

Research Article

Performance of Soybean Genotypes under Rhizobia Inoculation across Three Agro Ecologies of Nigeria

Tolorunse KD^{1*}, Gana AS¹, Sangodele EA² and Ngwu CH¹

¹Department of Crop Production, Federal University of Technology, Minna, Nigeria

²Olam Crown Flour Mill, Km 25, Kaduna-Abuja Express way, Kaduna, Nigeria

Abstract

There is need to improve soybean yield potentials per unit area in the tropics, at least to the world average productivity level. To achieve this, attention has to be paid to the selection of high yielding and stable genotypes through plant breeding improvement programmers. Twenty four soybean lines were investigated across three agro ecological zones in Nigeria to determine their productivity. In each of the sites, the experiments were laid out in randomized complete block design with three replications. Data were collected on growth and yield parameters. Results indicated that seven lines (TGx 1987-10F, TGx 1990-55F, TGx 1990-46F, TGx 1990-57F, TGx 1989-49FN, TGx 1989-48FN and TGx 1989-40F) were identified to be high yielding in both Northern and Southern Guinea Savannah, while TGx 1989-40F was high yielding in Sudan Savannah. This indicates that environmental differences could be responsible for soybean productivity from one agro ecology to another. Therefore, soybean lines could be recommended for cultivation according to their performances in a given environment.

Keywords: Agro ecology; Interaction; Performance; Soybean

Introduction

Soybean (*Glycine max* (L.) Merrill) is a legume native to East Asia perhaps in North and Central China [1] and belongs to the family

***Corresponding author:** Tolorunse KD, Department of Crop Production, Federal University of Technology, Minna, Nigeria; Tel: +234 07036411724; E-mail: kehinde.tolorunse@futminna.edu.ng

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Leguminosea. Soybean has been recognized as one of the premier agricultural crops today, thus it is the best source of plant protein and oil and has now been recognized as a potential supplementary source of nutritious food [2]. It has been found to substitute other sources of good quality protein such as milk, meat and fish. Therefore, it has become very suitable to other protein sources that are scarce or too expensive to afford [3].

Soybean contains a good quality protein of 42% and 19.5% oil [2]. Soybean protein is considered complete, because it supplies sufficient amounts of the types of amino acids that are required by the body for building and repair of tissues [4]. Essential amino acids found in soybean are methionine, isoleucine, lysine, cystine, phenylalanine, tyrosine, theonine, tryptophan as well as valine [5]. Amino acids are used in the formation of protoplasm, the site for cell division and therefore facilitate plant growth and development. Soybean has been found to have different uses; for example in food industry, soybean is used for flour, oil, cookies, candy, milk, vegetable cheese, lea thin and many other products [6].

There is need to improve on soybean yield potentials per unit area in the tropics, at least to the world average productivity level. To achieve this, attention has to be paid to the selection of high yielding and stable genotypes through plant breeding/improvement programmes. In plant improvement programmes, knowledge of the genetic variability and the adequate evaluation of breeding materials under several environments are of paramount importance. With the identification of high-yielding and well-adapted soybean genotypes, breeders can make recommendations to farmers, for soybean production in specific environments and across environments, which is expected to address the yield gap presently experienced in Nigerian agro ecologies. Therefore the objectives of the study was to evaluate the performance of soybean lines in individual environments and across environments, evaluate yield stability of the lines across the three environments and select superior advanced lines in the test environments for yield evaluation trial.

