

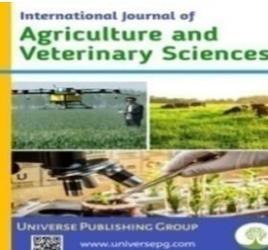


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Yield Stability Analysis of Late Set Pigeon Pea (*Cajanus cajan L.*) Genotypes

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ABSTRACT

Pigeon pea breeding program in Ethiopia has been started recently and is actively involved in improving the genetic yield potential to meet the needs of farmers in different parts of the country through genotype introduction. Since performance of the genotypes depends on the genetic potential of the crop and the environment in which the crop is grown, this study aimed at the evaluation of yield performance and stability of six late set pigeon pea genotypes including the standard check. Yield performances were evaluated at five locations namely Bako, Billo, Gute, Uke and Chewaka in parts of western Oromia during 2021 main growing seasons. The experiment in each location was arranged in a Randomized Complete Block Design with three replications. The results showed that the yield performances of late set pigeon pea genotypes were highly influenced by genotype-environment interaction (GEI). The yield components were significantly affected by GEI. The partitioning of the G + GE sum of squares showed that IPCA1 and IPCA2 were significant components which accounted for 29.72 % and 34.86 % of G + GE sum of squares, respectively. Highly significant mean square was observed for genotypes, genotypes by Environment interaction and environment indicating adaptation for high performance environments showing these genotypes were sensitive to environments and gave maximum yield when inputs are not limited. Genotypes ICEAP 01499 and ICEAP 01489 were stable and had relatively high yield performances across test environments. Hence, these two genotypes were identified as candidate genotypes to be verified for possible release in the subsequent season for Western Oromia and areas with similar agro-ecologies.

Keywords: Yield stability analysis, *Cajanus Cajan*, Genotype x environment, Late set, and Pigeon pea.

INTRODUCTION:

Pigeon pea (*Cajanus cajan L.*) ranked sixth globally after the peas, broad beans, lentils, chickpeas, and the common beans (Fatokimi and Tanimonure, 2021). Globally, it is cultivated on a 5.4 million hectare of land with an annual production of 4.49 million tons. It is grown in about 82 countries in the world. India accounts for about 72 % of the area grown for pigeon peas (FAO, 2017). In Africa (Eastern and Southern),

pigeon pea is grown on 0.56 million hectares (Esther and Victoria, 2021). Pigeon pea is an important crop in Malawi, Kenya, Uganda, Mozambique, and Tanzania. It is generally cultivated in association with yam, millet, sorghum, and cassava, among other crops (Egbe and Kalu, 2006). It is a tropical grain legume and is among the important pulses grown for food, feed, and soil fertility improvement. It is a deep-rooted and the drought-tolerant leguminous crop used in the several

countries as a source of dietary protein (Troedson *et al.*, 1990). It is endowed with rich dietary protein in its seed which provides the much-needed protein requirements. The seed contains 18 - 29% protein on a dry weight basis, which is about three times the value found in cereals, and is closer to soybean, which is 34% (Padhyaya and Reddy, 2006). The protein is 258 also of excellent quality, being high in lysine. The crop is, therefore, an important complement to cereal and root-based diets (Varshney *et al.*, 2009).

Pigeon pea offers great potential as an economic crop in the economy of some nations, as it constitutes their major cash crop, especially in India and Malawi (Silim and Mgonja, 2006). It does not only serve as protein for both humans and livestock but also is very useful in the pharmaceutical industry as medicine (Egbe, 2005). Pigeon pea enhancement program started with germplasm introduction from the ICRISAT and neighboring countries to identify high-yielding, disease, and pest-tolerant cultivars. Pigeon pea research in terms of crop improvement is still at its infant stage in Ethiopia. The production of pigeon peas in the present agro-ecological area is inadequate due to a scarcity of released and widely adapted pigeon pea varieties, which are better in both biotic and abiotic aspects.

