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Estimation of Genotype×Environment Interaction in Some Elite Pigeonpea [*Cajanus cajan* (L.) Millspaugh] Genotypes by AMMI and GGE Biplot Models

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ABSTRACT

The study was conducted with 14 elite genotypes of pigeon pea during *kharif* (June–January) of 2018, 2019 and 2020 at Regional Agricultural Research Station, Warangal, Telangana state, India. The objective of the study was to find out the stable genotypes and genotype by environment crossovers using AMMI and GGE Biplot stability models. Analysis of variance clearly showed that environments contributed highest (26.04%) in total sum of squares followed by genotypes × environments (21.34%) indicating very greater role played by environments and their interactions in realizing final grain yield and when the interaction was partitioned among the first two interaction principal component axis (IPCA) as they were significant in predictive assessment and capturing 80.50% and 19.50% of the total variation in the G×E interaction sum of squares, respectively. GGE biplot revealed that the environments E1 (*kharif*, 2018) and E3 (*kharif*, 2020) are the most discriminating. The What-Won-Where GGE Biplot for yield revealed that in E3 (*kharif*, 2020), G5 (WRG-437) was the winner and in E2, the genotype G13 (WRGE-134) followed by G11 (WRGE-143) and G8 (WRGE-138). In another mega environment E1, the genotype G9 (WRGE-141) was the winning genotype. AMMI and GGE bi plots analysis revealed that among environments, E1, E2 exerted strong interaction forces while, the environment E3 did less and in the genotypes WRGE-138, WRGE-134, WRGE-136 and WRGE-143 identified as the most adapted lines with stable performance coupled with negligible G×E interaction and can be considered as the potential genotypes, which can improve the Pigeon pea productivity.

KEYWORDS: AMMI, GGE biplot, G×E interaction, pigeon pea, yield

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1. INTRODUCTION

A variety of pulses are cultivated in India as well as in the world and among these pulse crops, Pigeonpea occupies the second position in terms of acreage, production and productivity after chickpea. Pigeon pea (*Cajanus cajan* L. Millsp.) is a climate-resilient pulse crop ranks sixth in global grain legume production. It is being cultivated in about 6.99 m ha area with an annual production of 5.96 mt and a mean productivity of 852 kg ha^{-1}, while, India ranks top in annual pigeon pea production with 4.29 mt accounting more than 80% of total world production. (Anonymous, 2020a). In Telangana state, pigeon pea is being cultivated in an area of 3.22 l ha^{-1} with productivity of 575 kg ha^{-1} (Anonymous, 2020b).

The $capita^{-1}$ availability of protein in the country is 37 g day^{-1}, while WHO recommended it should be 80 g day^{-1}, consequently most serious problem of the malnutrition existing among the poor people, where most of the people have vegetarian diet and avoid the animal protein (Singh et al., 2020). It needs fulfil of demand through pulses protein. Hence, the pulse requirement in the country is projected at 32 mt by the year 2030 and 39 mt by the year 2050. This necessitates an annual growth rate of 2.2% (Singh and Praharaj, 2020). Pigeon pea is considered to be an excellent and affordable source of plant-based protein, substantially higher (21.7 g 100 g^{-1}) coupled with other nutritional components as compared to major cereals (6.0–15.0 100 g^{-1}).

Genotype×environment interaction complements the selection process and recommendation of a genotype for a target environment and hence a number of different methods have been proposed to estimate G×E interaction (Gauch and Zobel, 1996, Gauch, 2006). These methods can be broadly classified into two main categories i.e., Parametric and Non-parametric methods (Huehn, 1996). Parametric methods mainly include ecovalence (W^2_i) method (Wricke, 1962), regression coefficient (b_i) and deviation from regression (S^2di) method (Eberhart and Russell, 1966), stability variance (σ_i^2) method (Shukla, 1972), coefficient of variance (CV_i) method (Francis and Kannenberg, 1978). An additive main effects and multiplicative interaction (AMMI) model-based stability parameters such as ASV (AMMI Stability Value) and YSI (Yield Stability Index) were also of parametric model (Bajpai and Prabhakaran, 2000). The non-parametric methods include $S_{(i)}$ measures of Huehn (1990) and Nassar and Huehn (1987), NP(i) measures of Thennarasu (1995) and KR or rank-sum of Kang (1988). These traditional parametric as well as non-parametric statistical methods for estimation of G×E interaction are either ANOVA based or PCA based have some limitations. Through addressing these limitations, Presently two types of biplots are being extensively used to visualize G×E interactions, and these are the AMMI (Gauch, 1988) and GGE biplots; (Yan et al., 2000) and also found effective as it captures a large portion of the interaction sum of squares; at the same time separates main as well as interaction effects and shows that which genotype will be suitable for which environment (Jeberson et al., 2017). The only difference among these models is the omission of E component in GGE biplot (Yan et al., 2000, Gauch, 2006, Yan et al., 2007)

