RJ-5: Semi-arid eastern plain zone
Kota	Rajasthan	25.12° N	75 51° E	235	8.3	Loamy sand	RJ-9: South-eastern humid plain zone
Navsari	Gujarat	20.57° N	72 55° E	9	7.9	Clayey	GJ-1: South Gujarat heavy rainfall zone
Pantnagar	Uttarakhand	29.01° N	79 29° E	344	7.5	Clay loam	UK-2: Bhabar and tarai zone
Raigarh	Chattisgarh	21.53° N	83 23° E	215	6.7	Sandy loam	CG-1: Chattisgarh plain zone

environments were least informative. Selection of genotypes and their relation with environment is posed with several problems as means offered no clues. But, the GGEbiplot (genotype main effect (G) plus genotype-by-environment (GE) interaction (G+GE) analysis) was found quite useful for analyzing the multi-environment data. Biplot analysis revealed clear delineation of mega-environment (sub), genotypes by performance and test-environments.

3.1. Mega-environment (genotype-by-environment data (GED)) analysis

The biplot (Figure 2) based on environment-focused partitioning revealed the relationships among the test environments. The biplot explained the 75% (53 and 22% by PC1 and PC2, respectively) of the total G+GE and adequately represents the environment-centered data. The analysishelped in visualization of complete mega-environment, and revealed the existence of sub-mega-environments in them in relation to coriander cultivation in India. The eleven test environments fall in to two (sub) mega-environments. The biplot visualization helped to achieve this in a robust manner forming two sub-mega-environment sectors i.e. sectors formed by ray 2 and 3, ray 4 and 5. The most important issue here was to identify a superior genotype across the environments (mega-environment). The genotypes at the verticeswere the highest yielder across these environments. These biplot sectors and environment grouping in relation to genotype performance revealed that the genotype DH-220 was highest yielder in test locations Jabalpur, Jobner, Hisar, Raigarh and Pantnagar. Among the test environments Kota, Jagudan, Ajmer, Navsari and Lam, RKD-18 was the highest yielder. The visualization was found more robust and clear than the raw data. However, the precise view of the genotype performance and stabilitycan be visualized in the sub-mega-environment microanalysis (Figure 3 and Figure 4).

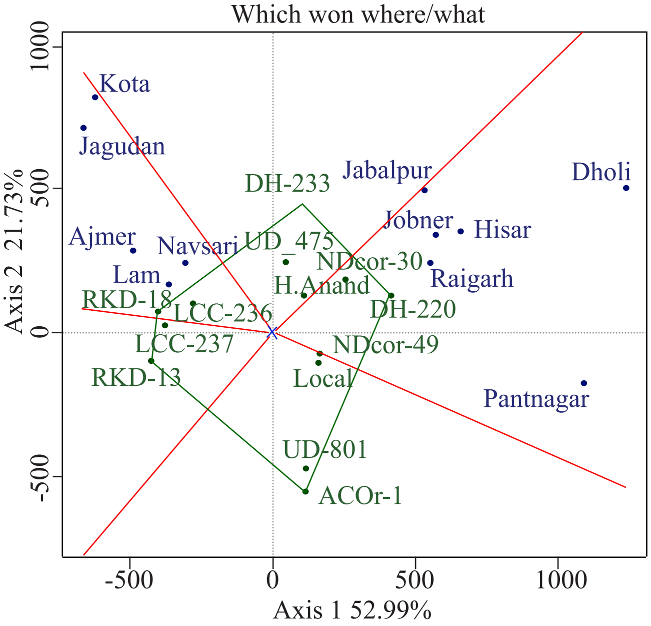

Figure 2: Genotype by environment data analysis

Table 2: Three years mean yield (kg ha^{-1}) of thirteen coriander genotypes tested at eleven locations in India

