# PERFORMANCE OF SOME SOYBEAN (*Glycine max* (L.) MERIIL) GENOTYPES IN THE SOUTHERN GUINEA SAVANNA OF NIGERIA

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## ABSTRACT

The study was conducted to evaluate the performance of ten soybean genotypes in Southern Guinea Savanna of Nigeria. The experiments were conducted in three locations across the Southern Guinea Savanna of Nigeria during the 2021 cropping season. In each location, the experiments were laid out in Randomized Complete Block Design (RCBD) with three replications. Data were collected on plant height, number of leaves, growth and yield parameters and analyzed using Analysis of Variance (ANOVA) and means were separated using Duncan Multiple Range Test (DMRT). The results revealed that five genotypes (NCRI-SOY AC 18, NCRI-SOY AC 17, NCRI-SOY AC 69, NCRI-SOY AC 77, NCRI-SOY AC 73) were outstanding in yield across the three locations. Therefore, only five genotypes were stable in high yield. These five genotypes are recommended as donor parents in breeding of soybean varieties with both stabilities in high yield across environments. Also, the five genotypes are recommended for large scale soybean production in order to ensure adequate production and food security.

Keywords: Performance, Yield, Soybean, Genotypes

## INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is one of the most important oil seed crops in the world. The crop has gained popularity in Nigeria, outranking cowpea (*Vigna unguiculata* (L) Walp), because of its potential to supply high quality protein (Akande *et al*., 2007). Soybean production constitutes 6 % of all arable land in the world and has the highest percentage increase in area under production among crops annually. The global demand for the crop is expected to increase due to the crop's potential to improve the dietary quality of the vast majority of people and livestock (Hartman *et al*., 2011). Stability analysis is performed to estimate the performance of genotypes as linear function of the level of productivity in each environment (Bernardo, 2010). The use of multiplicative models which include the additive main effect and multiplicative interaction (AMMI) model has also been used to assess the stability of other crops (Adjebeng-Danquah, *et al*., 2017). The AMMI model allows fitting of the sum of several multiplicative terms rather than only one multiplicative term in dissecting the performance of genotypes in different environments (Bernardo, 2010). Yan also suggested the use of the genotype and genotype × environment interaction (GGE) biplot to graphically visualize genotypic performance across several environments. The use of these strategies will enable the breeder to make informed decisions in

where to place which variety based on their adaptability for optimum performance. Effective identification of superior genotypes is generally complicated by the presence of G x E interactions, whereby cultivar relative yields vary across different environments. In many crops, variations of genotypes in time to flowering is a source of genotype x environment interaction and requires appropriate consideration. Soybean yield potential in various agro-ecological environments vary depending on the compatibility with the agro-ecosystem, biotic and abiotic stress magnitudes, and level of crop management (Penalba, 2007 and Zanon 2016). Environmental variables such as soil type, growing season, planting pattern and elevation often become a determinant of suitability adaptation of soybean varieties in Ethiopia (Adie, 2013 and Kuswantoro 2016). It also leads to the interaction between genotype and environment. (GEI), which caused difficulties in selecting superior lines (Kumar, 2014). Optimization of such diverse environments can be achieved by the provision of high yielding and stable adaptation soybean varieties. Therefore, the objectives of the study were to identify stable soybean genotype(s) for yield and its component traits and also to evaluate the performance of soybean genotypes in individual environment and across environments.

**MATERIALS AND METHODS**

Ten soybean genotypes were selected (NCRI SOY AC78, NCRI SOY AC18, NCRI SOY AC17, NCRI SOY AC69, NCRI SOY AC77, NCRI SOY AC73, NCRI SOY AC26, NCRI SOY AC29, NCRI SOY AC25, NCRI SOY AC28). The study was conducted in three locations across the Southern Guinea Savanna of Nigeria. The first location, was at Ayédè village (9°23'46"N 3°35'28"E) Pake Jebba Expressway, Ilorin, Kwara state; the second location was at *N*ational Cereals Research Institute (*NCRI*) Apata (7°23'46"N 3°50'26"E), Ibadan, Oyo state; while the third location was at the Teaching and Research Farm of the Department of Crop Production, Federal University of Technology Minna, Niger state (9°35'00"N 6°32'46"E). Randomized Complete Block Design (RCBD) with three (3) replications was used in each location. The gross plot size was 3 m x 2 m = 6 m$^2$; giving 4 ridges of 2 m long each. The net plot size was 1.5 m x 2 m = 3 m$^2$; to give 2 ridges of 2 m long each. Along each replication, gross plots were separated by a distance of 0.5 m, while 1 m distance separated one replication from the other. The total experimental area was 65 m x 11 m = 715 m$^2$. Three (3) soybean seeds were sown per hill and later thinned down to one plant per stand. The planting distance used was 75cm × 20cm between and within rows, respectively. This gave a plant population of 66,667 plants ha$^{-1}$. Single super phosphate (SSP) was applied at the rate of 40kg/ha at 2 weeks after planting. Weed and insects

