Indian J. Genet., 81(1): 63-73 (2021)
DOI: 10.31742/IJGPB.81.1.7

Identification of pigeonpea genotypes with wider adaptability to rainfed environments through AMMI and GGE biplot analyses

M. V. Nagesh Kumar*, V. Ramya, C. V. Sameer Kumar, T. Raju[1], N. M. Sunil Kumar[1], G. Seshu, G. Sathish[2], D. Bhadru and M. V. Ramana

Professor Jayashankar Telangana State Agricultural University, Rajendranagar 500 030, Hyderabad, Telangana; [1]University of Agricultural Sciences, Raichur 584 104, Karnataka; [2]Sri Konda Laxman Telangana State Horticultural University, Mulugu 502 279, Telangana

(Received: August 2020; Revised: January 2021; Accepted: January 2021)

Abstract

Pigeonpea [*Cajanus cajan* (L.) Millspaugh] is an important pulse crop grown under Indian rainfed agriculture. Twenty eight pigeonpea genotypes were tested for stability and adaptability across ten rainfed locations in the States of Telangana and Karnataka, India using AMMI (additive main effects and multiplicative interaction) model and GGE (genotype and genotype by environment) biplot method. The grain yields were significantly affected by environment (56.8%) followed by genotype × environment interaction (27.6%) and genotype (18.6%) variances. Two mega environments were identified with several winning genotypes *viz.,* ICPH 2740 (G15), TS 3R (G10), PRG 176 (G8) and ICPL 96058 (G22). E2 (Gulbarga, Karnataka), E3 (Bidar, Karnataka) and E6 (Vikarabad, Telangana) were the most discriminating environments. Genotypes, ICPH 2740, PRG 176 and TS 3R were the best cultivars in all the environments whereas PRG 158 (G9), ICPL 87119 (G12), ICPL 20098 (G19) and ICPL 96058 (G22) were suitable across a wide range of environments. Genotypes, ICPH 2740 and PRG 176 can be recommended on a large scale to the farmers with small holdings to enhance pigeonpea productivity and improve the food security.

Key words: Pigeonpea, GE Interaction, GGE biplot, AMMI, stability, ideal genotype

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millspaugh], also referred to as redgram, is an important legume crop grown in the semi-arid regions of Asia, Africa, Latin America and the Caribbean. It is a high-protein (22%), sulphur rich, hardy pulse crop with an ability to adapt to wide climatic conditions and be intercropped without allelopathic effects on the main crop (Singh et al. 2018). Globally, pigeonpea is cultivated in an area of 5.6 m ha with a production of 4.4 m t and a productivity of 788 kg/ha (FAOSTAT 2019). India is the leading pigeonpea producer in the world accounting for 87% of the global production. Myanmar, Tanzania, Kenya and Malawi are other major pigeonpea-producing countries. In India, it is grown in 4.5 m ha with a production of 3.8 m t and productivity of 843 kg/ha (INDIASTAT 2019). Though the average yield of pigeonpea in India is higher than the global average yield, it is very low compared to the potential yield of over 2000 kg/ha (Bhatia et al. 2006). To address the disproportionate yield gap, several cultivars with resistance to abiotic and biotic stresses were developed following pre-breeding of wild relatives and subsequent pedigree selection and heterosis breeding methods (Saxena et al. 2013). During the last five decades, over 140 cultivars have been developed for cultivation across different agroecological zones in India (Singh et al. 2018).

Developing high yielding cultivars suitable for cultivation in varied environments is the basic target in plant breeding. However, the inconsistent performance of genotypes due to genotype × environment interaction (GEI) is limiting the development of stable high yielding cultivars. It is critical that multi-environment trials (MET) are conducted each year to investigate GEI for selecting stable genotypes for yield and other important traits, after which, compatible and stable genotypes are recommended to the farmers (Ebdon and Gauch 2002;

---

*Corresponding author's e-mail: mvnag@rediffmail.com

Published by the Indian Society of Genetics & Plant Breeding, A-Block, F2, First Floor, NASC Complex, IARI P.O., Pusa Campus, New Delhi 110 012; Online management by www.isgpb.org; indianjournals.com

Zali et al. 2011). The data generated through the MET trials is quite large. There are two powerful methods which can effectively interpret the MET data, analyze GEI and evaluate genotypic adaptability and phenotypic stability - the additive main effects and multiplication interaction (AMMI) analysis and genotype and genotype × environment interaction (GGE) biplot model (Yan and Rajcan 2002; Samonte et al. 2005). Both the tools are used by plant breeders, geneticists and agronomists for identification of genotypes with high yield and wide adaptability.

The AMMI model proposed by Gauch (1992) is a multivariate method that uses analysis of variance (ANOVA) and principal component analysis (PCA) to describe the GEI in more than one dimension. The GGE biplot proposed by Yan et al. (2000) considers both genotype main effects and GEI effects for analysis. The major difference between these two models is that GGE biplot analyzes G plus GE (or GEI) and AMMI on the other hand separates G from GE (Neisse et al. 2018). GGE analysis is based on environment-centred PCA whereas AMMI analysis refers to double-centred PCA (Naroui et al. 2013). The AMMI Stability Value (ASV) developed through the AMMI model is a quantitative stability value to rank the stability of genotypes Purchase et al. (2000). The AMMI and GGE biplot analyses have been used extensively to identify stable cultivars with high yield and yield attributing characters in a wide variety of crops. In the last couple of years, their application was reported in evaluation of genotypes of rice (Dwivedi et al. 2020), wheat (Bavandpori et al. 2018; Lozada and Carter 2020; Manu et al. 2020), maize (Choudhary et al. 2019), barley (Kumar et al. 2018; Yadav et al. 2020), rapeseed (Sara et al. 2019), groundnut (Kumar et al. 2019; Ajay et al. 2020), pigeonpea (Pagi et al. 2017; Singh et al. 2018; Lal et al. 2019; Gaur et al. 2020), chickpea (Kanouni 2018), urdbean (Kumar et al. 2020a; Kumar et al. 2020b), and ashwagandha (Kumar et al. 2020).

Pigeonpea, in addition to its cultivation as sole crop and intercrop, can fit in unique cropping systems such as pigeonpea-wheat rotation, rice-fallows, high altitudes and post-rainy pigeonpea (Sameer Kumar et al. 2018). These systems offer excellent scope for expansion of pigeonpea to non-traditional regions and new niches. In this context, it is essential to not only develop but also identify high yielding genotypes with wider adaptability based on the cropping situation requirements, without underpinning the importance of cultivars with specific adaptability. The present study was conducted to identify pigeonpea genotypes with stable and high yield performance across rainfed environments situated in Telangana and Karnataka states of India using AMMI and GGE biplot analyses.