Methodology

The study was conducted during the 2015 and 2016 rainy seasons at three experimental sites across three different agro-ecologies of Nigeria. The experimental sites were; Abuja (Southern Guinea savanna) Latitude 9.52335N and Longitude 6.44791E, Igabi (Northern Guinea savanna) Latitude 10.94427N and Longitude 7.64443E, Gwarzo (Sudan savanna) Latitude 11.92996N and Longitude 7.98789E. The experimental treatment was a factorial combination of 24 soybean genotypes (TGx 1989-11F, TGx 1990-110FN, TGx 1989-42F, TGx 1990-95F, TGx 1989-45F, TGx 1990-114FN, TGx 1989-53FN, TGx 1993-4FN, TGx 1989-75FN, TGx 1990-78F, TGx 1987-62F (Check), TGx 1448-2E (Check), TGx 1989-40F, TGx 1990 -52F, TGx 1989-48FN, TGx 1990-40F, TGx 1989-49FN, TGx 1990-57F, TGx 1989-68FN, TGx 1990-46F, TGx 1990-55F, TGx 1987-10F (Check), TGx 1835-10E (Check), TGx 1485-1D (Check)) and three inoculation types (Without Inoculation, Legume Fix and Nodu Max) fitted into a Split-plot design with three replications. The main plots consisted of

the soybean genotypes and the sub-plots were the inoculation types. Gross plot size was 3 m × 4 m (12 m²) containing five ridges of 3 m long each. Net plot size was 3 m × 2.5 m (7.5 m²). An alley of 1 m was used to separate the blocks, and 0.5 m for the treatment plots. The experimental field in each location was ploughed, harrowed and ridged with tractor. Then followed by field layout in which 216 sub-plots were marked out as per the treatments. Single Super Phosphate (SSP) was applied by hand at the rate of 40 kg P₂O₅ ha⁻¹ at 2 weeks after sowing, using side placement method of fertilizer application.

Cypermethrin (Best) at the rate of 0.14 kg a.i ha⁻¹ [7] was applied once on the seedlings with knapsack sprayer to control insect pests infestation. In each of the location and year of research, seed yield was taken in which seeds were separated from the husk and kept in labelled bags representing respective plots and then converted to kilogram per hectare. Data collected were subjected to Analysis of Variance (ANOVA) using General Linear Model (GLM) procedure of SAS [8]. Level of significance was determined at 5%. Means were separated using Duncan Multiple Range Test at p = 0.05. To determine genotypic sensitivity and stability, linear regression and correlation model was used. Additive Main Effect and Multiplicative Interaction (AMMI) were used to determine the stability pattern of the genotypes across the locations. The AMMI model is

$$Y_{ij} = \mu + g_i + e_j + \sum \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

Where ε_{ij} is the mean of the Ith line in the jth environment, μ is the grand mean, g_i is the genotype effect, e_j is the site effect, λ_k is the singular value for principal components k , α_{ik} is the eigenvector score for genotype i and component k , γ_{jk} is the eigenvector score for environment j and component k , and ε_{ij} is the error for genotype i and environment j .

Results and Discussion

Table 1 shows seed yield of soybean as affected by genotypes and inoculation during the 2015 and 2016 cropping seasons and the combined data at the Abuja site. Seed yield was significant among the genotypes and the inoculation applications at both cropping seasons and their combined data. TGx 1990-110FN, TGx 1990-46F, TGx 1989-45F, TGx 1989-49FN and TGx 1990-55F recorded significantly higher seed yield during the 2015 cropping season while TGx 1990-95F had the least yield during the same cropping season. In 2016 cropping season, TGx 1990-46F produced the highest yield but not significantly different from four other entries. Also, the combined data revealed that TGx 1990-46F and TGx 1989-49FN had significantly higher yield compared to other entries. The result of inoculation indicated that plants without inoculation produced significantly lower yield at both cropping seasons and the combined data. Furthermore, the interaction between genotypes and inoculation was not significant except during the 2016 cropping season. Seed yield were generally higher in plants inoculated with either Nodu Max or Legume Fix compared to those plants without inoculation (Table 2). Among the inoculated plants, irrespective of the inoculants, TGx 1990-110FN, TGx 1989-49FN and TGx 1990-46F produced higher yield, similar to those produced by Nodu Max-inoculated TGx 1989-48FN, TGx 1990-40F and the Legume Fix-inoculated TGx 1989-42FN, TGx 1989-68FN and TGx 1990-55F plants. These were similar in yield as the checks TGx 1835-10E (Check), TGx 1835-10E (Check), TGx 1967-62F (Check) and TGx 1987-10F (Check) (Table 2). In the