The AMMI and GGE biplot analyses have been extensively used to identify high yielding stable cultivars in a variety of crops viz., sweet potatoes (*Ipomoea batatas*) (Osiru et al., 2009), finger millet (*Eleusine coracana*) (Lule et al., 2014) and grain sorghum (Patil et al., 2007). The present investigation was carried out to estimate the pattern of genotype×year interaction for few elite pigeon pea genotypes to make a decision on their yield potential and adaptability for Telangana state.

2. MATERIALS AND METHODS

2.1. Experiment description

The experimental materials comprised of 14 elite genotypes of pigeon pea and were evaluated in randomized complete block design with 3 replications during *kharif*, 2018, 2019 and 2020 (June–January of each respective years) under rainfed conditions of heavy black soils of pulses scheme at Regional Agricultural Research Station, Warangal, (Latitude,18°03' N, longitude of 79°22' E at 270 m of mean sea level), Telangana state, India. Each plot consisted of 4 rows of each 4 m row length was followed with spacing of 120 cm between rows and 20 cm between the plants. Crop was sown during 1st week of July and standard package of practices were followed to raise healthy crop. Observations were recorded for grain yield on plot basis.

2.2. Statistical analysis

The performance of genotypes was tested over three years using stability models *viz.,* (1) Additive Main effects and Multiplicative Interaction (AMMI) (Gauch and Zobel, 1996) and (2) GGE Biplot or Site Regression Model (Yan and Kang, 2003). The AMMI model (Gauch, 1988) was used in analyzing the stability and interaction for yield. These residuals include the experimental error and the effect of the GEI. The analytical model can be written as

$$Y_{ij}=\mu+g_i+e_j+\Sigma\lambda k+\alpha ikyjk+R_{ij} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (1)$$

Where,

Y_{ij} is the yield of i^{th}-genotypes in j^{th}-environment

μ is the overall mean

g_i is the effect of the i^{th} genotype

e_j is the effect of the j^{th} environment

λk is the eigen value of the PCA for axis k

α_{ik} and y_{jk} are the genotype and environment principal components scores for axis k, respectively

R_{ij} is the residual term. Environment and genotype PCA scores are expressed as unit vector times the square root of λk.

The GGE biplot graphically represents G and GEI effect present in the multi-location trial data using environment centered data. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also sources of variation in GEI analysis of multilocation trial data (Yan et al. 2000, Yan, 2001). The data was subjected to IRRI P.B. tools 1.4 version to get AMMI and GGE Biplots. Correlation studies were estimated through R Software package.

3. RESULTS AND DISCUSSION

The AMMI analysis of variance for grain yield (kg ha^{-1}) of 14 pigeon pea genotypes (Table 1) evaluated over three years revealed that the main effects of genotypes (G) and environments (E) accounted for 19.79% and 26.04% of the total sum of squares respectively. The G×E interaction also accounted for 21.34% of the total sum of squares indicating that the differences in the response of the genotypes across the environment were substantial and the presence of G×E interaction and it was clearly demonstrated by the AMMI model, when the interaction was partitioned among the first two interaction principal component axis (IPCA) as they were significant in predictive assessment. 2 PCAs were highly significant capturing 80.50% and 19.50% of the total variation in the G×E interaction sum of squares, respectively (Table 2). Previous reports confirmed that in most of the cases, the maximum GEI could be explained through using the first two PCAs (Varma et al., 2020).