Hence, considering the importance of pigeon peas in food security and its potential for the future in the Ethiopian economy, it is important to increase its production and productivity through developing new ones. Hence, the current research was started to evaluate introduced pigeon pea genotypes, for releasing and registering improved varieties for production in the Western part of Oromia and areas with similar agro-ecologies (Ray *et al.*, 2022; Mijena *et al.*, 2023).

MATERIALS AND METHODS:

Six late set pigeon pea genotypes including check (Table 1) were evaluated at five locations for one year, during 2021 main cropping season. Each plot consisted of four rows of 4- meter length, with 60 cm and 40 cm inter and intra row spacing, respectively. NPS fertilizer was applied at the rate of 100 kg ha⁻¹ at planting time. All other management practices were applied as per recommendation.

Data Analysis

Data Analysis an Additive Main Effects and Multiplicative Interaction (AMMI) model was used to assess genotype by environment interaction (GEI) pattern.

AMMI model is expressed as:

$$Y_{ger} = \mu + ag + \beta e + \epsilon_n \tilde{a}_n \tilde{d}_n + eger + \tilde{n}_g e$$

Where: Y_{ger} is the observed yield of genotype (g) in environment (e) for replication (r); μ is the grand mean; ag is the deviation of genotype g from the grand mean, βe is the deviation of environment e; ϵ_n is the singular value for IPCA, \tilde{a}_n is the genotype eigenvector for axis n, and \tilde{d}_n is environment eigenvector; $eger$ is error term and $\tilde{n}_g e$ is PCA residual.

Accordingly, genotypes with low magnitudes, regardless of the sign of interaction principal component analysis scores have general or wider adaptability; while genotypes with high magnitudes of IPCA scores have specific adaptability (Gauch, 1992; Umma *et al.*, 2014). Genotype plus genotype by environment variation (GGE) was used to assess the performance of genotypes in different environments. The environmental effects were removed from the data and results obtained from the data were used to calculate environment and variety scores and these scores were used to plot the standard principal component bi-plots (Yan and Kang, 2003).

Table 1: Pedigree and source of Late set pigeon pea genotypes used for the study.

| S. No. | Pedigree | Source of materials | Remark |
|--------|-------------|---------------------|--------|
| 1 | ICEAP 01489 | ICRSAT | Line |
| 2 | ICEAP 01517 | ICRSAT | Line |
| 3 | ICEAP 01204 | ICRSAT | Line |
| 4 | ICEAP 01499 | ICRSAT | Line |
| 5 | ICEAP 01485 | ICRSAT | Line |
| 6 | Dursa | OARI | Line |

Table 2: The study Environments and their main agro ecological features.

| Location | Longitude | Latitude | Altitude (m) | RF (mm) | Soil texture |
|----------|-----------------|---------------|--------------|---------|---------------|
| Bako | 37°09'E | 09°06'N | 1650 | 1431 | Sandy-clay |
| Gute | E:036038.196' | N:09001.061' | 1915 | NI | Clay |
| Billo | E:037°00.165' | N:09°54.097' | 1645 | 1500 | Reddish brown |
| Chewaka | 036.11703'E | 09.98285'N | 1259 | NI | Clay-loam |
| Uke | E:036032..391'E | N:09025.082'N | 1319 | NI | Sandy-loam |

NI = not identified RF= Rainfall

RESULTS AND DISCUSSION:

Combined analysis of variance there were statistically significant differences ($P < 0.01$) among late set pigeon pea genotypes, environments and their interaction for grain yield (**Table 3**). This indicates the presence of

genetic variation among the late set pigeon pea genotypes and possibility to select high yielding and stable genotype (s); the environments were variable and the responses of pigeon pea genotypes across environments were also variable.