Materials and methods

Twenty eight diverse pigeonpea genotypes (Table 1) were evaluated in ten rainfed environments (Table 2) of Telangana and Karnataka, India during the rainy seasons of 2016 and 2017. Among these, 16 were advance stage lines (ICPL 81-3, ICPL 88039, ICPL 161, ICPL 86022, ICPL 149, ICPL 88034, ICPL 92047, ICPH 2433, ICPH 3963, ICPL 20108, ICPL 20098, ICPL 99046, ICPL 96053, ICPL 96058, ICPL 20325 and ICPL 20338), six were recently released varieties (PRG 176, TS3 R, ICPH 2740, ICPH 3762, WRG 65 and WRG 53) and the remaining six were popular cultivars (PRG 158, ICPL 87119, ICPL 85063, ICP 8863, LRG 41 and PRG 100) that have been under cultivation for more than a decade. Standard agronomic practices were followed to maintain optimum crop growth. Each plot had six rows of 5 m in length. The row-to-row spacing and plant-to-plant spacing were kept at 1.5 m and 0.2 m, respectively. The experiments were laid out in a randomized complete block design with three replications. Observations were recorded on four central rows in each plot.

Statistical analyses were carried out using GENSTAT 20.0 software. Each location in two consecutive seasons was considered as an individual environment. Two types of analyses *viz.,* AMMI and GGE biplots were used to understand the pattern of genotype performance across the ten locations. Data from each location were analyzed first using single Analysis of Variance (ANOVA) and was later pooled for combined analyses of cultivars across the locations. Partitioning of the variation due to genotypes, environments and GEI was carried out. GGE biplots were generated to understand the which-won-where pattern and to rank the cultivars based on yield and stability. Similarities/dissimilarities were studied among the pairs of environments.

Results and discussion

An attempt was made to identify stable and widely adaptable pigeonpea genotypes from among 28 pigeonpea lines using AMMI and GGE biplot analyses. The mean grain yield of 28 genotypes evaluated across the rainfed environments during the rainy seasons of 2016 and 2017 ranged from 516 kg/ha to 2590 kg/ha (Table 3). Genotype, ICPH 2740 (G15) recorded highest

Table 1. Origin and pedigree of 28 pigeonpea genotypes tested in the study

Code	Name of the cultivars	Origin	Maturity (days)	Pedigree
G1	ICPL 81-3	ICRISAT[1]	120-140	Selection from ICP 11537
G2	ICPL 88039	ICRISAT	130-140	Selection from ICPL 161
G3	ICPL 161	ICRISAT	130-140	Pant A2 x ICP 6
G4	ICPL 86022	ICRISAT	130-140	ICPL 87 x ICPL 76115-H263-H4-HB
G5	ICPL 149	ICRISAT	120-140	SPS from ICP 6
G6	ICPL 88034	ICRISAT	120-140	ICPL 81 x ICPL 151
G7	ICPL 92047	ICRISAT	140-150	ICPL 84052 x ICPL 83027
G8	PRG 176	PJTSAU[2]	140-150	Pedigree selection ICPL 88039 x ICPL 88034
G9	PRG 158	PJTSAU	160-165	Pedigree selection of BSMR-16 x Maruthi
G10	TS 3 R	UAS[3], Raichur	150-160	TS 3 x ICP 8863
G11	ICPH 2433	ICRISAT	140-150	ICPA 2039 x ICPL 161
G12	ICPL 87119	ICRISAT	170-175	C 11 x ICPL 6
G13	ICPL 85063	ICRISAT	150-160	(T21 x BDN 1) x JA 275
G14	ICP 8863	UAS, Bangalore	140-160	Selection from local land race
G15	ICPH 2740	ICRISAT	170-180	CMS BSMR 736 x 2740 R
G16	ICPH 3762	ICRISAT	160-175	ICPA 2049 x ICPL 87051
G17	ICPH 3963	ICRISAT	160-175	ICPA 2078 x ICPL 87119
G18	ICPL 20108	ICRISAT	150-170	IPH 487 inbred-5
G19	ICPL 20098	ICRISAT	160-170	ICPL 87119 x ICPL 12746
G20	ICPL 99046	ICRISAT	150-160	ICPL 87119 x ICP 13232
G21	ICPL 96053	ICRISAT	150-160	ICPL 87051 x ICPL 83057
G22	ICPL 96058	ICRISAT	150-160	ICPL 88047 x ICPL 83057
G23	LRG 41	ANGRAU[4]	170-180	Selection from local land race
G24	WRG 65	PJTSAU	165-170	WRG 13 x ICPL 87051
G25	WRG 53	PJTSAU	160-165	ICPL 332 x ICPL 85063
G26	PRG 100	PJTSAU	150-160	Selection from Local land race
G27	ICPL 20325	ICRISAT	95-100	MN 5 x AL 1621
G28	ICPL 20338	ICRISAT	100-110	MN 5 x ICPL 85010

[1]ICRISAT= International Crop Research Institute for Semi-Arid Tropics, Hyderabad; [2]PJTSAU= Professor Jayashankar Telangana State Agricultural University, Hyderabad; [3]UAS= University of Agricultural Sciences; [4]ANGRAU= Acharya N.G. Ranga Agricultural University, Guntur

mean grain yield of 2590 kg/ha followed by PRG 176 (G8), ICPL 96058 (G22), ICPL 20098 (G19) and TS3R (G10). ICPL 20338 (G28) recorded the lowest yield of 516 kg/ha. Pigeonpea variety WRG 65 (G24) recorded a mean grain yield of 1603 kg/ha across the ten tested environments, which is higher than the mean grain yield of 1460 kg/ha recorded by Rao et al. (2020) across five environments. Among the environments, highest mean grain yield of 2282 kg/ha was obtained at E8 (Tajsultanpur and Gulbarga in Karnataka) followed by 2211 kg/ha at E9 (Ganjalkhed and Gulbarga, Karnataka), 2172 kg/ha at E1 (Palem and Nagarkurnool in Telangana) and 2111 kg/ha at E2 (Gulbarga, Karnataka). Rao et al. (2020) recorded a mean environment grain yield of 1256 kg/ha (E3) at Palem, Nagarkurnool which is lower than 2172 kg/ha (E1) recorded in the present study. The differences observed in the mean yields might be due to different genotypes and environments that were tested in both the studies.