Table 1: Mean performance of the pigeon pea genotypes across the environments

Sl. No.	Genotype	Grain yield (kg ha^{-1})			
		Kharif, 2018 (E1)	*Kharif*, 2019 (E2)	*Kharif*, 2020 (E3)	Mean grain yield (kg ha^{-1})
G1	WRG-423	1437.49	1669.44	1180.48	1429
G2	WRG-426	932.29	1405.09	1919.98	1419
G3	WRG-429	973.95	1556.25	1607.59	1379
G4	WRG-432	1187.49	1568.52	1363.12	1373
G5	WRG-437	1037.49	1927.55	1769.27	1578
G6	WRG-65	760.41	1577.78	1525.31	1288
G7	WRGE-137	1257.28	1544.81	1164.44	1322
G8	WRGE-138	1170.83	1768.52	1424.99	1455
G9	WRGE-141	1708.32	1665.97	1189.75	1521
G10	WRGE-142	940.62	1500.46	1408.34	1283
G11	WRGE-143	1249.99	1808.70	1416.31	1492
G12	PRG-176	695.20	894.21	1078.12	889
G13	WRGE-134	1898.50	2020.83	1610.35	1843
G14	WRGE-136	1520.00	1531.25	1178.46	1410
	Mean	1197.85	1602.81	1416.89	1406

Table 2: AMMI Analysis of Variance for G×E interaction

Source	d. f.	SS	MS	% Explained SS
Total	125	19389684	155117	
Genotypes (G)	13	3838844	295295	19.79
Environment (E)	2	5050593	2525296	26.04
G×E	26	4138271	159164	21.34
ICPCA 1	14	3333086.5	238077	80.50
ICPCA 2	12	805224.3	67102	19.50
Error	78	5480082	70257	32.83

3.1. AMMI biplot analysis

To probe the main effects and interaction across different environments, AMMI 1 and AMMI 2 biplots were constructed. AMMI 1 biplot of main effects (genotype and environments) are shown along the abscissa and the ordinate represents the first IPCA. The interpretation of a biplot assay is that if main effects have IPCA score close to zero, it indicates negligible interaction effects and when a genotype and an environment have the same sign on the IPCA axis, their interaction is positive, if different, interaction is negative (Rao et al., 2020).

3.2. AMMI 1 biplot display

The mean performance and PCA1 scores for both the varieties and environments used to construct the AMMI 1biplot (Figure 1). The AMMI 1 biplot analysis for the yield showed that the pigeon pea genotypes, G13 (WRGE-134), G5 (WRG-437), G9 (WRGE-141) and G11 (WRGE-143) recorded high yield and G12 (PRG-176) with lowest grain yield, out of which G13 (WRGE-134) and G5 (WRG-437) had high IPCA 1 score in which G13 (WRGE-134) is being the overall best genotype in terms of yield. On the other hand, G9 (WRGE-141), G11 (WRGE-143) and G8 (WRGE-138) were high yielding genotypes with negative IPCA 1 scores, While IPCA 1 for G4 (WRG-432) were near to zero score and hence have less interaction with the environments with average yield performance. Environments E2 (*kharif*, 2019) and E3 (*kharif*, 2020) having higher grain yield, whereas in environment E1 (*kharif*, 2018) lesser grain yield than the average was exhibited.

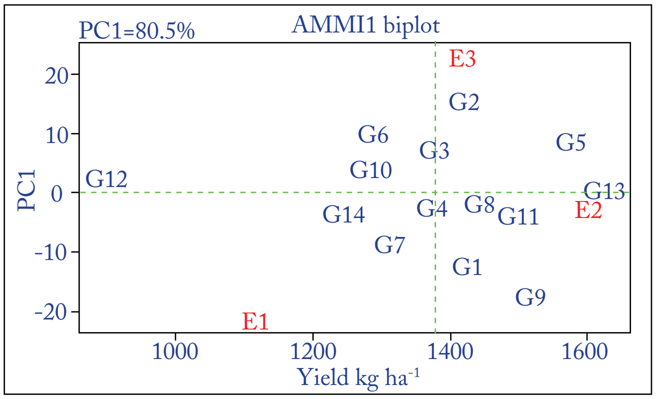

Figure 1: AMMI 1 Biplot for grain yield (kg ha^{-1}) of 15 pigeon pea genotypes (G) and 5 environments (E) using genotypic and environmental scores

3.3. *AMMI 2 Biplot display*

The IPCAI versus IPCA II biplot explains the magnitude of interaction of each genotype and environment. The genotypes and environments that are farthest from the origin being more responsive and fit the worst genotype. Genotypes and environments that fall into the same sector interact positively and negatively, if they fall into opposite sectors and the genotypes with less interaction in both axes are positioned near the origin (Anandan et al., 2009).

