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GGE biplot based assessment of yield stability, adaptability and mega-environment characterization for hybrid pigeonpea (*Cajanus cajan*)

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ABSTRACT

GGE biplot methodology is a powerful tool to study relationship among test environments (E), genotypes (G) and genotype-by-environment interaction (GE). Present study was conducted on 10 short-duration genotypes in five test environments for two years, and 16 medium-duration genotypes in six test locations for three years in randomized complete block design with two replications. In short-maturity group three mega-environments (ME) were found—ME1 comprised of Phaltan, Patancheru and Hyderabad1; ME2 and 3 constituted Jalna and Aurangabad, respectively. In scenario of limited resources, Patancheru may be a good testing location for general adaptability of short-duration hybrids, while Aurangabad and Hyderabad1 may be right environments for testing specific adaptation of short-duration cultivars in pigeonpea. ICPH 2433 was a winning genotype in ME1 in terms of high yield and stability. In medium-maturity group, two MEs were observed. Jalna, Jalna 1, Parbhani and Hyderabad grouped together as ME1, while Patancheru and Phaltan formed the second mega-environment (ME2). Parbhani was found to be most representative of all the six test locations. Jalna (ME1) and Phaltan (ME2) produced longest environment vectors, and hence may be regarded as highly discriminating. In medium-maturity group ICPH 2673 was found to be stable and high-yielding genotype for ME1.

Key words: *Cajanus cajan*, CMS, Cross over, $G \times E$, Hybrid, Mega-environment

Pigeonpea (*Cajanus cajan*) is an important food legume for the semi-arid tropics of Asia, Africa, Latin America and the Caribbean countries. It is grown in more than 80 countries in area of 4.86 Mha with an annual production of 4.10 Mt and mean productivity of 844 kg/ha (FAOSTAT 2011). India is the largest producer and consumer of pigeonpea with an area of 3.5 Mha followed by Myanmar (0.57 Mha), Kenya (0.19 Mha), Malawi (0.12 Mha), Uganda (0.09 Mha), Tanzania (0.07 Mha) and Nepal (0.02 Mha). It is a versatile hardy grain legume, which provides sustainability to various production environments and systems. It fixes atmospheric nitrogen, makes available phosphorous, supplies substantial organic matter in form of fallen leaves. Pigeonpea is an excellent nutrient re-cycler as it brings the nutrient from the deeper strata of the soil by virtue of its deep (which go as deep as 4 m) root system to the top layers. It also helps break the hard pan formed during farming operations. Pigeonpea is

a valuable source of grain protein (20–22%), fodder and fuel wood. It has all the necessary traits to make farming productive and sustainable, and can ensure nutritional security.

Since the last five decades the mean productivity of this crop has been fluctuating between 750–850 kg ha⁻¹, which is regarded as low by all standards. To address this long standing yield stagnation in pigeonpea, CMS-based hybrids were bred at ICRISAT, Patancheru. These hybrids were based on *C. cajanifolius* (A₄) cytoplasm, and exhibited up to 35% heterosis over the popular pure-line checks (Saxena *et al.* 2009, Saxena and Nadarajan 2010).

Hybrids, like pure line cultivars are thought to have differential response for various quantitative traits across environment—defined as the genotype \times environment interaction (G \times E), which is important at all stages of plant breeding, including selection based on trait or selection based on yield and ideotype design (Jackson *et al.* 1993, Yan and Hunt 1998). Mean genotype yield compared to others, adaptation (best performing environment for the given cultivar), and yield stability (measure of consistency of the genotype compared to others) are the three major focus areas for a successful breeding programme (Bilbro and Ray 1976). In pigeonpea information on yield stability and fertility

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restoration are important as it will help researchers identify and target appropriate cultivars for different environments. In the literature mention of various methods of measuring stability of performance can be found (Lin *et al.* 1986; Kang and Gauch 1996, Kang 1998, Yan and Kang 2003, Piepho 1999).