AMMI analysis

The results of AMMI analysis of variance of 28

Table 2. Environments for 28 pigeonpea genotypes used in the study

Code	Environment	Latitude (N)	Longitude (E)	Altitude (m)	Mean annual rainfall (mm)	Soil type	Approximate cultivated area (ha)
E1	Palem, Nagarkurnool, Telangana	16.48^0	78.32^0	458	460	Sandy	21,000
E2	Gulbarga, Karnataka	17.32^0	76.83^0	454	640	Clayey	3,75,000
E3	Bidar, Karnataka	17.91^0	77.51^0	710	720	Sandy loam	73,000
E4	Gadwal, Telangana	16.23^0	77.80^0	324	390	Sandy	42,000
E5	Mahabubnagar, Telangana	16.74^0	78.00^0	498	480	Sandy	1,30,000
E6	Vikarabad, Telangana	17.33^0	77.90^0	435	630	Clayey	1,36,000
E7	Narayanpet, Telangana	16.44^0	77.29^0	435	420	Sandy loam	1,55,000
E8	Tajsultanpur, Gulbarga, Karnataka	17.32^0	76.83^0	454	640	Clayey	-*
E9	Ganjalkhed, Gulbarga, Karnataka	17.43^0	76.84^0	489	640	Sandy loam	-*
E10	Patancheru, Medak, Telangana	17.52^0	78.26^0	522	730	Sandy loam	52,000

*Environments E8 and E9 are under the jurisdiction of E2

pigeonpea genotypes evaluated at ten rainfed locations are presented in Table 4. Environments (E), genotypes (G) and GEI had a significant effect on pigeonpea yield ($P < 0.01$). Environment contributed to the maximum variation of 56.8%, which might explain the differences in the cultivars among the environmental means of grain yield (Table 3). This was followed by the effect of GEI which contributed to 27.6% of the variation in grain yield. The genotypic effect was low with 18.6 % of the total sum of squares attributed to it. Srivastava et al. (2012) studied the yield stability and adaptability of pigeonpea hybrids separately for short-duration and medium-duration hybrids. The 56.8% variation due to E obtained in this study is higher than that obtained in short duration pigeonpea (43%) and lower than the medium duration genotypes (69%) that were tested across six environments (Srivastava et al. 2012). In a similar study by da Cruz et al. (2020) in cowpea, further decomposition of significant GEI interactions revealed complex GEI with over 50% estimate levels in all the environments thus corroborating the importance of GGE biplot in identifying superior cowpea genotypes with phenotypic stability and adaptability.

The GEI was further partitioned by PCA (Gollob 1968) into first three principal component axes which were highly significant ($p < 0.01$) explaining 35.8, 20.2 and 11.2% of GEI sum of squares respectively. The first two interaction PCAs accounted for 67.2% of GEI sum of squares. Similar results, where the first two interaction PCAs explained the maximum GEI were reported by Srivastava et al. (2012), Fikere et al. (2014), Biswas et al. (2019) and Rao et al. (2020). On the same note, IPCA1 (interaction effects) and mean grain yield (main effect) were used for the construction of AMMI1 biplot (Fig. 1). The four quadrants (Q) of the biplot corresponded to higher mean (QI and II), lower mean (QIII and IV), +ve IPCA1 score (QI and IV) and -ve IPCA1 score (QII and III). Accordingly, a genotype and environment with same sign on PCA1 axis denote positive interaction and vice-versa. A genotype with a PCA1 score near zero is considered to be stable over wide environments due to small interaction effect. Conversely, a genotype with large PCA score is suitable for specific environments (Rao et al. 2020).

Pigeonpea genotypes, ICPL 81-3 (G1), ICPH 2672 (G16) and ICPL 96053 (G21) had higher mean grain yields and positive IPCA1 scores. ICPL 81-3 (G1) with the highest IPCA1 score is considered as the best overall genotype in this study. Cultivars G13 (ICPL 85063) and G15 (ICPH 2740) with high yields and IPCA score near zero are high-yielding genotypes with lowest interaction (Fig. 1). Genotypes, ICPL 81-3 (G1), ICPH 2762 (G16), ICPL 20098 (G19) and ICPL 96053 (G21) had yields higher than the mean grain yield and showed specific adaptability with positive interaction for environment E8 (Tajsultanpur and Gulbarga, Karnataka). However, specific adaptability was shown by ten genotypes (Fig. 1) with rainfed environments at E1 (Palem and Nagarkurnool, Telangana), E2 (Gulbarga, Karnataka) but at E9

Table 3. Mean grain yield (kg/ha) of 28 pigeonpea genotypes under ten environments tested during 2016 and 2017

Code	Name of the cultivar	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	Mean
G1	ICPL 81-3	2543	2070	1412	2301	2322	2372	2153	2691	2454	2188	2251^{fg}
G2	ICPL 88039	1566	1273	1004	1656	1837	1917	1902	2055	1858	1675	1674^{kl}
G3	ICPL 161	2719	2692	2021	2368	2121	2013	1854	2560	2526	2030	2290^{ef}
G4	ICPL 86022	1659	1630	1317	1649	1647	1625	1629	1923	1850	1514	1644^{l}
G5	ICPL 149	2447	2219	1578	2169	2059	2028	1853	2455	2327	1946	2108^{hi}
G6	ICPL 88034	2383	2460	1894	2109	1874	1754	1658	2279	2282	1780	2047^{i}
G7	ICPL 92047	2274	2383	1927	2099	1920	1816	1775	2280	2285	1817	2058^{hi}
G8	PRG 176	2830	2694	2086	2562	2421	2366	2219	2816	2726	2313	2503^{ab}
G9	PRG 158	2641	2522	1944	2399	2270	2216	2086	2653	2567	2159	2346^{cdef}
G10	TS 3 R	2954	2745	1946	2521	2293	2218	1974	2764	2661	2200	2428^{bcd}
G11	ICPH 2433	2678	2758	2177	2390	2143	2020	1917	2556	2561	2052	2325^{def}
G12	ICPL 87119	2705	2628	2041	2445	2285	2214	2086	2678	2613	2179	2387^{bcde}
G13	ICPL 85063	2548	2436	1931	2374	2291	2252	2156	2641	2551	2172	2335^{def}
G14	ICP 8863	2453	2395	1844	2223	2077	2009	1899	2456	2396	1969	2172^{gh}
G15	ICPH 2740	2766	2704	2243	2623	2539	2493	2425	2877	2806	2421	2590^{a}
G16	ICPH 3762	2350	2347	2034	2334	2317	2286	2293	2596	2536	2186	$2328d^{ef}$
G17	ICPH 3963	1927	2028	1673	1849	1744	1667	1670	2057	2048	1628	1829^{j}
G18	ICPL 20108	2011	1747	1259	1885	1900	1917	1806	2222	2061	1766	1857^{j}
G19	ICPL 20098	2695	2475	1901	2478	2409	2390	2247	2776	2645	2289	2431^{bcd}
G20	ICPL 99046	2023	2178	1901	2008	1924	1846	1893	2209	2216	1804	2000^{i}
G21	ICPL 96053	2406	2319	1899	2306	2265	2237	2183	2581	2494	2139	2283^{efg}
G22	ICPL 96058	2921	2569	1791	2538	2407	2386	2130	2848	2679	2299	2457^{bc}
G23	LRG 41	1996	1958	1479	1830	1720	1662	1588	2070	2011	1606	1792^{jk}
G24	WRG 65	1535	1569	1342	1594	1614	1591	1643	1859	1806	1477	1603^{l}
G25	WRG 53	1322	1413	1229	1409	1425	1392	1472	1659	1628	1288	1424^{m}
G26	PRG 100	1519	1680	1481	1576	1542	1481	1564	1792	1794	1413	1584^{l}
G27	ICPL 20325	547	656	427	587	563	512	574	819	801	432	592^{n}
G28	ICPL 20338	396	552	398	498	499	450	554	727	722	364	516^{n}
	Mean	2172	2111	1649	2028	1944	1898	1829	2282	2211	1825	1995
	LSD (0.01)											42.46(SEM)118.29