AMMI 2 Biplot for grain yield (kg ha^{-1}) was constructed using interaction of IPCA2 against IPCA1 scores of 15 pigeon pea genotypes (G) in 5 environments (E) (Figure 2). As a result, environments E1 (*kharif*, 2018), E2 (*kharif*, 2019) exerted strong interaction forces while, the environment E3 did less. In the present study, the genotypes G10 (WRGE-142), G4 (WRG-432), G14 (WRGE-136) and G11 (WRGE-143) and G8 (WRGE-138) were close to origin and hence they were less sensitive to environmental forces, While G10 (WRGE-142) recorded high mean yield with high stability. G2 (WRG-426) and G12 (PRG-176) had more responsive since they were away from the origin and were influenced by environmental forces.

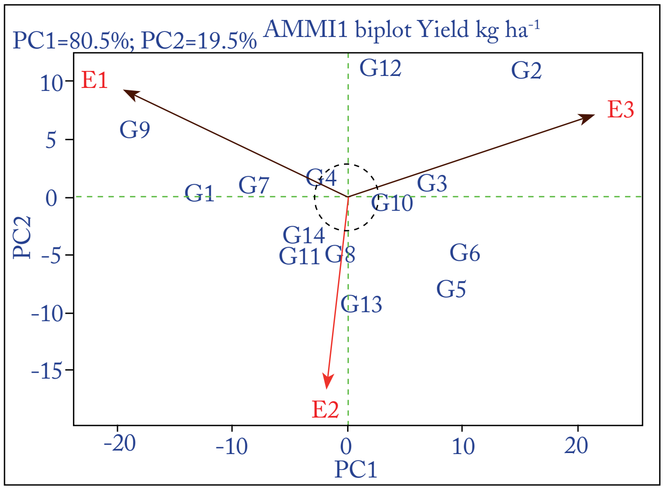

Figure 2: AMMI 2 Biplot for grain yield (kg ha^{-1}) showing the interaction of IPCA2 against IPCA1 scores of 15 pigeon pea genotypes (G) in five environments (E)

3.4. *GGE bi plot of environment-view for yield*

Environment centered GGE biplot used to estimate the pattern of environments (Figure 3). To compare the relationship between environments, some lines are drawn to connect the test environments to the biplot origin as environment vectors. The angle cosine between 2 environments is used to extent of the correlation between them (Dehghani et al., 2010). Environments E3 (*kharif*, 2020) and E2 (*kharif*, 2019) are positively correlated (an acute angle). The presence of wide obtuse angle among environments is an indication of high cross over genotype×environment interaction (Yan and Tinker, 2006). In the present study, the environments E1 (*kharif*, 2018) are negatively correlated (an obtuse angle).