were intensively controlled in each location. Seed yield was taken during harvest after threshing the pods from the net plot and weighed in kg and converted to ton/ha. To determine the effect of genotype by environment interaction (GEI) and stability on yield and pod shattering, the data collected were subjected to Additive Main Effect and Multiplicative Interaction (AMMI) using Breeding Management System (BMS). The ANOVA model is $Y_{ij.} = \mu + g_i + e_j + ge_{ij} + \varepsilon_{ij.}$; AMMI model is $Y_{ij.} = \mu + g_i + e_j + \sum_k \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij.}$; where $Y_{ij}$ is the mean of the $i$th line in the $j$th environment, $\mu$ is the grand mean, $g_i$ is the genotype effect, $e_j$ is the site effect, $\lambda_k$ is the singular value for principal components $k$, $\alpha_{ik}$ is the eigenvector score for genotype $i$ and component $k$, $\gamma_{jk}$ is the eigenvector score for environment $j$ and component $k$, and $\varepsilon_{ij.}$ is the error for genotype $i$ and environment $j$. The result of the AMMI model analysis was interpreted by a biplot between Principal Component (PC) Axis 1 versus PC Axis 2. Genotype plus genotype × environment interaction (GGE) biplot was used to identify the best-performing genotype across environments. The polygon view of the GGE-biplot was used to show "which-won-where"; that is the best genotype in each environment and it summarized the GEI pattern of a multi environment yield trial data. The GGE biplot used is based on the Sites Regression (SREG) linear-bilinear (multiplicative) model (Hailemariam, 2021), which is given as $\bar{y}_{ij} - \mu_j = \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$; where $\bar{y}_{ij}$ is the cell mean of genotype $i$ in environment $j$; $\mu j$ is the mean value in environment $j$; $i = 1, \cdots g$; $j = 1, \cdots e$, $g$ and $e$ being the numbers of cultivars and environments, respectively; and $t$ is the number of principal components (PC) used or retained in the model, with $t \leq \min (e, g - 1)$. The model is subject to the constraint $\lambda_1 \geq \lambda_2 \geq \cdots \lambda_t \geq 0$ and to orthonormality constraints on the $\alpha_{ik}$ scores, with similar constraints on the $\gamma_{jk}$ scores [defined by replacing symbols $(i, g, \alpha)$ with $(j, e, \gamma)$]. The $\varepsilon_{ij}$ are assumed normally and independently distributed $(0, \sigma^2/r)$, where $r$ is the number of replications within an environment.

**RESULTS AND DISCUSSION**

Table 1 shows means performance for soybeans genotypes seed yield per plot. In Ibadan location, soybeans seed yield ranged from 0.965kg to 0.269kg. Genotype NCRI SOY AC 18 had the highest mean seed yield per plot (0.9649) while genotype NCRI SOY AC 73 had the least (0.2690). In Ilorin location, mean seed yield ranged from 0.427kg to 0.186kg. Genotype NCRI SOY AC 77 had the highest mean seed yield per plot (0.4267) while genotype NCRI SOY AC 69 had the least (0.1827). In Minna location, mean seed yield ranged from 0.441-0.141kg. Genotype NCRI SOY AC 18 had the highest mean performance (0.4413) for seed yield per plot while genotype G6 had the least (0.1407). Table 2 shows genotype ranking using Finlay and Wilkinson regression