Table 3: Combined analysis of variance for grain yield of six late set pigeon pea genotypes evaluated at parts western Oromia, Ethiopia.

| Source | DF | Type III SS | Mean Square |
|--------------------------|----|-------------|---------------|
| Environments | 4 | 96664800.37 | 24166200.09** |
| Genotypes | 5 | 3055106.62 | 611021.32** |
| Block within environment | 8 | 162053.22 | 20256.65* |
| Interaction | 20 | 4987682.22 | 249384.11** |
| CV (%) | | 5.84 | |

DF=Degree of freedom Gen=Genotype Loc=Location Rep=Replication **= significant at $P = 0.01$, *=significant at $P=0.05$ ns = non-significant

Performance of Genotypes across Environments

The result presented in **Table 4** indicates the average mean grain yield of six late set pigeon pea genotypes including standard check evaluated across five environments in western Oromia in 2021 main cropping season. The pooled mean grain yield ranged from 1508.4 to 2039.3kg ha⁻¹. Among all genotypes, genotype ICEAP 01204, ICEAP 01517 and ICEAP 01485 was lower yielder at Chewaka and Gute respectively. Higher grain yield was obtained from genotype ICEAP 01499 at Billo, Bako and Uke followed by genotype

ICEAP 01489 at the same location while genotype ICEAP 01485 was the highest yield at Uke. This difference could be due to their genetic potential of the genotypes. Hence, genotype 260 ICEAP 01489 was found to be the top yielder at all locations followed by genotype ICEAP 01499 at three locations: Billo, Bako and Uke. The differences in yield rank of late set pigeon pea genotypes across the test environments revealed that there was high genotype by environment interaction in terms of yield.

Table 4: Mean grain yield for late set Pigeon pea for individual and across location.

| Genotypes | Grain yield kg ha ⁻¹ | | | | | Comb. GY (kg ha ⁻¹) | Yield Adv. (%) check |
|-------------|---------------------------------|--------|---------|--------|--------|---------------------------------|----------------------|
| | Bako | Uke | Chewaka | Gute | Billo | | |
| ICEAP 01489 | 1321.3 | 2649.1 | 1136.1 | 997.2 | 2902.5 | 1801.2 | 19.4 % |
| ICEAP 01517 | 1126.8 | 2813 | 470.4 | 437.97 | 2893.1 | 1548.3 | |
| ICEAP 01204 | 1325.9 | 2987.1 | 393.5 | 471.3 | 2830.5 | 1601.7 | |
| ICEAP 01499 | 1845.4 | 3045.4 | 736.1 | 709.3 | 3860.2 | 2039.3 | 35.2 % |
| ICEAP 01485 | 1377.8 | 3243.5 | 387.9 | 492.6 | 2479.5 | 1596.3 | |
| Dursa | 1588 ^b | 2297.2 | 569.4 | 350.9 | 2736.5 | 1508.4 | |
| Mean | 1430.9 | 2839.2 | 615.6 | 576.6 | 2950.4 | 1682.5 | |

| | | | | | | | |
|------------|-------|-------|------|------|-------|-----|--|
| LSD (0.05) | 233.8 | 271.5 | 66.9 | 76.8 | 144.3 | 72 | |
| CV (%) | 9.1 | 5.3 | 6.1 | 7.3 | 2.7 | 5.8 | |
| P-value | ** | ** | ** | ** | ** | ** | |

AMMI analysis

An output of the ANOVA table of AMMI model analysis of variance for grain yield is presented in **Table 5**. This analysis also revealed the presence of highly significant (P< 0.01) differences among late set

pigeon pea varieties for grain yield. From the total treatment sum of squares, the largest portion (92.3%) was due to the environment's main effect; followed by genotype's main effect (63.35 %) and the effect of genotype by environment interaction was 25.9 %.