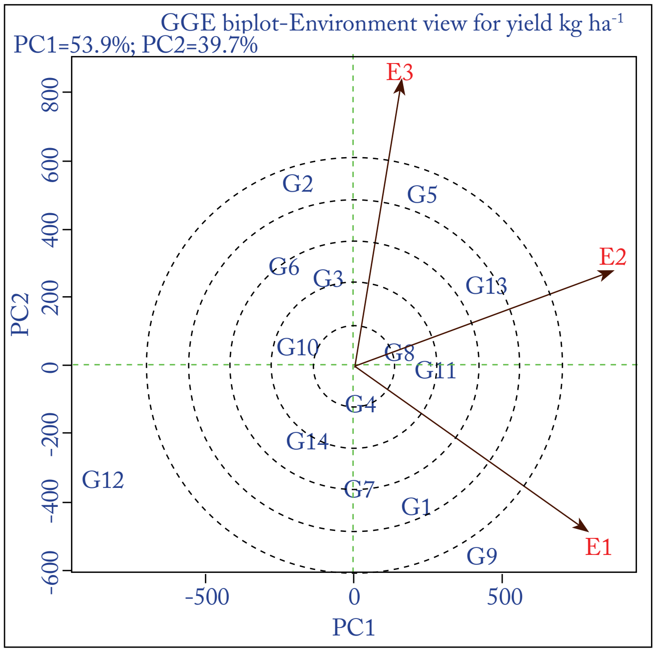

Figure 3: Vector view of GGE biplot of environment-focused scaling

3.5. *GGE bi plot of genotype view for grain yield*

Vector of GGE biplot in the genotype focused scaling also measures their dissimilarity in discriminating the genotypes. Genotypes G5 (WRG-437) and G13 (WRGE-134) showed same group position (Figure 4). Genotypes G8 (WRGE-138) and G11 (WRGE-143) felt in different group, while, G12 (PRG-176) with poor grain yield and not suitable for any environment. Likewise, genotypes can be discriminated based on dissimilarity.

3.6. *GGE biplot on environment for comparing environments with ideal Environment*

Discriminating ability and representativeness of the testing environments are an important measure in the GGE biplot. The concentric circles can help us to visualize the length of the environment vectors (Figure 5), which are a measure of the discriminating ability of the environments as well as standard deviation within the respective environments (Kang et al., 2015). The environments E1 (*kharif*, 2018) and E3 (*kharif*, 2020) are the most discriminating. The average environment which is drawn as small circle at the end of arrow has the average coordinates of all test environments and average environment axis (AEA) is the line passing through the average environment and the biplot origin (Figure 6). A test environment showing a smaller angle with the AEA is more representative than test environments (Yan and Rajcan, 2002). Accordingly, the environments E2 (*kharif*, 2019) is the most representative where as the environments E1 (*kharif*, 2018) and E3 (*kharif*, 2020) are least representative. Test environments with both discriminating and representative are good test environments for selecting adaptable genotypes.

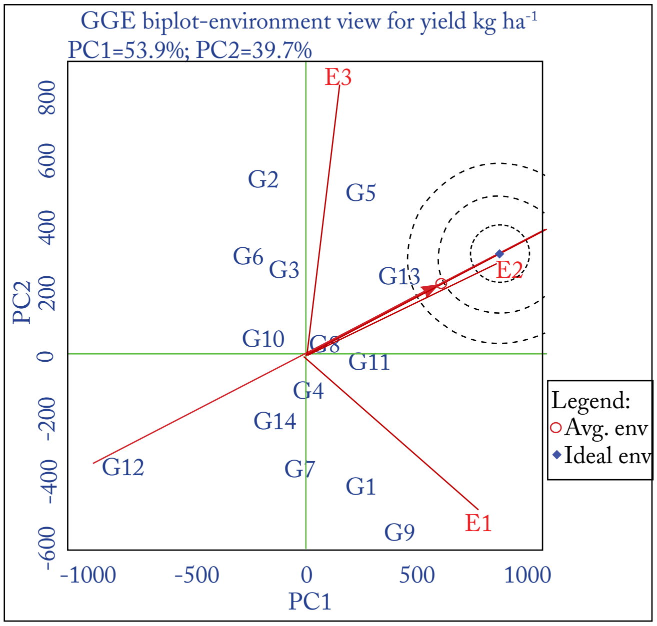

Figure 4: GGE biplot on environment focused for comparing environments with ideal Environment

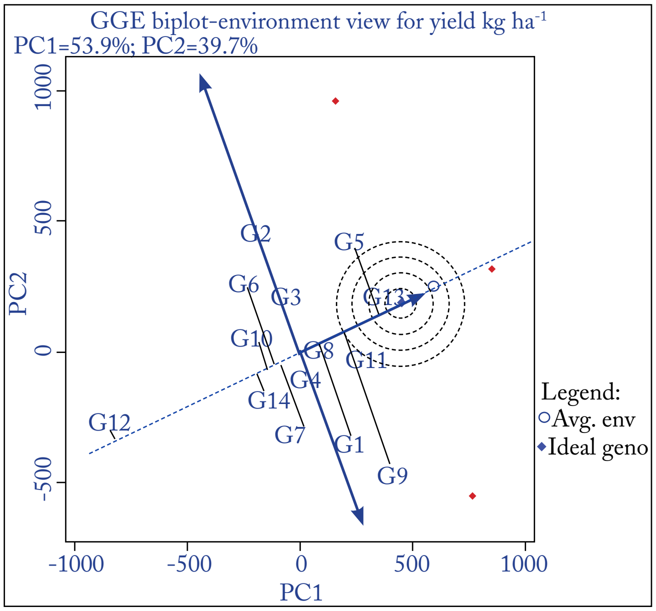

Figure 5: Biplot of stability and mean performance of genotypes across average environments