analysis. Using coefficient of regression (bi) to rank genotypes. Genotype NCRI SOY AC 78, NCRI SOY AC 69 and NCRI SOY AC 17 are stable genotypes. Genotype NCRI SOY AC 73, NCRI SOY AC 18 and NCRI SOY AC 26 had specific adaptation which is the high yielding environment while genotype NCRI SOY AC 77 and NCRI SOY AC 73 had specific adaptation to low yielding among the three environments. Ranking of genotypes with deviation from regression ($S^2$di) shows that genotype NCRI SOY AC 26, NCRI SOY AC 28 and NCRI SOY AC 73 are stable genotypes. Figure 1 shows the GGE biplot for seed yield of some soybean genotype. The biplot shows that the first interaction principal component accounted for 85.6% of the total variations explained by genotype by environment interaction sum of square while the second interaction sum of square accounted for 9.4 % of the variation explained by genotype by environment sum of square. Genotype G1 and G10 had IPCA1 scores closer to zero. Genotype G6, G4, G7 and G2 had high IPCA score values.

Figure 1 shows GGE biplot of which genotype won where or which genotype performed best in a particular location. The biplot revealed that genotype at the vertex of the polygon performed optimally in that location. Genotype G2 performed best in Ibadan and Minna locations while genotype G5 and G9 performed best at Ilorin location. Genotypes G6 and G4 found on the vertex of the polygon without any environment performed poorly in all the sites. Figure 2 show mean seed yield per plot of soybeans genotypes verses stability biplot. The biplot shows that the red line with a single arrow head represent the average seed yield for soybeans genotypes while the blue line with double arrow head represent the degree of stability. The small red circle represents the ideal genotype. Genotype with short stability vector represent stable genotypes while genotypes with long stability vector are not stable. Figure 3 show mean seed yield per plot of soybeans genotypes verses stability biplot. The biplot shows that the red line with a single arrow head represent the average seed yield for soybeans genotypes while the blue line with double arrow head represent the degree of stability. The small red circle represents the ideal genotype. Genotype with short stability vector represent stable genotypes while genotypes with long stability vector are not stable. Positive correlation was observed between Ibadan location and Minna this is because the angle between these two environmental vectors is less than 90° this implies that the genotypes would perform similarly in both locations. Positive correlation between Ilorin and Minna also implies that genotypes that performed optimally in Minna would also perform optimally in Ilorin. Negative correlation between Ilorin and Ibadan and between Ilorin and Minna is because the angle between the environmental vectors is greater than 90°. This implies that the

genotypes under evaluation would perform differently across these two environments (Hailemariam, 2021). Genotypes that performed optimally in one location would not perform optimally in the other location. Similar result pattern was reported by Hailemariam and Hebtegebriel, (2022) who reported positive correlation when stability and adaptability analysis was conducted for soybeans genotypes in Ethopia. Ideal environment is the most powerful in genotype discriminating. However, from the study, Ibadan location is the Ideal location being the closest to the Ideal environment. Ideal environment is the most representative of all the overall environment. Ranking of genotypes using Finlay and Wikinson Joint regression analysis reveals that genotypes with regression coefficient approaching unity, mean square deviation from regression equal to zero or not significantly different from zero and with high seed yield. Genotype with bi values greater than 1 had specific adaptation to high yielding environment while genotype with bi value less than 1 had specific adaptation to poor yielding environment.

**CONCLUSION**

The Study revealed that stability analyses according to various principles can result in better identification of stable genotypes, even when there were no interactions among the parameters. Genotype by environment interaction was confirmed among the genotypes under evaluation. Ranking genotypes with joint regression analysis showed that genotype NCRI SOY AC 78, NCRI SOY AC 17 and NCRI SOY AC 25 would perform optimally in the three locations under evaluation while genotype with specific adaptation such as genotype NCRI SOY AC 18 and NCRI SOY AC 26 for high yielding environment (Ibadan) and genotype NCRI SOY AC 77 and NCRI SOY AC 73 for poor yielding environment. Genotype NCRI SOY AC 18 performed optimally in Ibadan and Minna while genotype NCRI SOY AC 25 and NCRI SOY AC 77 performed optimally in Ilorin and are recommended for cultivation in locations where they perform optimally. Genotype G9 NCRI SOY AC 25 is the most stable genotype while Ibadan location is the ideal location among the location under evaluation.