The process of identifying stable genotypes involve repetitive field testing, trait evaluation, and selection of genotypes which rank high during series of field trials conducted across a range of environments and years. There are two important parts of G×E testing i) statistical analysis that directly detect presence of G×E and measure stability of genotype performance, ii) mega-environments which involves grouping of similar non-discriminating environments using cluster analysis and principal component analysis (Carver *et al.* 1987, Geng *et al.* 1987) using models such as additive main effects and multiplicative interaction (AMMI) which combines principal component analysis with analysis of variance (Gauch and Zobel 1997). Such mega-environments will make testing more efficient and cost-effective. It may also help reduce Type 2 error during the selection process (Kang 1993).

The GGE biplot methodology of analyzing multi-environment trial (MET) data has emerged as a powerful tool for G×E analysis with nifty visual outputs for plant breeders, quantitative geneticist and agronomists (Yan *et al.* 2000, Yan and Hunt 2002; Yan and Kang 2003, Yan and Tinker, 2006). This methodology puts G and GE interaction together called GGE (Yan *et al.* 2000), on a graphic biplot visualization tool based on methodology suggested by Gabriel (1971).

GGE (Genotype and Genotype-Environment Interaction) biplots are thought to be an improvement over the AMMI (additive main effects and multiplicative environments) model. The AMMI model, for a long time was perhaps the most widely used tool. This was due to availability of large technical interpretations (Duarte and Vencovsky 1999). AMMI analysis translates the effects of genotype (G) and location (E) as additive effects plus treats GE as a multiplicative component for arriving at principal component estimates. The biplots generated by AMMI were named as GE biplots by Yan *et al.* (2000), who further proposed an improvement in the model in which the genotypic effects (G) were pooled with the multiplicative GE effects for generation of principal component analysis. This modified biplot was named as GGE biplot. GGE biplot scores over AMMI due to the fact that biplot always explains an intercession proportion of the sum of squares of genotypes + genotypes by environments (G + GE), compared AMMI1 and AMMI2 mega-environment graphs. Therefore, it is believed that GGE biplots are more accurate than AMMI1 and more pragmatic than AMMI2 mega-environment (Yan *et al.* 2007).

In pigeonpea there are no published reports for genotype by environment interaction for grain yield and fertility

restoration in A₄ based CMS hybrids. Hence, this research was carried out.

MATERIALS AND METHODS

Single cross hybrids were separated into groups (depending upon their days to flower and maturity) of short and medium maturity. Performance data of eight short maturity (along with two checks) were evaluated for two years (2007 and 2008) and 14 medium-maturity hybrids (along with two checks) for three (2006, 2007 and 2008) years. Short maturity group hybrids were assessed in a total of five locations (Aurangabad, Hyderabad 1, Jalna, Patancheru, and Phaltan), while medium-maturity group hybrids were evaluated in six environments (Hyderabad, Jalna, Jalna 1, Parbhani, Patancheru, and Phaltan). The experimental sites spanned a wide array of agro-ecologies of south and south-western regions of India. Details of soil type, latitude, longitude and altitude are given in Table 1.

In short maturity group the hybrid tested were ICPH 2433, ICPH 2363, ICPH 2438, ICPH 2429, ICPH 2364, ICPH 2431, and ICPH 2447, and ICPH 3310 with the pure line varieties ICPL 88039 and UPAS 120 as checks. Medium-maturity hybrids included ICPH 2673, ICPH 2671, ICPH 3341, ICPH 3464, ICPH 2740, ICPH 2751, ICPH 3462, ICPH 3337, ICPH 3477, ICPH 3472, ICPH 3491, ICPH 3494, ICPH 3461, and ICPH 3340 along with the pure line varieties Asha and Maruti as control cultivars. These hybrids were selected for multi-location, multi-year evaluation on the basis of superior station trial performance in terms of grain yield and fertility restoration at ICRISAT, Patancheru.