combined data, all the growth and yield attributes measured correlated positively and significantly with the seed yield (Table 3). The strongest relationship between any two growth parameters and seed yield in the combined data, was that between 100-seed weight and seed yield ($r = 0.889^*$). This was in turn also the strongest relationship between any two growth parameters recorded. Table 4 indicated the combined analysis for sensitivity and stability coefficients for seed yield from soybean genotypes across environments during the 2015 and 2016 cropping seasons. TGx 1989-19F recorded mean seed yield (1577 kg ha⁻¹) greater than average mean 1570 kg ha⁻¹ and showed average genotypic sensitivity ($b = 1$) hence averagely stable. Also, five genotypes TGx 1990-40F, TGx 1989-11F, TGx 1990-52F, TGx 1448-2E (Check) and TGx 1990-55F recorded more than average mean performance and above average sensitivity, thus less stable. Furthermore, four genotypes, TGx 1989-45F, TGx 1989-75FN, TGx 1990-110FN and TGx 1990-95F had more than average mean performance and below average sensitivity ($b < 1$) making it more stable.

Treatment	2015	2016	Combined
Genotypes (G)			
TGx 1989-11F	1659.2 ^{cd}	1545.1 ^{dc}	1602.1 ^c
TGx 1990-110FN	2717.5 ^{ab}	1839.0 ^{ab}	2278.3 ^a
TGx 1989-42FN	1590.6 ^{cd}	1676.5 ^{bc}	1633.6 ^c
TGx 1990-95F	1514.2 ^d	1544.6 ^{cd}	1529.4 ^c
TGx 1989-45F	1989.8 ^{ab}	1820.1 ^{ab}	1905.0 ^{ab}
TGx 1990-114FN	1558.8 ^{cd}	1611.3 ^{cd}	1585.0 ^c
TGx 1989-53FN	1613.0 ^{cd}	1498.9 ^d	1556.0 ^c
TGx 1993-4FN	1581.8 ^{cd}	1601.0 ^{cd}	1591.4 ^c
TGx 1989-75FN	1573.1 ^{cd}	1592.3 ^{cd}	1582.7 ^c
TGx 1990-78F	1563.6 ^{cd}	1582.8 ^{cd}	1573.2 ^c
TGx 1967-62F(Check)	1722.7 ^{bc}	1738.6 ^{bc}	1730.7 ^{bc}
TGx 1448-2E(Check)	1658.7 ^{cd}	1655.7 ^{bc}	1657.2 ^c
TGx 1989-40F	1583.3 ^{cd}	1647.0 ^{bc}	1615.2 ^c
TGx 1990-52F	1657.3 ^{cd}	1693.2 ^{bc}	1675.3 ^c
TGx 1989-48FN	1752.9 ^{bc}	1816.5 ^{bc}	1784.7 ^{bc}
TGx 1990-40F	1699.1 ^{bc}	1762.7 ^{bc}	1730.9 ^{bc}
TGx 1989-49FN	1996.4 ^{ab}	1982.3 ^{ab}	1989.4 ^{ab}
TGx 1990-57F	1707.4 ^{bc}	1771.1 ^{bc}	1739.2 ^{bc}
TGx 1989-68FN	1696.7 ^{bc}	1727.0 ^{bc}	1711.9 ^{bc}
TGx 1990-46F	2060.0 ^a	2145.9 ^a	2102.9 ^a
TGx 1990-55F	1859.5 ^{ab}	1801.0 ^{bc}	1830.2 ^{bc}
TGx 1987-10F(Check)	1741.8 ^{bc}	1794.4 ^{bc}	1768.1 ^{bc}
TGx 1835-10E(Check)	1743.7 ^{bc}	1851.9 ^{ab}	1797.8 ^{bc}
TGx 1485-1D(Check)	1753.0 ^{bc}	1872.2 ^{ab}	1812.6 ^{bc}
±SE	112.7	109.3	122.2
Inoculation(I)			
Without inoculation	1204.0 ^c	1250.2 ^b	1239.7 ^c
Nodu Max	1882.1 ^b	1912.8 ^a	1892.0 ^b
Legume Fix	1988.1 ^a	2008.3 ^a	1991.0 ^a
±SE	38.3	42	39.5
Interaction			
G x I	NS	*	NS