Geno-types	Test environments												
	Ajmer	Lam	Navsa-ri	Jagu-dan	Kota	Niche-1^*	Hisar	Jabal-pur	Dholi	Pant-nagar	Rai-garh	Jobner	Niche-2^*	Mean
RKD-13	786	616	665	1760	1723	1110	1342	1258	808	1286	323	1238	1043	1073
RKD-18	712	727	675	1843	1955	1182	1363	1501	902	1364	335	1192	1110	1142
UD-475	420	569	868	2052	1248	1031	1932	1752	1724	1570	352	1741	1512	1293
UD-801	355	531	390	1273	684	647	1751	1590	1328	1784	470	1308	1372	1042
LCC-236	911	897	930	2221	1096	1211	1590	1528	1455	1251	338	1054	1203	1206
LCC-237	693	959	834	2114	1364	1193	1503	1589	992	1285	365	1023	1126	1156
DH-220	509	646	592	1461	1029	847	2054	2063	2070	2140	1022	1521	1812	1373
DH-233	648	507	566	1933	1670	1065	2104	1984	1764	1671	805	1536	1644	1381
ND-Cor-30	464	561	410	1589	1528	910	1799	1977	1940	2146	544	1555	1660	1319
ND-Cor-49	437	591	574	1347	1234	837	1801	1592	1743	1824	454	1669	1514	1206
ACor-1	330	374	438	1350	698	638	1601	1483	1363	2043	350	1122	1327	1014
H. Anand	550	531	675	1929	1305	998	1758	1749	1668	2054	562	1494	1548	1298
Local	277	456	794	1491	1264	856	1638	1340	1697	1988	851	1517	1505	1210
Mean	545	613	647	1720	1292	963	1710	1646	1496	1724	521	1382	1413	1209

3.2. Genotype evaluation: Mean performance and stability of the genotypes

The average environment view (AEC view) of the GGEbiplot of the two (sub) mega-environments i.e. Niche-1 (Figure 3) and Niche-2 (Figure 4) revealed superior genotypes in each sub-megaenvironments.

The genotype ranking in Niche-1-mega-environment was LCC-236>LCC-237>RKD-18>RKD-13>DH-233>UD-475>HisarAnand>NDCor-30>Local>DH-220>NDCor-49>ACor-1>UD-801. The national check RKD-18 niche environment, Hisar Anand was found to be most stable though with average performance. The genotypes, LCC-236 and RKD-18 were found to havemean performance above the average, though lessstable. However, an ideal genotypeis a combination of both mean performance and stability. LCC-236 with highest mean performance ranked first among the genotypes evaluated in this niche environment evaluated.

In the, Niche-2-mega-environment the genotype ranking was DH-220>NDCor-30>DH-233>Hisar Anand>NDCor-49=UD-475>UD-801>ACor-1>LCC-236>LCC-237>RKD-18>RKD-13. In this mega-environment, the entry DH-220 ranked first in yield among all genotypes and was found to be the most stable genotype, with maximum average mean performance followed by NDCor-30. From this AEC view and micro GED analysis, the entries LCC-236 in the RKD-18 niche-mega-environment and DH-220 in the DH-220 niche-mega-environment were found promising and were the winning genotypes in respective niches. The ranking of genotypes was reported to be useful in various crops (Al-Ubaidi et al., 2013; Baxevanos et al., 2008; Hamayoon et al., 2011; Roostaei et al., 2014; Xing-Ming et al., 2007; Yan and Kang, 2002).

3.3. Evaluation of test environments

The evaluation of test environments revealed two mega-environments (Figure 5 and Figure 2). It also helped to identify the ideal test environment for a set of mega environments. This model can be further evaluated by using certain test genotypes. The advantage of identifying a mega environment is that we can restrict to a fewer test centers thus saving resources and energy. The AEC view based on environment based on scaling is used to delineate the mega-environments. Among the test environments, the environments of Dholi, Pantnagar, Kota and Jagudan were most discriminative for the tested genotypes. Lam and Navsari are the less discriminative of for testing the genotypes, when all test environments are considered as one mega-environment. The reason Lam and Navsari are less discriminative was mainly due to rainfed models of cultivation here and thus the PC scores may not have explained the GGE data from these centers. On a holistic view of Lam, Navsari and Ajmer with short vectors, least discriminationof genotypes, may not be ideal test environments. The test environments Pantnagar and Dholi are most discriminative and ideal for selecting superior genotypes. The test environments with long vectors and large angles, Kota, Jobner and Jabalpur, are ideal for culling unsuitable genotypes. Gedif and Yigzaw (2014); Kaya et al. (2006); Sarkar et al. (2014) demonstrated the utility of AEC view in bread wheat, potato and barley respectively.