The experimental design in each environment was a randomized completed block design with two replications. Each plot consisted of six rows of 4 m length with 75 cm between rows. In all the three years trials were sown during

Table 1 Test environments for short and medium-maturity group pigeonpea cultivars

Environment	Latitude	Longitude	Elevation (m above msl)	Soil type
Aurangabad	20°51'	75°25'	574	Vertisol
Hyderabad 1	17°42'	78°35'	533	Alfisol
Hyderabad	17°37'	78°11'	548	Alfisol
Jalna	19°54'	75°53'	552	Vertic Inceptisol
Jalna 1	19°48'	75°49'	510	Deep Vertisol
Parbhani	19°14'	76°46'	410	Deep Vertisol
Phaltan	17°59'	74°24'	557	Deep Vertisols
Patancheru	17°30'	78°16'	510	Deep Vertisols for medium maturity group, Alfisols for short maturity group

normal sowing time (between 1 June and 31 July). At all the locations, irrigation was provided to the crop whenever necessary to avoid moisture stress, and optimum crop management practices were followed to raise a healthy crop.

Data were recorded on important phenological traits including grain yield, days to flower, days to maturity and fertility restoration. Grain yield was recorded at the time of maturity with 12% grain moisture. Five random competitive plants were sampled from each entry and pods were separated manually from the plants to get seeds. Plot yield in kg/plot was converted to kg/ha. Days to flower was recorded on the day 50% of the plants flowered, days to maturity was recorded when 75% of the pods attained maturity.

Statistical analysis experiment were carried out in randomized complete block design (RCBD) at all the locations. Data from all locations was pooled and tested for presence of significant G×E by using Analysis of Variance by considering all effects as fixed. To pool data from multiple experiments, Bartlett's Test for homogeneity of variance was carried out and was found significant. To make variance homogeneous among the environments, grain yield for each maturity group was standardized using environment wise error mean square. A significant G×E was detected for both the short and medium maturity groups (Tables 4, 5), hence to explore the data further, GGE biplots were drawn for grain yield to identify (a) which-won-where pattern, i.e performance of specific genotypes to specific environments, (b) genotype evaluation for stability, (c) most discriminative environment

(the longest environment vector), and, (d) ideal test environment. Software used for the analysis was SAS 9.2 version.

RESULTS AND DISCUSSION

Pooled analyses of variance for grain yield, for both short and medium-duration groups revealed that genotype (G), environment (E) and genotype × environment (GE) interaction were significantly ($P < 0.0001$) different among the pigeonpea genotypes tested (Tables 2,3). Ideally, GGE biplot analysis should be applied to multi-environment trial (MET) data when GE interaction is significant. It can, however, also be applied to MET data when it is not significant (Bhan *et al.* 2005).

The results indicated that pigeonpea yields were significantly influenced by environment in both short and medium-maturity groups. In short-maturity group, environment accounted for 43% of the total variation, while G and GE explained 9 and 11% of the variation (with P value less than 0.0014), respectively (Table 2).

In medium-maturity group environment accounted for 69% of the total variation while G and GE explained, respectively, 2 and 4% of the variation at P value of less than 0.0007 (Table 3). The effect of GE was more than two times that of G effect in medium-maturity group, while in short-duration both were comparable. The magnitude of E and GE vis-à-vis G indicated probable existence of different mega-environments (MEs).

Partitioning of GGE using GGE biplot analysis revealed

Table 2 Analysis of variance for short-maturity group pigeonpea cultivars

Source	DF	Type III SS	Mean Square	F Value	Pr>F	Per cent variation explained
Environment	4	310.53	77.63	77.63	<.0001	43.1
Rep (env)	15	111.81	7.45	7.45	<.0001	15.51
Treatment	9	67.20	7.47	7.47	<.0001	9.32
Env. × treat	36	76.24	2.12	2.12	0.0013	10.58
Error	123	123.00	123.00	1.00		
Corrected total	187	720.48				

R-Square=0.83, Coeff Var=25.25, Grain yield mean=3.96 (tonnes/ha)

Table 3 Analysis of variance for medium-maturity group pigeonpea cultivars

Source	DF	Type III SS	Mean square	F Value	Pr>F	Per cent variation explained
Environment	5	2 010.30	402.06	402.06	<.0001	68.82
Rep (env)	30	328.97	10.97	10.97	<.0001	11.26
Treatment	15	63.87	4.26	4.26	<.0001	2.19
Env. × treat	75	128.41	1.71	1.71	0.0006	4.39
Error	404	404.00	404.00	1.00		
Corrected total	529	2 921.08				

R-Square, 0.86; Coeff Var, 24.66; grain yield mean, 4.05 (tonnes/ha)

a total of 90% variation explained by PC1 (69%) and PC2 (21%) for short-duration (Fig 1). In medium-maturity group GGE biplot analysis revealed a total of 79% variation explained by PC1 (64%) and PC2 (14%) (Fig 2).