Ganjalkhed and Gulbarga, Karnataka) with grain yields higher than the mean yield. The remaining cultivars had yields less than the mean grain yield and showed specific adaptation to tested environments (Fig. 1).

Based on ASV and IPCA scores, ICPL 88039 (G2), ICPL 161 (G3) and ICPH 2433 (G11) were most unstable cultivars (Table 5). Environments E5 (Mahabubnagar, Telangana), E6 (Vikarabad, Telangana), E8 (Tajsultanpur and Gulbarga, Karnataka) and E10 (Patancheru and Medak, Telangana) stood out with small contribution to the interaction whereas E1 (Palem, Nagarkurnool, Telangana), E3 (Bidar, Karnataka) and E7 (Narayanpet, Telangana) had higher contribution and were favorable for obtaining high grain yields (Table 6). Overall, G13 (Laxmi) , G15 (ICPH 2740), G19 (ICPL 20098) and G21 (ICPL 96053) were categorized as the most ideal genotypes with the combining attributes of high yield and stable performance across wide environments (Table 5; Fig. 1). Similar findings on genotypic stability based on IPCA and ASV were made in chickpea (Zali et al.

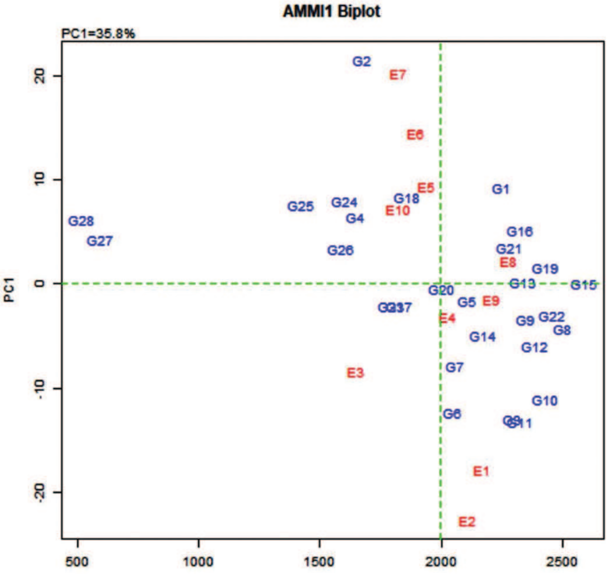

Fig. 1. **Biplot analysis of GEI based on AMMI 1 model for the PCA1 scores and grain yield (kg/ha) of 28 pigeonpea genotypes tested across 10 environments**

Table 4. Analysis of variance (mean squares) for grain yield (kg/ha) of 28 pigeonpea genotypes across ten environments during 2016 and 2017

Source of variation	Degrees of freedom	Sum of Squares	Mean Sum of Squares	% Explained
Total	1679	611245182	364053	
Treatments	279	575792961	2063774**	94.2**
Genotypes	27	107097490	3966573**	18.60**
Environments	9	327050401	36338933**	56.8**
Replications	20	17887037	894352	3.20
G x E interactions	243	158918857	653987**	27.60**
IPCA 1	35	56887622	1625361**	35.8**
IPCA2	33	321016091	9727260**	20.2**
IPCA 3	31	17798912	574158**	11.2**
Residuals	175	36710256	209773*	23.1**
Error	1380	17619112	12767	

**Significant at 1% probability level

2011), sorghum (Rakshit et al. 2014), soybean (Kumar et al. 2014), maize (Bo•oviæ et al. 2018), pigeonpea (Gaur et al. 2020) and groundnut (Ajay et al. 2020).

In addition to AMMI biplot I and II and ASV, Gaur et al. (2020) used another stability parameter AMMI biplot I and II and ASV stability parameter *viz.,* yield stability index (YSI) to analyze elite pigeonpea genotypes across three environments in Pantnagar, India. They identified genotypes PA 620 (seed yield per plant and number of secondary branches), YPAS 120 (plant height and number of pods), PA 622 (number of primary branches) and PA 620 (number of primary branches) as the most stable and high yielding genotypes. Ajay et al. (2020) have used 12 AMMI stability parameters and simultaneous selection for yield and stability (SSI) to evaluate GEI and yield stability in groundnut under phosphorus stress conditions. Nine out of the 12 AMMI parameters showed a significant positive correlation with yield and three parameters *viz.,* Stability parameters Modified AMMI stability index (MASI), Modified AMMI stability value (MASV), Sums of the absolute value of the IPC scores (SIPC) were shortlisted to identify stable high yielding genotypes.

Polygon view of the GGE biplot

The GGE biplot of 28 pigeonpea genotypes tested at 10 environments indicated the extent of genotype and environment interaction given in Fig. 2. The biplot was divided into five sectors with genotypes present in all the five sectors. Genotypes, ICPL 81-3 (G1), ICPL 88039 (G2), ICPL 88034 (G6), ICPH 2433 (G11), ICPH 2740 (G15), ICPL 20325 (G27) and ICPL 20338 (G28) situated at the vertices of the polygon were considered to be superior. All the 10 tested environments were scattered in two of those sectors, with E3 in one sector and the rest nine environments in another sector indicating the presence of two mega environments.