Table 1: Mean seed yield (kg ha⁻¹) of soybean as affected by genotypes and inoculation during the 2015 and 2016 cropping seasons across the environments.

Note: Means followed by the same letter(s) within a set of treatment column are not significantly different at P = 0.05 using DMRT; NS = Not significant; * = Significant at P = 0.05; SE = Standard error

Genotypes	Without Inoculation	Nodu Max	Legume Fix
TGx 1989-11F	1189.1 ¹	1530.9 ^f	1915.2 ^b
TGx 1990-110FN	1299.4 ⁴	2118.3 ^a	2099.3 ^a
TGx 1989-42FN	1236.1 ¹	1777.5 ^d	2016.0 ^a
TGx 1990-95F	1185.6 ¹	1836.3 ^c	1611.8 ^c
TGx 1989-45F	1122.7 ¹	1965.6 ^b	1772.1 ^d
TGx 1990-114FN	1172.6 ¹	1746.4 ^d	1915.0 ^b
TGx 1989-53FN	1158.9 ¹	1701.9 ^d	1636.0 ^c
TGx 1993-4FN	1197.9 ¹	1828.7 ^c	1776.4 ^d
TGx 1989-75FN	1270.5 ¹	1743.7 ^d	1762.6 ^d
TGx 1990-78F	1181.5 ¹	1696.4 ^c	1870.7 ^c
TGx 1967-62F(Check)	1238.1 ¹	1814.3 ^c	2163.5 ^a
TGx 1448-2E(Check)	1317.6 ^b	1734.7 ^d	1914.9 ^b
TGx 1989-40F	1317.8 ^b	1874.3 ^c	1748.8 ^d
TGx 1990-52F	1244.3 ¹	1931.3 ^b	1904.0 ^b
TGx 1989-48FN	1345.6 ^b	2125.2 ^a	1978.7 ^b
TGx 1990-40F	1212.7 ¹	2148.9 ^a	1926.5 ^b
TGx 1989-49FN	1168.3 ¹	2229.3 ^a	2549.3 ^a
TGx 1990-57F	1329.9 ^b	1904.0 ^b	2079.1 ^a
TGx 1989-68FN	1341.6 ^b	1759.0 ^d	2080.3 ^a
TGx 1990-46F	1326.8 ^b	2588.8 ^a	2521.9 ^a
TGx 1990-55F	1144.8 ¹	1911.6 ^b	2346.3 ^a
TGx 1987-10F(Check)	1314.1 ^b	1987.0 ^b	2081.8 ^a
TGx 1835-10E(Check)	1245.0 ¹	2025.7 ^a	2284.7 ^a
TGx 1485-1D(Check)	1443.7 ^b	1929.2 ^b	2243.7 ^a

Table 2: Interaction effect of genotypes and inoculation on the seed yield (kg ha⁻¹) of soybean during the 2016 cropping season across the environments.