Table 5: Partitioning of the explained sum of square (SS) and mean square (MS) from AMMI analysis for grain yield of six late set pigeon pea genotypes used as testing materials.

| Source of variation | Degree of freedom | SS | Explained SS (%) | MS |
|---------------------|-------------------|-----------|------------------|------------|
| Total | 89 | 105360555 | | 1183826 |
| Treatments | 29 | 104707648 | | 3610609** |
| Genotypes | 5 | 3055200 | 2.9 | 611040** |
| Environments | 4 | 96664674 | 92.3 | 24166169** |
| Interactions | 20 | 4987773 | 4.8 | 249389** |
| Block | 10 | 170655 | | 17065ns |
| IPCA1 | 8 | 2293213 | 45.98 | 286652** |
| IPCA2 | 6 | 2017093 | 40.44 | 336182** |
| Residuals | 6 | 677468 | | 112911 |
| Error | 50 | 482252 | | 9645 |

ns= non- significant, **= significant at 1% and *= significant at 5% probability level. SS= sum of square, MS= mean square

A large yield variation explained by the environments indicated the existence of both spatial and temporal diversity in test-environments, with large differences among environmental means that caused most of the variation in grain yield. In line with this result Tolessa and Gela, (2014) reported large yield variation of common bean genotypes due to environments. This also indicates the existence of a considerable amount of deferential response among the 261 evaluated pigeon pea genotypes to changes in growing environments and the differential discriminating ability of the test environments. Substantial percentage of G × E interaction was explained by the IPCA-1 (45.98%); followed by IPCA-2 (40.44 %) and, therefore, used to the plot a two-dimensional GGE biplot. Amare and Tamado, (2014) and Temesgen *et al.* (2014) suggested the most accurate model for AMMI could be predicted by using the first two IPCA.

AMMI biplot analysis

AMMI biplot graphs with X-axis plotting IPCA1 (52.96 %) and Y-axis plotting IPCA2 (26.13 %) scores illustrate stability and adaptability of late set pigeon pea genotypes to tested environments (**Fig. 1**). The

more the IPCA scores approximate to zero, the more stable or adapted the genotypes are over all the environments sampled. The variation of seed yield for each genotype was significant in the different environments. G4 was specifically adapted to high yielding environments (**Fig. 1**). G5, G6, G3 and G2 were the most unstable genotypes and also adapted to low yielding environments and not stable. Billo, Uke and Bako locations were the potentially environmentally friendly than other testing locations (**Fig. 1**). G4 had the highest seed yield followed by G1. G4 had higher GEI in the environments of Bako and Billo. It has been reported that the genotypes that have the lowest IPCA score in AMMI biplot are an indication of the stability or adaptation over environments (Dolinassou *et al.*, 2016). It is further stated that the greater the IPCA scores, negative or positive, the more specific adapted genotypes to certain environments.

GGE biplot analysis

In GGE biplot (**Fig. 2**), IPCA1 and IPCA2 explained 52.98 and 26.13 %, respectively, of the pigeon pea genotypes by environment interaction and made a total of 79.1%.

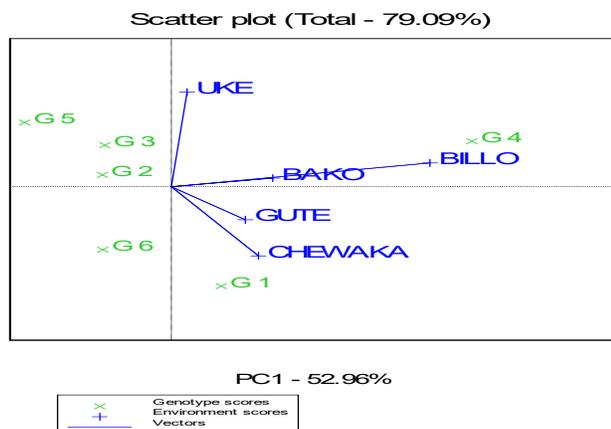


Fig. 1: Biplot of interaction principal component axis (IPCA1) against interaction principal component axis (IPCA2) of late set pigeon pea genotypes evaluated across environments.