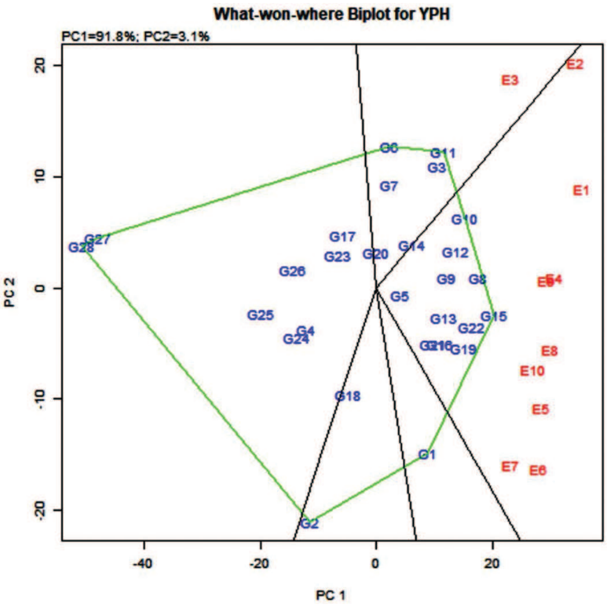

Fig. 2. Polygon views of the GGE biplot based on symmetrical scaling of 28 pigeonpea genotypes across ten environments

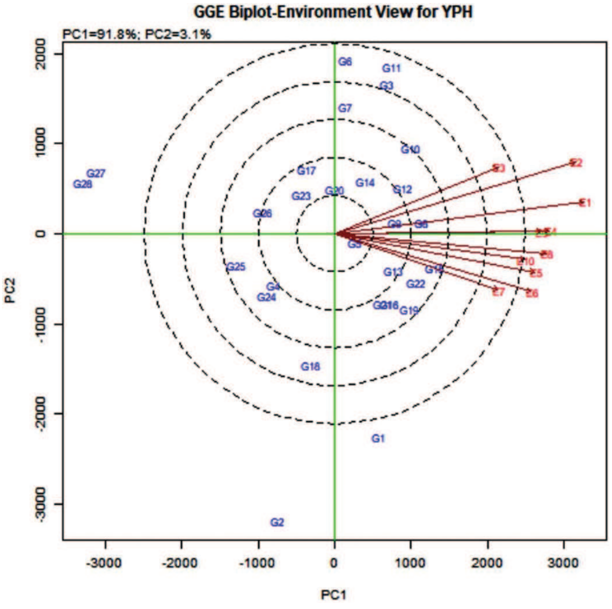

Fig. 3. GGE biplot graph showing relationships between 10 tested environments of 28 pigeonpea gernotypes

The genotypes, ICPL 88034 (G6) and ICPH 2433 (G11) were at the apexes of the sector containing E3 (Bidar, Karnataka) indicating that these two cultivars were the best performers in that location whereas ICPH 2740 (G15) is the best performer in the remaining of the nine environments. Cultivars G1 (ICPL 81-3), G2 (ICPL 88039), G27 (ICPL 20325) and G28 (ICPL 20338) were located at the apexes in the sectors that did not show any environment, indicating that these genotypes were not superior in mega environment. Genotypes G5 (ICPL 149), G14 (Maruthi) and G20 (ICPL 99046) were closest to the centre of origin indicating low variation in GEI (Fig. 2). In a similar study, Das et al. (2020) identified ideal (LGG 460) and desirable (COGG 912) genotypes with durable resistance and genetic homeostasis in which could be used in mungbean resistance breeding programme. In the same study, close relationship was found among three tested environments as revealed by consistent genotypic response towards leaf spot severity suggesting lowering the number of testing centres for screening of mungbean genotypes thereby saving natural resources and costs.

Relationship among the test environments

A total of 94.9% the variance was clarified by the first two principal components (PC) with PC1 clarifying 91.8% and rest 3.1% clarified by PC2 (Fig. 3). With longest vectors from the origin, environments E2 (Gulbarga, Karnataka), E3 (Bidar, Karnataka) and E6 (Vikarabad, Karnataka) were the most discriminating of the cultivars, while E1 (Palem and Nagarkurnool, Telangana), E5 (Mahabubnagar, Telangana), E8 (Tajsultanpur and Gulbarga, Karnataka) and E10 (Patancheru and Medak, Telangana) were moderately discriminating among the tested environments. Environment E4 (Gadwal, Telangana), with the shortest vector was considered as least discriminating environment as it offered little information on the differences among cultivars. With angles smaller than 90°, environments E4 (Gadwal, Telangana), E8 (Tajsultanpur and Gulbarga, Telangana), E10 (Patancheru and Medak, Telangana), E5 (Mahabubnagar, Telangana), E6 (Vikarabad, Telangana), E7 (Narayanpet, Telangana) were positively correlated. On the contrary, with an approximate angle of 90°, E3 (Bidar, Karnataka) and E7 (Narayanpet, Telangana) were not correlated (Fig. 3). Similar results where the first two PCs clarified most the variance were reported in soybean (Kumar et al. 2014), groundnut (Lal et al. 2019), urdbean (Kumar et al. 2020a) and mungbean (Kumar et al. 2020b).

Evaluation of environments and genotypes

Environment E4 (Gadwal, Telangana), with its location in the first concentric circle, was identified as the most ideal environment (Fig. 4). Cultivar evaluation in E4

Table 5. Mean grain yield (kg/ha), scores of two principal components (IPCA-1 and 2) and AMMI stability value (ASV) of 28 pigeonpea genotypes