Note: Means followed by the same letters are not significantly different at P = 0.05 using DMRT; SE = Standard error

	1	2	3	4	5	6	7	8	9	10
1	1									
2	0.564*	1								
3	0.621*	0.719*	1							
4	0.581*	0.603*	0.709*	1						
5	0.156*	0.298*	0.253*	0.186*	1					
6	0.599*	0.696*	0.752*	0.589*	0.240*	1				
7	0.599*	0.696*	0.752*	0.589*	0.240*	0.000*	1			
8	0.242*	0.335*	0.340*	0.307*	0.145*	0.333*	0.333*	1		
9	0.478*	0.424*	0.539*	0.393*	0.177*	0.455*	0.455*	0.199*	1	
10	0.591*	0.597*	0.696*	0.509*	0.234*	0.789*	0.789*	0.264*	0.889*	1

Table 3: Combined analysis for correlation matrix between growth and yield attributes against seed yield of some soybean genotypes as influenced by inoculation type during the 2015 and 2016 cropping seasons across environments.

Note: * = Significant at 5%, ns = not significant, 1 = Chlorophyll content, 2 = Plant height, 3 = Number of leaves, 4 = Number of pods per plant, 5 = Number of branches per plant, 6 = Above ground biomass yield, 7 = Total biomass yield, 8 = Harvest index, 9 = 100-seed weight, 10 = Seed yield

The genotype and environment interaction clearly plays a significant role in breeding adaptable genotypes to the wide environment. This interaction was validated by the highly significant difference for seed yield. These results relate the findings of Gebeyehu and Assefa [9] who reported that selections based on the highest yielding genotypes appeared less stable than the average of all genotypes. Furthermore, Gebeyehu and Assefa [9] stated that selection solely for seed

yield could result in rejection of several stable genotypes. TGx 1989-45F and TGx 1990-110FN out yielded others because of its yield components such as plant height, number of leaves, number of pods per plant and some other growth traits that have contributed to the high yield. In contrast, Arslanglu and Aytac [10] reported contrary finding on the effect of genotype, environment and genotype by environment interaction on soybean pod number per plant, whereby plant height, seed yield and one hundred-seed weight were found to be significant at (P = 0.01). From the findings of this study, it was evident that total biomass yield and seed yield declined in the same trend. The mean performance analysis revealed that high yielding genotypes across the environments over the two years were TGx 1989-45F, TGx 1990-110FN and TGx 1989-53FN. Thus, the outstanding performance by TGx 1989-45F in terms of yield and yield related traits made it the best performer across the three environments over two years. These conform to [11] explanation for soybean performance that yield variation across environments and years was associated with changes in number of seeds per unit area. A contrary explanation is that an ideal soybean cultivar is one that achieves the greatest yield across many environments [12].

Genotype	Mean	Sensitivity (b value)	Static Stability	Mean square Deviation
TGx 1989-53FN	1493	0.7377	62849	909
TGx 1989-45F	1631	0.7381	64383	3846
TGx 1989-75FN	1571	0.8235	79986	12118
TGx 1990-114FN	1539	0.8239	83799	4325
TGx 1990-110FN	1594	0.8509	91675	17353
TGx 1485-1D(CK)	1570	0.8553	98997	32982
TGx 1993-4FN	1564	0.9010	100316	19412
TGx 1989-68FN	1537	0.9180	100367	7392
TGx 1990-78F	1488	0.9270	102786	973
TGx 1989-42F	1568	0.9485	104917	3565
TGx 1987-62F(CK)	1585	0.9533	105135	1887
TGx 1835-10E(CK)	1567	0.9676	118586	22522
TGx 1990-95F	1607	0.9848	118601	61738
TGx 1989-40F	1577	1.0000	124557	4196
TGx 1990-40F	1592	1.0414	136271	426
TGx 1989-11F	1579	1.0881	139353	18149
TGx 1987-10F(CK)	1566	1.0900	142051	125
TGx 1990-52F	1587	1.0970	144824	2772
TGx 1448-2E(CK)	1596	1.1146	146514	8178
TGx 1990-55F	1632	1.1271	149189	7093
Grand mean	1570			

Table 4: Combined analysis for sensitivity and stability coefficients for seed yield from soybean genotypes across environments during the 2015 and 2016 cropping seasons.