Other studies conducted on groundnut by Amare and Tamado, (2014) and white lupines by Atnaf *et al.* (2017) explained an interaction of 81.8 and 63.4%, respectively, extracted from IPCA1 and IPCA2. An ideal genotype is defined as genotype which has the greatest IPCA1 score (mean performance) and with zero GEI, as represented by an arrow pointing to it (Fig. 2). A genotype is more desirable if it is located closer to the ideal genotype. Thus, using the ideal genotype as the center, concentric circles were drawn

to help visualize the distance between each genotype and the ideal genotype. Therefore, the ranking based on the genotype-focused scaling assumes that stability and mean yield are equally important. In this study, genotype 4 which fell closest to the ideal genotype was identified as the most desirable genotypes as compared to the rest of the tested late set pigeon pea genotypes (Fig. 2). Similar results were reported by Dabessa *et al.* (2016) for groundnut.

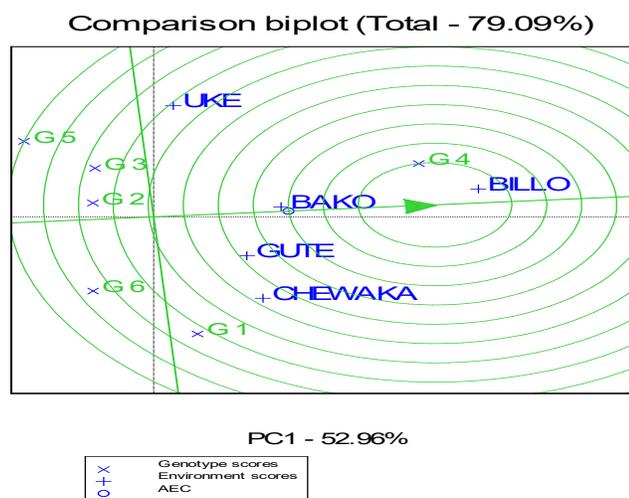


Fig 2: GGE-biplot based on genotype-focused scaling.

CONCLUSION AND RECOMMENDATIONS:

Combined analysis of variance indicated that grain yield performances of the tested late set pigeon pea were highly influenced by environment, varieties and GEI. This indicated that particular genotypes do not exhibit uniform performance under different environmental conditions or different genotypes may respond

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differently to a specific environment. The varieties and environment main effects and genotype-by-environment interaction effect were highly significant for late set pigeon pea genotypes. The environment contributed most to the variability in grain yield. Genotype 4 was closer to the ideal genotype and can thus be used as bench marks for the evaluation of the rest late set

pigeon pea genotypes in western Oromia. Considering simultaneously mean yield and stability, genotype 4 was the best late set pigeon pea genotypes and recommended for further evaluation under variety verification trial.

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CONFLICTS OF INTEREST:

The authors declare no potential conflict of interest.

REFERENCES:

- 1) Amare, K. and Tamado, T. (2014). Genotype by environment interaction and stability of pod yield of elite breeding lines of groundnut (*Arachis hypogaea L.*) in Eastern Ethiopia. *Star Journal*, 3(1), 43-46. <https://doi.org/10.4314/star.v3i2.6>
- 2) Atnaf, M., Dagne, K. and Tesfaye, K., (2017). Genotype by Environment Interaction and Grain Yield Stability of Ethiopian White Lupin (*Lupinus Albus L.*) Landraces. *Experimental Agriculture*.
- 3) Dabessa, A., Abebe, Z. and Lule, D. (2016). Genotype by environment interaction and kernel yield stability of groundnut (*Arachis hypogaea L.*) varieties in Western Oromia, Ethiopia. *J. of Agriculture and Crops*, 2(11), 113- 120. <https://ideas.repec.org/a/arp/jacarp/2016p113-120.html>
- 4) Dolinassou, S., Djirantal, A. K. and Njintang, Y. N. (2016). Genotype x environment interaction and kernel yield-stability of groundnut (*Arachis hypogaea L.*) in northern Cameroon. *J. of Applied Biology and Biotechnology*, 4(01), 001-007.
- 5) Egbe O. M., (2005). Evaluation of Some Agonomic Potentials of Pigeonpea Genotypes for Intercropping with Maize and Sorghum in Southern Guinea Savanna, University of Agriculture, Makurdi, Nigeria.
- 6) Egbe O. M. and B. A. Kalu, (2006). "Farming systems study: participatory rural appraisal of pigeon pea cropping systems in southern Guinea savanna of Nigeria," *The Review*, 5(1), pp. 37-47.
- 7) Esther O. and A. Victoria, (2021). "Analysis of the current situation and future outlooks for pigeon pea (*Cajanus cajan*) production in Oyo State, Nigeria: a Markov chain model approach," *J. of Agriculture and Food Research*, 6, Article ID 100218, 2021. View at: Google Scholar <https://doi.org/10.1016/j.jafr.2021.100218>
- 8) FAO, (2017). Statistics Pigeon Producing Countries. Production and Area Harvested Food and Agriculture Organization of the United Nations, Rome, Italy.
- 9) Fatokimi E. O. and V. A. Tanimonure, (2021). "Analysis of the current situation and future outlooks for pigeon pea (*Cajanus cajan*) production in Oyo State, Nigeria: A Markov Chain model approach," *J. of Agri. & Food Res.*, 6, p. 100218. <https://www.sciencedirect.com/science/article/pii/S2666154321001204>
- 10) Gauch, G., (1992). Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Amsterdam, the Netherlands: Elsevier Science Publishers.
- 11) Gwata E. T., S. N. Silim, and M. Mgonja, (2006). "Impact of a new source of resistance to Fusarium wilt in pigeon pea," *J. of Phytopathology*, 154(1), pp. 62-64.
- 12) Hari, D. K. N. U padhyaya, and L. L. Reddy, (2006). "Patterns of diversity in pigeon pea *Cajanus cajan (L.)* Germplasm collected from different elevations in Kenya," *J. of Genetic Research Crop Evolution*, 54, pp. 1787-1795. <https://oar.icrisat.org/481/>
- 13) Mijena D, Getiso A, Islam MR, and Shafi KM. (2023). Herbage yield evaluation of Pennisetum purpureum grass genotypes. *Int. J. Agric. Vet. Sci.*, 5(4), 64-74. <https://doi.org/10.34104/ijavs.023.064074>
- 14) Ray BP, Nath UK, and Azad MAK. (2022). Genetic analysis of submergence tolerance rice genotypes by introgression of Sub1 QTL to Indica HYV through breeding populations (F2) with marker assay. *Am. J. Pure Appl. Sci.*, 4(1), 10-21. <https://doi.org/10.34104/ajpab.022.010021>

- 15) Temesgen, A., Mammo, K. and Lule, D., (2014). Genotype by Environment Interaction (G x E) and Grain Yield Stability Analysis of Ethiopian Linseed and Niger Seed Varieties. *J. of Applied Biosciences*, **80**(1), pp.7093-7101.
- 16) Tolessa, T.T. and Gela, T.S., (2014). Sites regression GGE biplot analysis of haricot bean (*Phaseolus vulgaris L.*) genotypes in three contrasting environments. *World J. of Agricultural Research*, **2**, pp.228-236.
- 17) Troedson R. J., E. S. Wallis, and L. Singh, (1990). Pigeon Pea Adaptation, *CAB Inter, Wallingford, UK*.
<https://doi.org/10.1017/S0014479700020688>
- 18) Umma, K., Jamil, H., and Niaz, F. R., (2014). "Stability for BRRRI developed Promising Hybrid Rice for Yield and its related traits." *J. of Applied Science and Agriculture*, **9**, pp. 56-62.
- 19) Varshney R. K., R. V. Penmetsa, S. Dutta. (2009). Pigeon Pea Genomics Initiative (PGI): An International Effort to Improve Crop Productivity of Pigeon Pea (*Cajanus cajan L.*), *Springer, Berlin, Germany*.
- 20) Yan W. and Kang M.S (2003). GGE Biplot Analysis. A Graphical Tool for Geneticists, Breeders and Agronomists. *CRC Press, Boca Raton, FL*.

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