Geno-type No.	Genotype	Mean	IPCA-1	IPCA-2	ASV
G1	ICPL 81-3	2251	9.29	15.53	22.65
G2	ICPL 88039	1674	21.52	5.41	38.58
G3	ICPL 161	2290	-12.91	1.19	22.94
G4	ICPL 86022	1644	6.41	-2.69	11.69
G5	ICPL 149	2108	-1.59	7.40	7.92
G6	ICPL 88034	2047	-12.29	-3.33	22.07
G7	ICPL 92047	2058	-7.88	-5.57	15.05
G8	PRG 176	2503	-4.30	4.02	8.63
G9	PRG 158	2346	-3.44	3.15	6.87
G10	TS 3 R	2428	-10.98	8.50	21.27
G11	ICPH 2433	2325	-13.18	-3.26	23.61
G12	ICPL 87119	2387	-5.97	1.88	10.75
G13	ICPL 85063	2335	0.16	2.13	2.15
G14	ICP 8863	2172	-4.92	0.89	8.79
G15	ICPH 2740	2590	0.06	0.02	0.12
G16	ICPH 3762	2328	5.13	-3.51	9.77
G17	ICPH 3963	1829	-2.09	-6.42	7.42
G18	ICPL 20108	1857	8.28	6.86	16.22
G19	ICPL 20098	2430	1.57	6.37	6.96
G20	ICPL 99046	2000	-0.51	-9.05	9.09
G21	ICPL 96053	2283	3.43	0.37	6.10
G22	ICPL 96058	2457	-3.01	12.90	13.97
G23	LRG 41	1792	-2.08	-0.55	3.73
G24	WRG 65	1603	8.01	-5.67	15.31
G25	WRG 53	1424	7.54	-7.99	15.58
G26	PRG 100	1584	3.37	-10.09	11.74
G27	ICPL 20325	592	4.26	-8.08	11.07
G28	ICPL 20338	516	6.11	-10.42	15.04

maximized the observed genotypic variation for grain yield among the 28 tested pigeonpea cultivars. With close proximity to the ideal environment, E1 (Palem and Nagarkurnool, Telangana), E8 (Tajsultanpur and Gulbarga, Karnataka), E9 (Ganjalkhed and Gulbarga, Karnataka) and E10 (Patancheru and Medak, Telangana) were desirable environments. The differences among the environments could be due to the variations in weather, climate and soil factors etc., which can further change from year to year. Pigeonpea cultivars G8 (PRG 176), G10 (TS 3 R), G15 (ICPH 2740) and G19 (ICPL 20098) were situated close to the first concentric circle and were also in close proximity to the ideal genotype position. All these four high-yielding cultivars maximize the environment variation for grain yield suggesting their suitability and potential as reference genotypes in evaluation trials.

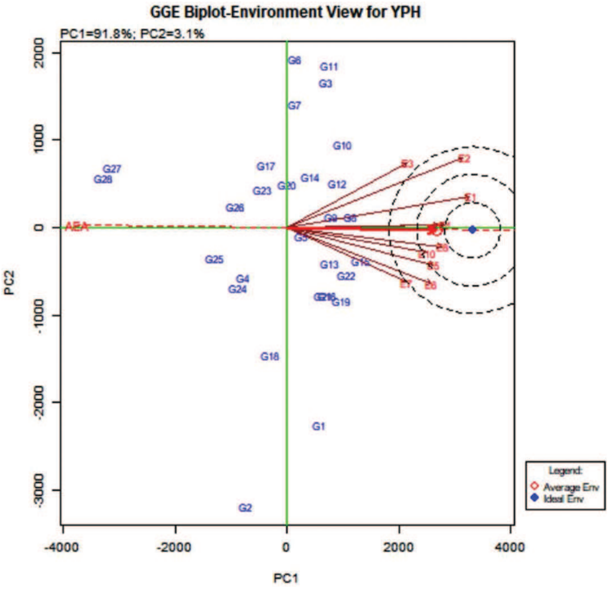

Fig. 4. GGE biplot graph based on environment-focused scaling for comparison of ten tested environments with the ideal environment for 28 pigeonpea genotypes

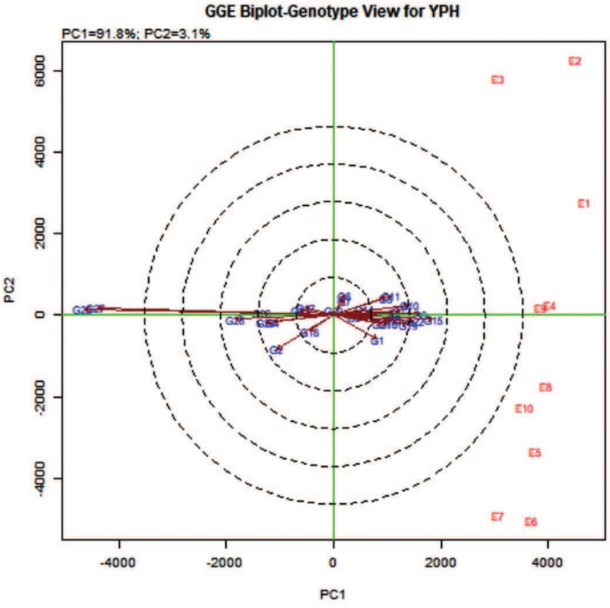

Fig. 5. GGE biplot graph based on genotype-focused scaling for comparison of 28 tested pigeonpea lines with ideal genotype

Table 6. Mean grain yield (kg/ha), scores of two principal components (IPCA-1 and 2) and AMMI Stability Value (ASV) across 10 environments

Environment	Mean	IPCA-1	IPCA-2	ASV
E1	2172	-17.79	18.06	36.29
E2	2111	-2.63	-5.57	7.25
E3	1649	-8.35	-26.76	30.53
E4	2028	-3.16	3.01	5.86
E5	1944	9.36	2.26	16.71
E6	1897	14.43	5.44	26.11
E7	1829	20.24	-7.68	36.61
E8	2282	2.17	8.57	9.38
E9	2211	-1.52	0.07	2.70
E10	1825	7.25	2.57	13.08

Cultivars G9 (PRG 158), G12 (ICPL 87119), G19 (ICPL 20098) and G22 (ICPL 96058) were more desirable and cultivars G2 (ICPL 88039) and G18 (ICPL 20108) were undesirable suggesting the adaptation of latter to specific environments. Three cultivars G5 (ICPL 149), G20 (ICPL 99046) and G14 (ICP 8663) were least sensitive to environment owing to their nearness to the biplot origin. Singh et al. (2018) identified nine superior and stable pigeonpea genotypes suitable for rainfed agriculture in Manipur, India. In addition to more recent GGE biplot approach, Pagi et al. (2017) also used Eberhart and Russell model for evaluating pigeonpea phenotypic stability using three linear kinds of linear responses of regression coefficient (bi), which were interpreted as bi=1, average stability and widely adaptable to different environments; bi>1, below average stability and well adapted to favorable environments and bi<1, above stability and specific adaptability to poor yielding environment. Pigeonpea genotypes G_{54} was recommended for recommended for cultivation across different environments in Western India using both Eberhart and Russell model and GGE biplot approach.