These results indicate that most of the genotypes performed differently across testing locations due to presence of large GE, over G. The results also indicate presence of significant cross overs. Therefore, the genotype selection on basis of overall mean would be misleading. The performance of genotypes, instead, should be on basis of its performance in the respective mega-environments.

Clustering and cosine of angles between the vectors of different environments gives approximation of the relationships between them, and may help in deciphering mega-environments (Yan and Tinker 2006). In the short-maturity group, three probable mega-environments are evident from Fig 1. In this group Phaltan, Patancheru (PATAN) and Hyderabad 1(HYD1) formed mega-environment 1 (ME1), whereas Jalna and Aurangabad (AUR'BAD), respectively, formed ME2 and ME3. In this maturity group no environment had significant negative correlation with each other by virtue of lack of obtuse angle between them (Fig 1). However, the angle between Jalna and Aurangabad is nearly 90°, therefore, these two environments bear no correlation between them (nearly zero correlation). Patancheru may be regarded as most ideal environment for testing general adaptation as it makes a very small angle with the average environment axis. This location may be the most ideal test environment for deciphering the general adaptability of the cultivars, and

may help in selecting widely adapted hybrids. Interestingly, testing location Hyderabad 1 which is close to Patancheru, has the longest environment vector, and may be suitable for testing specific adaptation for short-duration cultivars.

In short-maturity group, except for ICPH 2429 all other cultivars exhibited inconsistent yield ranking from environment to environment indicating cross over. Such cross overs are not uncommon and were also described by Baker (1988), Crossa (1990), and Yan and Hunt (1998). Out of 10 cultivars tested, ICPH 2433 was not only high-yielding (barring Jalna where it was low yielding), but also exhibited stable yield across all location (Table 4). This is also evident from Fig 1 where it falls on the vertex of the polygon, and hence highest yielding for ME1, comprising Phaltan, Patancheru and Hyderabad 1. Other high yielding and stable hybrids include ICPH 2438 and ICPH 2363 in ME1. For ME2, ICPH 2447 was high yielding and stable, whereas ICPH 2431 was a winning genotype in ME3 (Fig 1). Care must be taken to select stable cultivars that are high yielding, otherwise most of the times stability may be associated with poor yield.

Testing of 14 medium-maturity group hybrids along with two checks for three years in six locations revealed the presence of two mega-environments. On the basis of clustering between the radiating lines, Jalna, Jalna 1, Parbhani and Hyderabad grouped together as ME1, while Patancheru (PATAN) and Phaltan formed the second mega-environment (ME2) (Fig 2). Parbhani recorded a very small angle with average environment axis, and hence may be the most

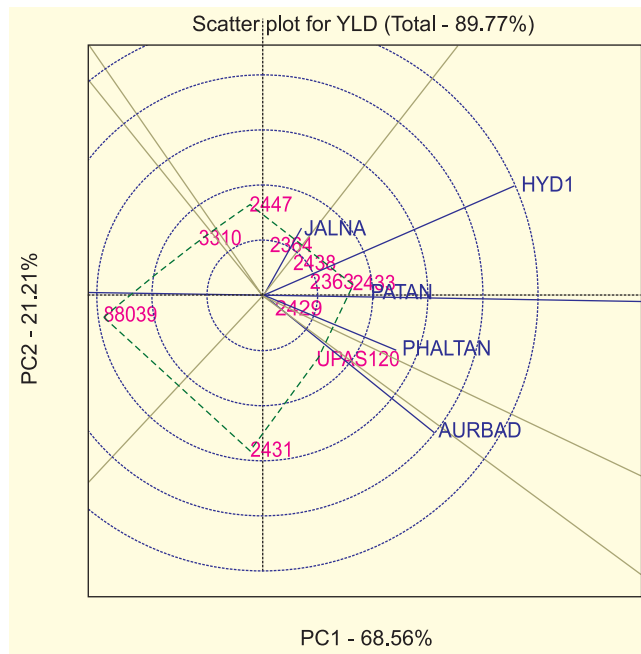


Fig 1 Polygon view for which-won-where pattern for short-duration cultivars based on grain yield