Table 1 Mean seed yield of soybean genotypes across the three locations (kg/ha)

| Genotypes | Ibadan | Ilorin | Minna |
| --- | --- | --- | --- |
| NCRI SOY AC 78 | 0.6404d | 0.2447bc | 0.4113ab |
| NCRI SOY AC 28 | 0.8453bc | 0.2783b | 0.3677abc |

| NCRI SOY AC 18 | 0.9649a | 0.1860c | 0.4413a | |
| NCRI SOY AC 17 | 0.6453d | 0.3617a | 0.3033cd | |
| NCRI SOY AC 69 | 0.5747d | 0.1827c | 0.3777abc | |
| NCRI SOY AC 77 | 0.3913e | 0.4267a | 0.3367bcd | |
| NCRI SOY AC 73 | 0.2690f | 0.2510bc | 0.1407e | |
| NCRI SOY AC 26 | 0.8940ab | 0.2203bc | 0.3150cd | |
| NCRI SOY AC 29 | 0.4437e | 0.2707b | 0.2680d | |
| NCRI SOY AC 25 | 0.7730c | 0.3753a | 0.3613bc | |
| Overall mean | | | | 0.4187 |
| CV | | | | 6.80 |

Means with the same alphabet(s) are not significantly different at $P \leq 0.05$. CV = Coefficient of Variation

Table 2 Genotype ranking using Finlay and Wilkinson Regression analysis

| Genotypes | Mean | Bi | rank | $S^2di$ | Rank |
|---|---|---|---|---|---|
| NCRI SOY AC 78 | 0.432133 | 0.963878 | 1 | 0.000978 | 7 |
| NCRI SOY AC 28 | 0.497133 | 1.547402 | 6 | 0.203425 | 2 |
| NCRI SOY AC 18 | 0.530733 | 1.97802 | 8 | 0.001666 | 10 |
| NCRI SOY AC 17 | 0.436778 | 0.888927 | 4 | 0.000803 | 6 |
| NCRI SOY AC 69 | 0.378333 | 0.921481 | 2 | 0.001562 | 9 |
| NCRI SOY AC 77 | 0.384889 | -0.00241 | 10 | 0.000587 | 5 |
| NCRI SOY AC 73 | 0.220222 | 0.175155 | 9 | 0.001039 | 8 |
| NCRI SOY AC 26 | 0.476444 | 1.851371 | 7 | 0.345728 | 1 |
| NCRI SOY AC 29 | 0.327444 | 0.505482 | 5 | 0.105672 | 3 |
| NCRI SOY AC 25 | 0.503222 | 1.17069 | 3 | 0.000415 | 4 |
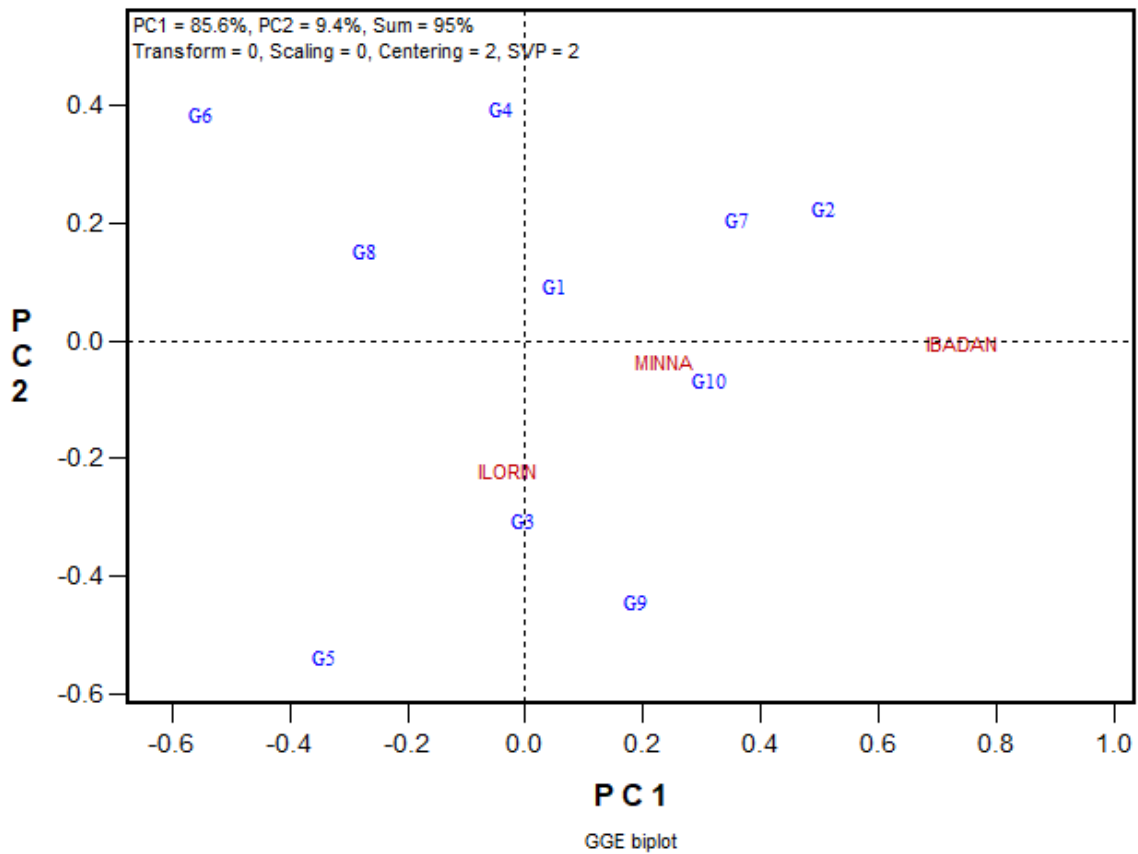
Figure 1. GGE biplot for seed yield of some soybean genotypes