Using both the AMMI and GGE biplot methods, the present study has identified high yielding and stable pigeonpea genotypes, ICPH 2740 and PRG 176 with highest yield across the tested environments.. Two mega environments were identified with the first consisting of only one environment E3 (Bidar, Karnataka) and the rest of the nine environments were scattered within the second mega environment, thus indicating the appropriateness of environmental selection for evaluation of genotypic stability. Two genotypes, CPL 88034 and ICPH 2433 were identified as best performers recording high grain yield in E3 environment, while ICPH 2740 was identified as best performer in the remaining nine environments. Environments E2 (Gulbarga, Karnataka), E4 (Gadwal, Telangana) and E9 (Ganjalkhed and Gulbarga, Karnataka) were favourable for achieving higher grain yields. Genotype ICPH 2740 could be recommended for large scale adoption under rainfed agriculture to enhance pigeonpea productivity and ensure food security among the farmers with small holding.

Authors' contribution

Conceptualization of research (MVNK, CVSK); Designing of the experiments (MVNK, TR, NMSK); Contribution of experimental materials (MVNK, TR, NMSK, MVR); Execution of field/lab experiments and data collection (MVNK, VR, TR, NMSK); Analysis of data and interpretation (MVNK, GS, GST, VR); Preparation of the manuscript (MVNK, VR, DB).

Declaration

Authors declare no conflict of interest.

Acknowledgements

The large scale testing of pigeonpea genotypes was done under the India Morocco Food Legumes Initiative Project (IMFLI) (2014-2017) partnered by ICRISAT, PJTSAU, Telangana and UAS, Raichur, Karnataka. The authors are highly grateful for the funding provided by OCP foundation, Morocco and ICRISAT, towards implementation of the project.

References

Ajay B. C., Bera S. K., Singh A., Kumar N., Gangadhar and Praveen K. 2020. Evaluation of genotype × environment interaction and yield stability analysis in peanut under phosphorus stress condition using stability parameters of AMMI model. Agric. Res., **9**: 477-486. doi: 10.1007/s40003-020-00458-3.

Bavandpori F., Ahmad J. and Hossaini S. 2018. Stability analysis of bread wheat landraces and lines using biometrical genetic models. Genetika, **50**: 449-464. doi: 10.2298/GENSR1802449B.

Bhatia V. S., Singh P., Wani S. P., Rao A. K. and Srinivas K. 2006. Yield gap analysis of soybean, groundnut, pigeonpea and chickpea in India using simulation modeling: global theme on agroecosystems. Report no. 31. Patancheru 502 324. Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), 156.

Bo•oviæ D., Tivanoviæ Z., Popovic V., Tatiæ M., Gospavic Z., Miloradoviæ Z., Stankoviæ G. and Dokiæ M. 2018. Assessment stability of maize lines yield by GGE-biplot analysis. Genetika., **50**: 755-770.

Choudhary M., Kumar B., Kumar P., Guleria S.K., Singh N.K., Khulbe R., Kamboj M.C., Vyas M., Srivastava R.K., Puttaramanaik, Swain D., Mahajan V. and Rakshit S. 2019. GGE biplot analysis of genotype × environment interaction and identification of mega-environment for baby corn hybrids evaluation in India. Indian J. Genet., **79**(4): 658-669. doi: 10.31742/IJGPB.79.4.3.

da Cruz D. P., de Amaral G. G., Vivas M., Entringer G. C., Rocha R. S., da Costa Jaeggi M. E. P., Gravina L. M., Periera I. M., do Amaral A. T., de Moraes R., de Oliveira T. R. A. and Daher R. F. 2020. Analysis of the phenotypic adaptability and stability of strains of cowpea through the GGE biplot approach. Euphytica, **216**: 160. doi: https://doi.org/10.1007/s10681-020-02693-9.

Das A., Gupta S., Parihar A. K., Singh D., Chand R., Pratap A., Singha K. D. and Kushwaha K. P. S. 2020. Delineating Genotype × Environment interactions towards durable resistance in mungbean against Cercospora leaf spot (*Cercospora canescens*) using GGE biplot. Plant Breed. **139**(3): 639-650. doi: https://doi.org/10.1111/pbr.12789.

Dwivedi A., Basandrai D. and Sarial A. K. 2020. AMMI biplot analysis for grain yield of basmati lines (*Oryza sativa* L.) in North Western Himalayan Hill regions. Indian J. Genet., **80**(2): 140-146. doi: 10.31742/IJGPB.80.2.3

Ebdon J. S. and Gauch H. G. Jr. 2002. Additive main effect and multiplicative interaction analysis of national turf grass performance trials: I Interpretation of Genotype x Environment interaction. Crop Sci., **42**: 489-496.

FAO STAT. 2019. Food and Agriculture Organization of the United Nations, Rome, Italy www.fao.org. Accessed on 04-02-2021.

Gauch H. G. 1992. Statistical analysis of regional yield trials: AMMI analysis offactorial designs. Elsevier, Amsterdam.

Gaur A. K., Verma S. K., Panwar R. K. and Sharma R. K. 2020. Estimation of G x E interaction by AMMI model in some elite pigeonpea [*Cajanus cajan* (L.) Millspaugh] genotypes. Indian J. Genet., **80**(2): 173-178. doi: 10.31742/IJGPB.80.2.7.

Gollob H. F. 1968 A statistical model that combines features of factor analysis and analysis of variance techniques. Psycrometrika, **33:** 73-115.

INDIA STAT. 2019. https://www.indiastat.com. Accessed on 04-02-2021.

Kanouni H. 2018. Stability of Chickpea (Cicer arietinum L.) landraces in National Plant Gene Bank of Iran for Drylands. J. Agril. Sci. Technol., **20**: 387-400.

Kumar A., Kumar S., Kapoor C., Bhagawati R., Pandey A. and Pattanayak A. 2014. GGE Biplot Analysis of Genotype×Environment interaction in soybean grown in NEH regions of India. Env. & Eco., **32**: 1047-50.

Kumar M., Patel M.P., Chauhan R.M. Tank C. J., Solanki S. D., Gami R. A., Soni N. V., Patel P. C., Patel P. T., Bhadauria H. S., Patel N. B., Patel R. M. and Rani K. 2020. Delineating G × E interactions by AMMI method for root attributes in ashwagandha [*Withania somnifera* (L.) Dunal] Indian J. Genet., **80**(4): 441-449. doi: 10.31742/IJGPB.80.4.10.