Note: CK = Check

The exhibited non-significance by these traits, number of branches per plant, number of pods per plant and one hundred-seed weight was confirmed by Baker [13] who defined the non-significant difference as failure of genotypes to achieve the same relative performance in different environment. Thus, the genotype by environment interaction might have made it difficult for breeders to identify the best genotypes, during selection and recommendation. The positive and significant correlation estimated between seed yield and other traits agreed

with the findings of Malik, et al., [14]. This implies that selections aimed at increasing seed yield would invariably select for higher plant height, higher leaf number and earliness to flower and as against one hundred-seed weight, number of branches per plant and number of pod per plant. This finding was in agreement with Karasu, et al., [15], who revealed that crop yield variations are strongly influenced by growth and yield parameters. The positive correlation reported agrees with Maesri, et al., [16], whereas, Rajanna, et al., [17], were of the view that one hundred-seed weight had negative association with seed yield. The positive correlation of number of pods per plant with seed yield obtained conformed to Karasu, et al., [15], study in Turkey. But Haliloglu, et al., [18], reported a contradictory result that the number of pods per plant indicated a positive association with seed yield. On the other hand, the positive correlation estimated between number of branches per plant and seed yield, total biomass yield, number of pods per plant agrees with Malik, et al., [14]. Thus the correlation estimation in this study clearly defines the contribution of various other traits such as plant height, number of leaves, branches per plant and total biomass yield to seed yield through path analysis. The highest and the lowest seed yields level attained by the genotypes were mostly due to plant height, number of leaves, number of branches per plant and number of pods per plant. In this study, it could be cited that the correlation coefficient of the genotypes across the environments in two years indicated that plant height had significant correlation with seed yield. This finding conformed to the report of Rajanna, et al., [17]. Although number of branches per plant correlated non-significantly with other traits, positive trend was recorded. The chlorophyll content was significantly associated with seed yield. This indicated that with the greenish nature of the leaves more efficient utilization of solar radiation could be achieved. The finding was in agreement with [19] who explained that the higher the chlorophyll content, the more improved the yield due to increased intercepted solar radiation and enhanced carbon exchange rate. The little variability recorded among genotypes was due to their response to climate changes in the three environments. This agrees with [20] findings that environment played major role in phenotypic expressions of agronomic traits. To overcome genotype by environment effect, [21] partitioned genotype by environment interaction into two; adaptability and phenotypic stability. These researchers defined adaptability as the capability that a genotype has to make use of the environmental effects that warrants a high yield level and phenotypic stability was related to yield maintenance or yield predictability in diverse environment. However, in the present study, genotype by environment was not partitioned. Phenotypically, all the studied genotypes followed similar trend of performance over two years. The non-significant differences posed by genotype by environment were confirmed by [22] who reported that traits do influence performance and seed yield. The yield variations explained by environments indicates that the environments were diverse, with large differences between environmental means contributing most of the variations in yield. According to [23], an ideal cultivar would have both a high average performance over a wide range of environments plus stability. Although genotypic main effect was highly significant this shows difference in genotypic performance across environments resulting in genotype by environment interaction. The existence of genotype by environment interaction raised the need to identify stable and high yielding genotypes.

Conclusion and Recommendations

Out of the twenty-four genotypes evaluated for genotype by environment interaction and yield stability, two (TGx 1989-45F and

TGx 1990-110FN) were identified by the analytical tools used as the overall best in relation to seed yield and stability as compared to the checks an grand mean performance of the genotypes. In terms of the environment, Gwarzo produced the least interaction scores, while Abuja and Igabi produced the highest interaction scores. Therefore, Gwarzo was most stable than Abuja and Igabi. However, the average yield performance of Gwarzo was poor when compared with the yield performance of the other two environments.

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