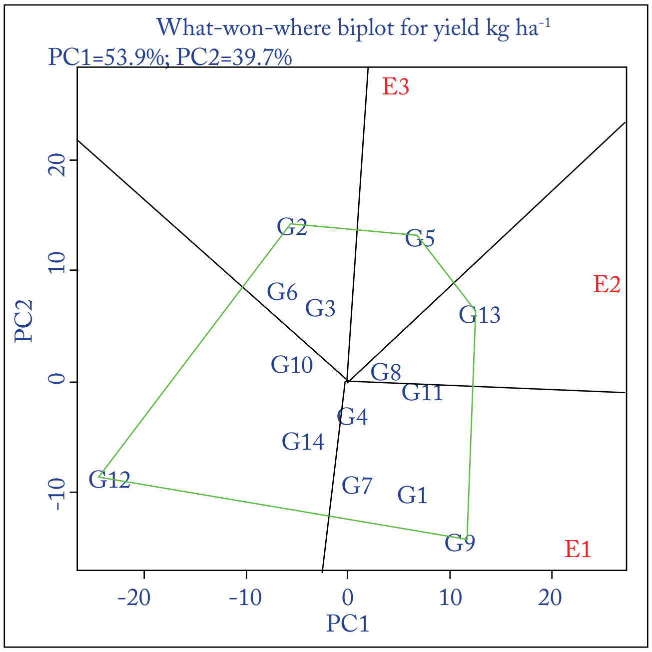

Figure 6: What-Won-Where GGE- Biplot for Yield (kg ha^{-1})

3.7. Biplot of stability and mean performance of genotypes across average environments

In Figure 6, the line that passes through the biplot origin and the average environment with single arrow is the average environment axis (AEA). Projections of genotype markers to the average environment axis show the mean yield of genotypes. Genotypes are ranked along the ordinate. The AEA ordinate is the double arrowed line that passes through the biplot origin and is perpendicular to the AEA abscissa. Greater projection onto AEA ordinate regardless of the direction means poor stability. Accordingly, the genotypes G9 (WRGE-141) and G1 (WRG-423) are unstable. The genotypes G11 (WRGE-143), G8 (WRGE-138), G10 (WRGE-142) and G14 (WRGE-136) with shorter projections are stable over environments.

3.8. "What-Won-Where" GGE Biplot

For differentiation of three environments into similar environmental groups, the "What-Won-where" pattern of GGE biplot was used. The decision as to whether each group of locations could be considered as representative of an environmental group was based on the similarity of grouping of winning genotypes across environments (Yan et al., 2000, Yan et al., 2007). In "What-Won-Where" biplot the genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments. The polygon is drawn on genotypes that lie farthest from the biplot origin in such way that all other genotypes are contained within in polygon. The What-Won-Where GGE Biplot for yield revealed that in E3 (*kharif*, 2020), G5 (WRG-437) was the winner and in E2, the genotype G13 (WRGE-134) followed by G11 (WRGE-143) and G8 (WRGE-138). In another mega environment E1, the genotype G9 (WRGE-141) was the winning genotype.

4. CONCLUSION

As revealed by AMMI and GGE bi plots, the genotypes G8 (WRGE-138), G13 (WRGE-134), G14 (WRGE-136) and G11 (WRGE-143) with negligible G×E interaction identified as stable genotypes coupled with high grain yield 1455 kg ha^{-1}, 1843 kg ha^{-1}, 1410 kg ha^{-1} and 1492 kg ha^{-1} respectively. Therefore, WRGE-138, WRGE-134, WRGE-136 and WRGE-143 could be popularized through large scale demonstrations in farmer's fields which can improve the Pigeon pea productivity and ensure livelihood of the resource poor farming communities.

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