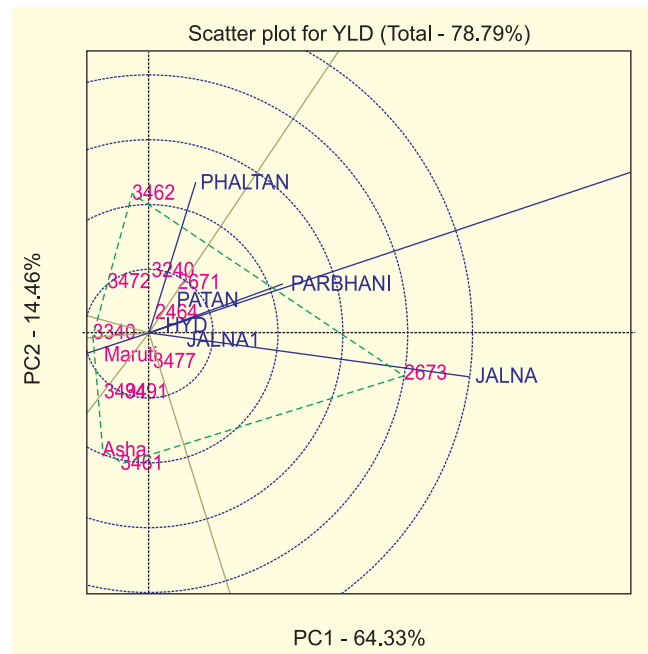


Fig 2 Polygon view for which-won-where pattern for medium-duration cultivars based on grain yield

representative environment of all the six test locations. This location will help in selecting cultivars that are widely adapted and bear general adaptation. On the other hand, Jalna (ME1) and Phaltan (ME2) produced longest environment vectors. Therefore, these two environments may be regarded as highly discriminating and may form good testing locations for examining specific adaptation of the medium maturing cultivars.

None of the test entries (14 hybrids and two checks) in medium-maturity group recorded consistent performance

across the six test locations. However, ICPH 2673 may be considered as high-yielding genotype for ME1, since it is located on the vertex of the polygon falling in ME1 (Fig 2, Table 5). In second mega-environment ICPH 3462 may be promising in terms of high yield and stability for the same reason. ICPH 3464 and ICPH 2751 may be considered stable genotypes as they are situated close to the average environment axis. Since ICPH 2671 recorded second rank in its mean yield performance (Table 5) it may be suited for environments of Jalna 1, Patancheru, Phaltan, Jalna and

Table 4 Mean performance of short-duration pigeonpea hybrids over two years (2007 and 2008) and five environments

Genotype	Environment					Mean	SEm
	AUR [*] BAD	HYD1	JALNA	PATAN	PHALTAN		
ICPH 2433	2 814.60	4 287.13	930.38	1 339.63	2 130.05	2 300.36	593.32
ICPH 2363	2 539.58	3 852.10	1 001.38	1 347.08	1 955.40	2 139.11	502.50
ICPH 2438	2 662.53	3 710.40	1 418.95	1 148.15	1 428.58	2 073.72	486.16
ICPH 2429	2 541.68	3 434.18	1 130.15	766.75	1 915.25	1 957.60	480.94
ICPH 2364	2 279.18	3 636.25	1 291.53	909.53	1 598.58	1 943.01	479.12
ICPH 2431	3 137.50	2 637.50	607.22	1 071.10	1 736.00	1 837.86	471.24
ICPH 2447	1 937.50	3 638.75	1 275.15	820.65	1 408.25	1 816.06	489.22
ICPH 3310	1 620.83	2 993.33	1 020.50	767.40	1 468.30	1 574.07	386.32
ICPL 88039	1 519.76	1 885.92	753.85	284.73	1 026.70	1 094.19	281.39
UPAS120	3 012.41	3 598.42	1 204.50	700.92	2 414.55	2 186.16	543.09
Mean	2 406.56	3 367.40	1 063.36	915.59	1 708.17		
SEm	176.68	217.81	79.93	102.28	128.40		