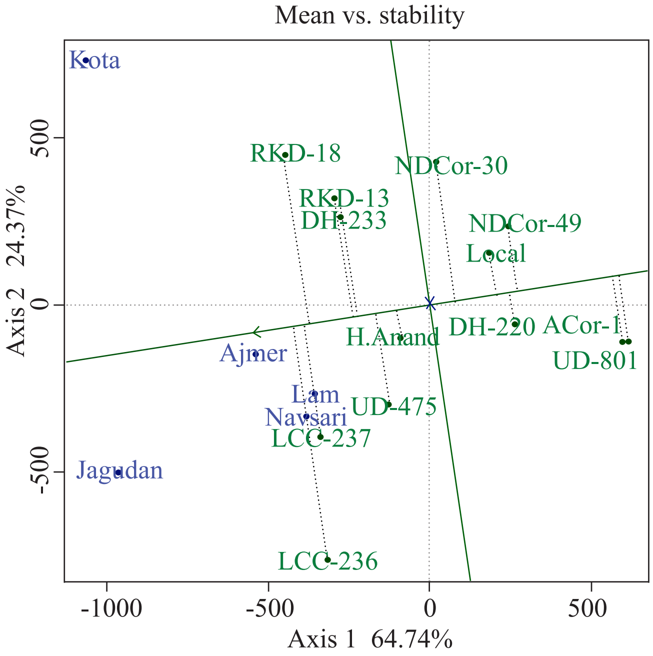

Figure 3: Genotype evaluation through mean performance and stability in Niche-1

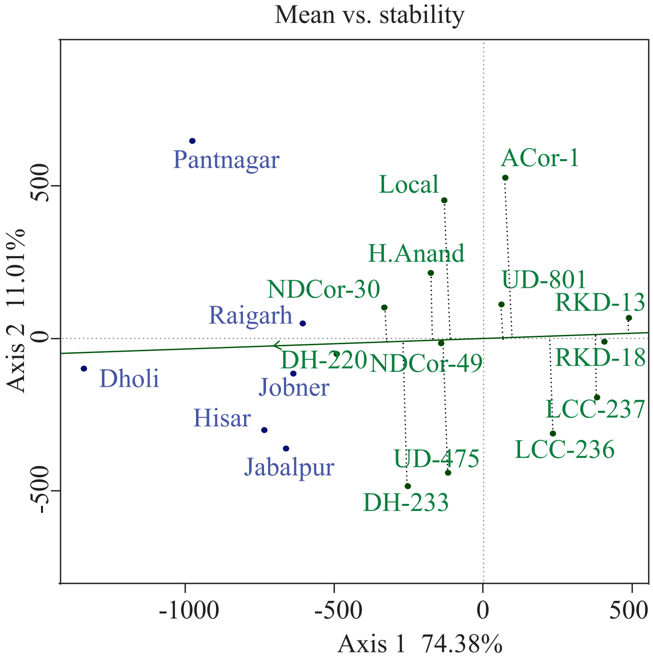

Figure 4: Genotype evaluation through mean performance and stability in Niche-2

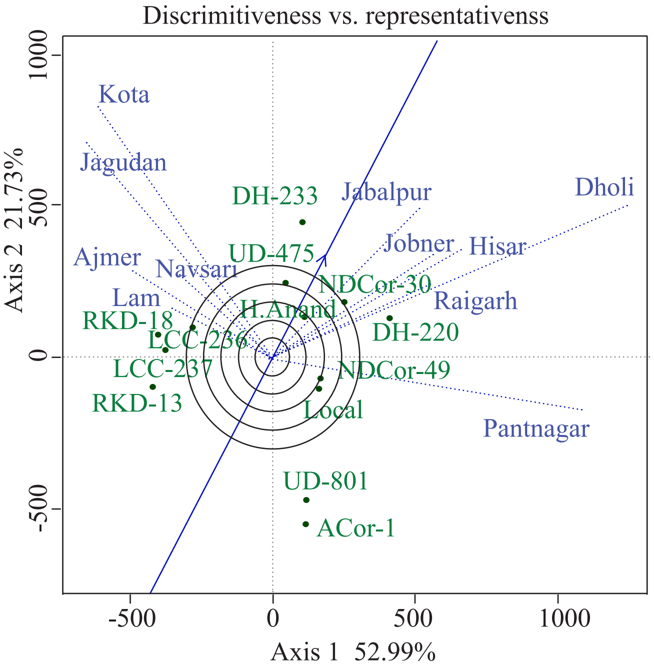

Figure 5: Evaluation of test environments

Micro-analysis of the above environment analysis revealed two diverse mega-environments i.e. Niche-1: Lam, Ajmer, Navsari, Jagudan and Kota; Niche-2: Pantnagar, Raigarh, Dholi, Hisar, Jobner and Jabalpur. The micro-analysis of Niche-1 mega-environment revealed that Jagudan is ideal for selecting superior genotypes and Kota is ideal for culling the unsuitable genotypes. In this niche-mega-environment. The other test centers are useful for robustness of the genotype selection process. This niche when further subjected to GED analysis (figures not presented), clearly delineated two sub-environments i.e. Sub-environment1: Kota, Sub-environment 2: Ajmer, Jagudan, Navsari and Lam. The micro-analysis of Niche-2 mega-environment projectedthat all the test centers in the niche did not differentiate in to any sub-environments.