G1= NCRI SOY AC 78; G2 = NCRI SOY AC 18, G3 = NCRI SOY AC 17; G4= NCRI SOY AC 69; G5= NCRI SOY AC 77; G6 = NCRI SOY AC 73; G7 = NCRI SOY AC 26; G8 = NCRI SOY AC 29; G9 = NCRI SOY AC 25; G10 = NCRI SOY AC 28
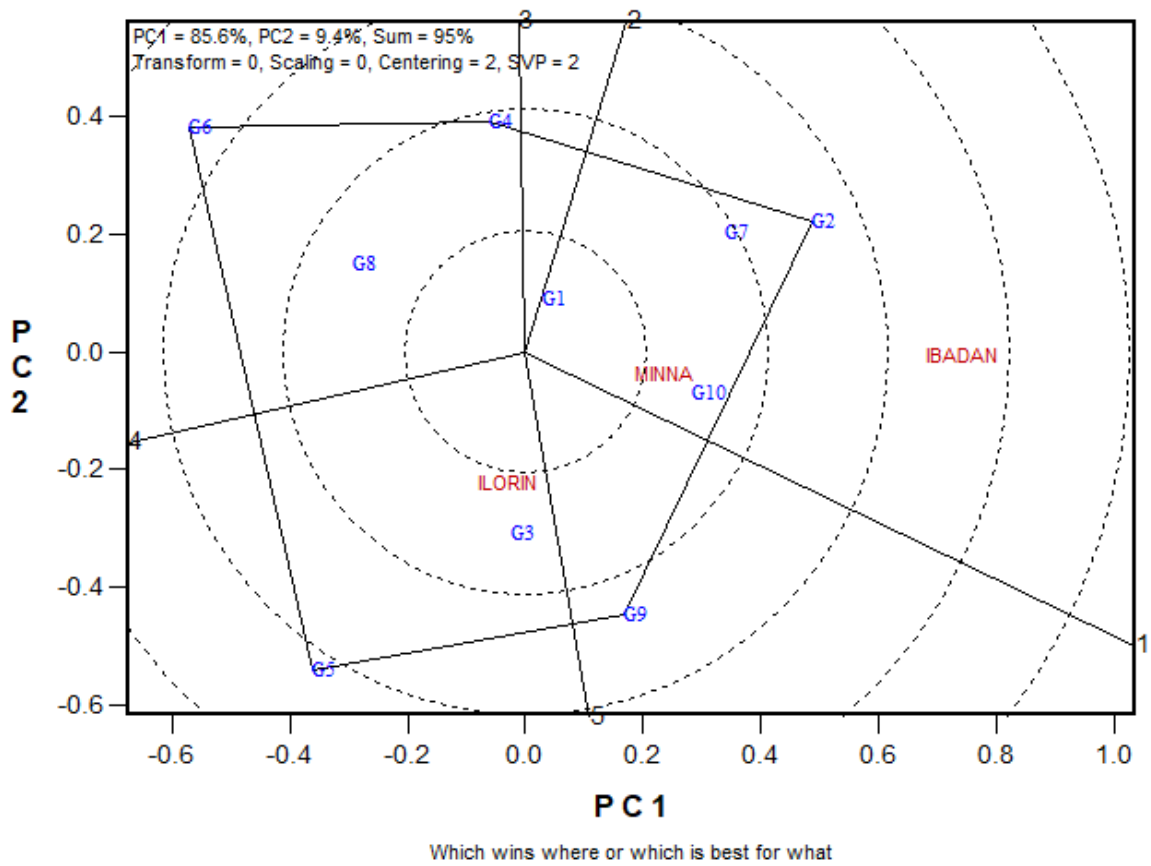
Figure 2 GGE biplot for which genotype won where or which genotype performed best