AUR^{*}BAD, Aurangabad; HYD1, Hyderabad1; PATAN, Patancheru

Table 5 Mean performance of medium-duration pigeonpea hybrids over three years (2006–08) and six environments

Genotype	Environment						Mean	SEm
	HYD	JALNA	J ALNA1	PARBHANI	PATAN	PHALTAN		
ICPH 2673	1 868.17	5 052.25	1 866.02	3 867.41	2 229.27	2 789.43	2 945.43	521.27
ICPH 2671	1 863.33	1 923.08	1 904.73	3 377.11	2 420.22	2 652.95	2 356.90	242.81
ICPH 3341	2 144.67	1 674.00	1 627.83	3 047.00	2 582.38	2 700.33	2 296.04	235.64
ICPH 3464	2 327.83	1 858.23	1 619.33	2 887.76	2 224.63	2 572.62	2 248.40	188.74
ICPH 2740	2 034.00	1 733.53	1 817.12	3 025.41	1 990.20	2 887.88	2 248.02	229.23
ICPH 2751	2 088.17	1 538.08	1 563.92	3 964.01	1 864.35	2 173.4	2 198.66	368.80
ICPH 3462	1 858.5	1 555.4	1 428.8	2 603.72	2 252.32	3 441.27	2 190.00	307.29
ICPH 3337	2 091.33	1 474.4	1 243.2	3 434.29	2 119.23	2 620.43	2 163.81	324.17
ICPH 3477	1 941.83	1 823.48	1 456.82	3 095.11	2 026.45	2 220.77	2 094.08	225.48
ICPH 3472	1 956.00	1 410.67	1 341.25	2 360.82	2 120.27	2 876.07	2 010.85	237.67
ICPH 3491	1 985.00	1 663.37	1 408.28	2 646.96	2 222.72	2 056.00	1 997.06	176.53
ICPH 3494	2 066.67	1 328.9	1 485.48	2 644.51	2 138.57	1 983.83	1 941.33	194.40
ICPH 3461	2 324.67	1 736.08	1 399.9	2 382.86	2 063.05	1 682.5	1 931.51	159.00
ICPH 3340	1 473.5	1 236.78	1 483.22	2 349.09	2 119.45	2 489.12	1 858.53	214.64
Maruti	1 426.7	1 338.47	1 826.34	2 595.37	1 791.83	2 372.5	1 891.87	205.17
Asha	1 570.3	1 474.55	1 774.24	2 329.72	1 810.92	1 823.33	1 797.18	121.18
Mean	1 938.79	1 801.33	1 577.91	2 913.20	2 123.49	2 458.90		
SEm	66.072	222.517	51.422	131.508	52.140	113.811		

HYD, Hyderabad; PATAN, Patancheru

Parbhani for higher and stable grain yield realization.

The presence of large G×E precludes selection of cultivars that are high yielding and stable across agro-ecologies. The report of three MEs in short-maturity group, and two in medium-maturity group in this study will help optimize testing location by selecting the most discriminating and representative locations, leading to better understanding of G×E. This study also calls for micro-zoning of the test locations in pigeonpea in India. Currently for release of a variety at zonal level its overall mean is considered in India, which may be misleading. ICPH 2433, ICPH 2363 and ICPH 2438 in the short-maturity group, and ICPH 2673 and ICPH 2671 in medium-maturity group were winning high-yielding and stable hybrids. We need to better understand G×E in pigeonpea, and with help of these testing locations (MES) develop location- and environment-specific, high-yielding, and disease-resistant cultivars.

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