Kumar N., Ajay B. C., Dagla M. C., Rathnakumar A. L., Radhakrishnan T., Lal C., Samdur M.Y., Mathur R. K. and Manivel P. 2019. Multi-environment evaluation of Spanish bunch groundnut genotypes for fresh seed dormancy. Indian J. Genet., **79**(3): 572-582. doi: 10.31742/IJGPB.79.3.7.

Kumar S., Sharma J. P., Kumar A., Choudhary H. K., Singh A. P., Sandghu R., Gupta R., Singh M. and Singh A. K. 2020a. Genotype x environments interactions for grain yield and its components in urdbean (*Vigna mungo* L Wilczek) under rainfed conditions of Jammu region Indian J. Genet., **80**(2): 194-203. doi: 10.31742/IJGPB.80.2.10 .

Kumar S., Choudhary H. K., Sharma J. P., Kumar A., Sandhu R., Gupta R., Gupta V. and Singh A. K. 2020b. Study on genotype x environment interactions and AMMI analysis for agronomic traits in mungbean (*Vigna radiata* L. Wilczek.) under rainfed conditions. Indian J. Genet., **80**(3): 354-358. doi: 10.31742/IJGPB.80.3.19.

Kumar V., Verma R. P. S., Kumar D., Kharub A. S. and Singh G. P. 2018. Assessment of barley genotypes for malting quality: Genotype x environment interactions. Indian J. Genet., **78**(4): 523-526. doi: 10.31742/IJGPB.78.4.16.

Lal C., Ajay B. C., Chikani B. M. and Gor H. K. 2019. AMMI and GGE biplot analysis to evaluate the phenotypic stability of recombinant inbred lines (RILs) of peanut under mid-season water stress conditions. Indian J. Genet., **79**(2): 420-426. doi: 10.31742/IJGPB.79.2.5.

Lozada D.N. and Carter A.H. 2020. Insights into the genetic architecture of phenotypic stability traits in winter wheat. Agron **10**(3):368. doi:10.3390/agronomy 10030368

Manu B., Kumara P. S., Biradar S., Chauhan D., Phuke R., Ambati D., Sai Prasad S. V., Mishra P. C., Mishra K. K., Harikrishna Jain N., Singh P. K., Singh G. P. and Prabhu K. V. 2020. Genetic gain and morpho-physiological characterization of BILs (Backcross Inbred Lines) under different moisture regimes in wheat (*Triticum aestivum* L). Indian J. Genet., **80**(1): 84-93. doi: 10.31742/IJGPB.80.1.11.

Naroui R., Mohammad R., Abdul Kadir M, Rafii Hawa M Y, Jaafar Naghavi M. R. and Ahmadi F. 2013. Genotype x environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (Triticum aestivum) under normal and drought stress conditions. Aust. J. Crop. Sci., **7**(7): 956-961.

Neisse A. C., Kirch J. L. and Hongyu K. 2018. AMMI and GGE bipot for genotype x environment interaction: a medoid-based hierarchical cluster analysis approach for high-dimensional data. Biomet. Lett., **55**(2): 97-121.

Pagi N., Dharajiya D., Ravindrababu Y., Pachchigar K., Soni N., Parmar L., Patel J., Chauhan R. and Patel M. S. 2017. Phenotypic stability and GGE biplot analysis in Pigeonpea [*Cajanus cajan* (L.) Mill sp.] genotypes across the environments. J. Exp. Biol. Agric. Sci., **5**(3): 359-367.

Rakshit S., Ganapathy K. N., Gomashe S., Rathore A., Ghorade R., Kumar N., Ganesmurthy K., Jain S., Kamatar M., Sachan J., Ambedkar S., Ranwa B., Kanawade D., Balusamy M., Kadam D., Sarkar A., Tonapi V. and Patil J. 2014. GGE biplot analysis to evaluate genotype, environment and their interactions in sorghum multi-location data. Euphytica, **185**: 465-469.

Rao P. J. M., Kishore N. S., Sandeep S., Neelima G., Rao P. M., Das D. M. and Saritha A. 2020. Evaluation of Performance and Yield Stability Analysis Based on AMMI and GGE-Biplot in Promising Pigeonpea [*Cajanus cajan* (L.) Millspaugh] Genotypes. Legume Res., doi: 10.18805/LR-4299.

Sameer Kumar C. V., Singh I. P., Vijaykumar R., Patil S. B., Tathineni R., Mula M. G., Saxena R. K., Hingane A. J., Rathore A., Reddy Ch. R., Nagesh Kumar M., Sudhakar C. and Varshney R. K. 2016. Pigeonpea – A unique jewel in rainfed cropping systems. Legume Pers., **11**: 8-10.

Samonte S. O. P., Wilson L. T., Mc Clung A.M. and Medley J. C. 2005. Targeting cultivars on to rice growing environments along AMMI and SREG GGE biplot analysis. Crop Sci., **45**: 2414-2424.

Sara M., Abbas R., Reza A. and Alireza E. 2019. Yield stability of rapeseed genotypes under drought stress conditions. Indian J. Genet., **79**(1): 40-47. doi: https://doi.org/10.31742/IJGPB.79.1.6.

Singh J., Kumar A., Fiyaz R. A. and Singh M. K. 2018. Stability analysis of pigeonpea genotypes by deployment of AMMI model under rainfed environment. Legume Res., **41**(2): 182-188.

Srivastava R., Rathore A., Vales M. I., Kumar V. R., Panwar S. and Thanki H. 2012. GGE biplot based assessment of yield stability, adaptability and mega-environment characterization for hybrid pigeonpea (*Cajanus cajan*). Ind. J. Agric. Sci., **82**: 928-933.

Yadav O. P., Razdan A. K., Kumar B., Singh P. and Singh A. K. 2020. Using AMMI approach to delineate genotype by environment interaction and stability of barley (*Hordeum vulgare* L.) genotypes under northern Indian Shivalik hill conditions. Indian J. Genet., **80**(3): 339-342. doi: 10.31742/IJGPB.80.3.15.

Yan W. and Rajcan I. 2002. Biplots analysis of the test sites and trait relations of soybean in Ontario. Crop Sci., **42**: 11-20.

Yan W., Hunt L. A., Sheng Q. and Szlavnics Z. 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci., **40**(3): 597-605.

Yan W. and Kang M. S. 2003. GGE biplot analysis: A graphical tool for breeders, Geneticists and Agronomists, Boca Raton F L, CRC Press.

Zali H., Farshadfar E. and Sabaghpour S. H. 2011. Non-parametric analysis of phenotypic stability in chickpea (*Cicer arietinum* L.) genotypes in Iran. Crop Br. J., **1**(1): 89-100.