G1= NCRI SOY AC 78; G2 = NCRI SOY AC 18, G3 = NCRI SOY AC 17; G4= NCRI SOY AC 69; G5= NCRI SOY AC 77; G6 = NCRI SOY AC 73; G7 = NCRI SOY AC 26; G8 = NCRI SOY AC 29; G9 = NCRI SOY AC 25; G10 = NCRI SOY AC 28
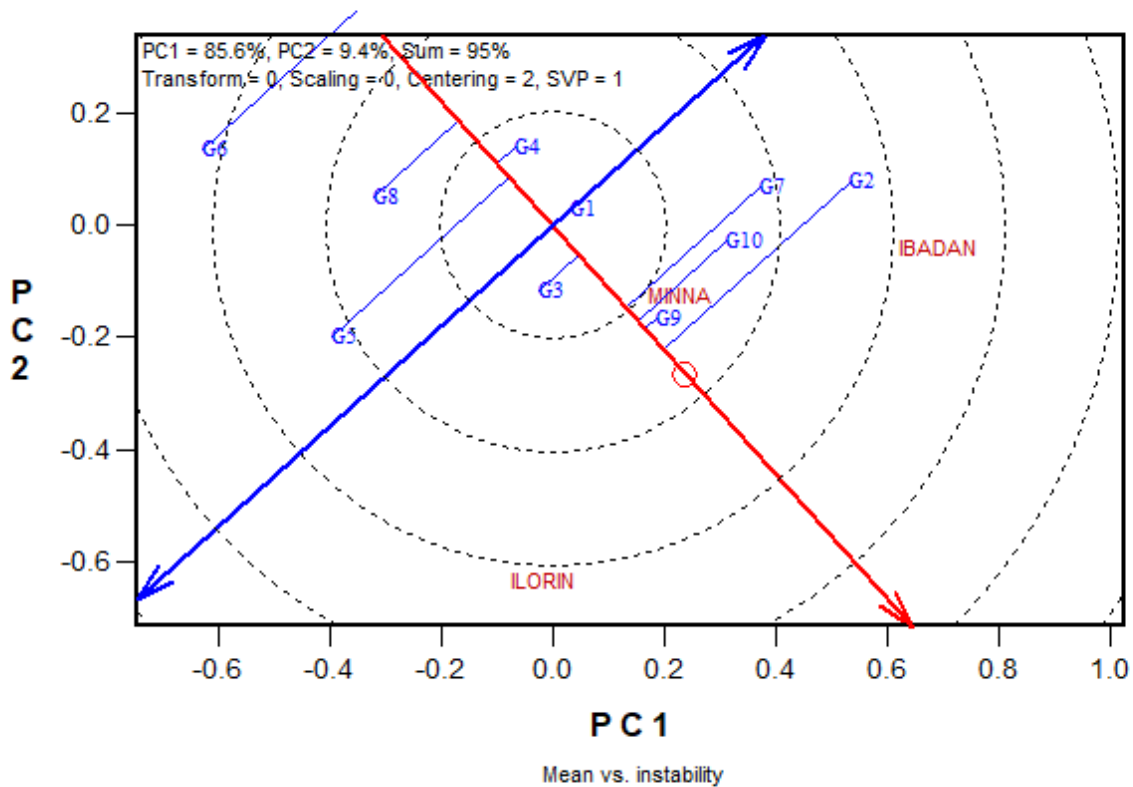
Figure 3. Genotype ranking based on their mean performance and stability

G1= NCRI SOY AC 78; G2 = NCRI SOY AC 18, G3 = NCRI SOY AC 17; G4= NCRI SOY AC 69; G5= NCRI SOY AC 77; G6 = NCRI SOY AC 73; G7 = NCRI SOY AC 26; G8 = NCRI SOY AC 29; G9 = NCRI SOY AC 25; G10 = NCRI SOY AC 28

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