3.4. *Efficacy of the model*

The Mega-environment analysis in which the biplot sectors and environment grouping in relation to genotype performance clearly focussed the superiority of the genotypes DH-220 and RKD-18 in respective environments. The view explained 74.7% of the total G+GE. Yang et al. (2009) opined that as a rule of thumb, that the first two PCs should account for > 60% of the (G+GL) variability and the combined (G+GL) effect should account for > 10% of the (L+G+GL) variability before claiming the usefulness of biplots. The present data set fits this amply thus confirming the utility of GGEbiplot model. Ding et al. (2007); Yan (2015); Yan et al. (2007); Yan and Holland (2010) vividly presented the utility and superiority of GGEBiplot analysis for discriminating test environments and genotypes. The GED analysis is presently widely used and accepted by the plant breeders and is quite useful for discrimination of genotypes (Akçura et al., 2011; Al-Ubaidi et al., 2013; Badu-Apraku et al., 2011; Farshadfar et al., 2013; Hamayoon et al., 2011; Jandong et al., 2011; Shojaei et al., 2011; Ullah et al., 2011; Rakshit et al., 2012; Rad et al., 2013; Noerwijati and Prajitno 2014; Zanetta et al., 2015; Olayiwola et al., 2015). The potential of GGEbiplot was expanded and utilized to study F1 hybrid performance under water stressed environment (Sabaghnia et al., 2011) in rape seed, wheat-barley disomic addition lines (Farshadfar et al., 2012), wheat land races for organic breeding (Koutis et al., 2012), potato for tuber yield (Gedif 1 and Yigzaw, 2014), black stem isolates (Hatami Maleki and Darvishzadeh, 2014) and multiple trait selection in sweet potato (Laurie and Booyse, 2015). The AEC view of the GGEbiplot revealed superior genotypes in respective niche environments. The view which is generally referred as the "Mean vs. Stability" view, showed the critical genotype comparisons based on mean performance and stability across environments within a mega-environment. The target environment constituted multiple mega-environments. Hence, selection of specifically adapted genotypes for each megaenvironment is advantagious. Yan et al. (2007) opined in such scenario asingle year multilocation trial would be sufficient. Hence, it may be rather judicious to take up scrupulous screening of genotypes in Niche1 and Niche 2 rather only a single year, which is quite sufficient to discriminate the genotypes. As Yan and Holland (2010) observed that microanalysis of megaenvironments help in delineation of multiple sub-environments within a mega environment. From this study, when a need for evaluating large number of genotype such as germplasm pools it is possible to evaluate at Pantnagar, Dholi and Jagudan, then elite ones may be tested across two mega environments. When there is a need for evaluating a few genotypes and resources are limited, these three environments may be deployed for reasonable discrimination among the genotypes. There is no doubt that a biplot, whether it is based on AMMI, GGE, or any other linear-bilinear model, is a useful visualization technique to quickly explore patterns of similarity or dissimilarity among genotypes or environments, and extract useful information from complex GE data (Yang et al., 2009). Genotype selection for their superiority in crop improvement programmes vested with recommendation of best cultivars from MET data. These decisions are critical for all the stake holders including breeders, agronomists, farmers and processers. However, these propositions need validation with the analysis of existing and future Multi Environment Data (MET) for further conformation and conclusions. There is a need for more understanding of the GE structure with supplementary information like the genetic correlation among the environments and relationship between genotypes for better decision making.

4. Conclusion

The mega-environment analysis effectively discriminated the genotypes over the environments. The evaluation of test environments revealed the nature of mega-environment and ideal test environments among the environments evaluated. The AEC view of the individual GGEbiplot facilitated ranking of genotypes within the environment. A simplistic environment model arrived from this study indicated that for reasonable discrimination of large number of coriander genotypes, only three ideal test environments (Pantnagar, Dholi and Jagudan) maybe deployed thus saving time, resources and energy.

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