

Evaluation of soybean lines for resistance to rust (*phakopsorapachyrhizi*)

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Abstract—Among the diseases that can reduce soybean production is rust disease caused by the fungus *Phakopsorapachyrhizi*. The aim is to evaluate the resistance of soybean genotypes to rust disease and to study there interactions between agronomic traits. The study was conducted at field and screen house in the University of Agriculture Makurdi between July to November 2016. A total of 10 soybean genotypes were evaluated for resistance to rust disease. After inoculation in the laboratory, three lines TGX-1835-10E, TGX-1987-10F and TGX-1945-4F showed a consistent moderate resistance to *Phakopsorapachyrhizi*. These soybean Genotype flowered earlier and had the highest seed yield per plant (799.51kg/ha, 766.75K g/ha and 742.63 respectively). In contrast, the lines TGX-1949-10F and TGX-1485-1D which is the control, flowered at about 43 days after planting, had seed yield per plant of (404.30 and 254.23kg/ha, respectively), these lines had significantly lower yield and susceptible to rust. In the field, four lines had seed weight per plant significantly heavier than TGX-1949-10F and TGX-1485-1D, namely TGX-1835-10E, TGX-1987-10F, TGX-1904-6F and TGX-1945-4E and using a polygon view, the best performing lines were visualized as TGX-1987-10F was best in Environment one and TGX-1835-10E in two. Based on average environment coordination (AEC) procedure, TGX-1945-1F and TGX-1945-4E had yields above the grand means and stable while TGX-1945-4F and TGX-1935-3F were identified with high but unstable yield, the soybean lines with heavier seed weight per plant should potentially serve as genetic material to develop high yielding soybean varieties and resistant to rust disease.

Keywords— Genotype, rust resistance, yield component, grain yield, genotype x environment Interaction (GEI).

I. INTRODUCTION

Soybean rust, caused by *Phakopsorapachyrhizi*, is a major disease limiting soybean production and has caused significant economic annual yield loss of up to 60 to 80% been reported in the eastern and southern parts of the country Levy et al. (2005). The disease originates from Japan Kitani et al. (1960) and mainly was associated with

Asia and Australia. Within the last 10 years, soybean rust was reported in South America and in the continental United States. In west and central Africa, soybean rust has been reported in Nigeria, Ghana, and Democratic Republic of Congo Akinsanmi et al. (2001). The disease is now endemic in most soybean-producing areas in Nigeria. Soybean rust also has become one of the obstacles to increase soybean production in central and north East Nigeria due to climatic condition (high temperature and humidity) providing suitable conditions for disease development, especially during the raining season Adeleke et al. (2006). Soybean rust becomes the most destructive foliar disease of soybean worldwide due to the widespread distribution and the potential for severe yield losses Hartman et al. (2005). Soybean rust symptoms generally occur first on the leaves at the base of the plant and spread up to the canopy as the disease severity increases. Rust symptoms include presence of tan to dark brown or reddish brown lesions Hartman et al. (1994). An increase in leaf density will result in leaf yellowing, early leaf senescence, and yield losses Tschanz et al. (1980). The heavy defoliation due to rust disease affects pod formation and pod filling Yang et al. (2007). According to the USDA (2010), severity of losses in yield depends on the susceptibility of the soybean variety, time of the growing season in which the rust becomes established in the field and weather conditions during the growing seasons. The extent of yield loss is also dependent on crop growth stage at which the disease starts and the intensity. Time of planting also affects soybean rust severity on plant leaves Twizeyimana et al. (2007). The most susceptible stages are between early flowering and mid-seed development.

Resistance to soybean rust is manifested phenotypically by red-brown lesions and characterized by the plant response that have been shown to be associated with single dominant genes for soybean rust resistance, i.e. an immune response, reddish-brown lesions (or incomplete resistance), and the susceptible tan lesions Bromfield, (1984). Plant breeders routinely test genotypes in multiple locations and years to determine whether or not environment affects the magnitude of specific traits of

genotypes, such as disease severity, as well differences of the values of the traits among genotypes Piepho, (1996). Several methods have been proposed to analyze the genotype– environment (GEI) interaction such as joint regression (Finlay and Wilkinson, 1963; Perkins and Jinks, 1968), sum of squared deviations from regression (Eberhart and Russel, 1966), stability variance (Shukla, 1972), coefficient of determination (Pinthus 1973), coefficient of variability (Francis and Kanneberg 1978), and Type B genetic correlation (Burdon 1977). These methods are commonly used to analyze multi-location environment trials data to reveal patterns of GE interaction. Alternatively, the additive main effects and multiplicative interaction (AMMI) model have led to more insight in the complicated patterns of genotypic responses to the environment (Gauch and Zobel 1988, Zobel et al, 1988, Gauch 1992, 2006). Yan et al. (2000) proposed another methodology known as GGE-biplot for graphical display of GE interaction pattern of Multi-environment trial (MET) data with many advantages, among which is the graphical visualization of the interrelationship among environments, genotypes, and interactions between genotypes and environments. The objective of the study was to evaluate soybean lines for resistance to rust disease, *Phakopsora pachyrhizi*.

II. MATERIALS AND METHODS

Experiment 1;

Evaluation of Soybean Genotypes in Wukari and Makurdi Environments.

The study was conducted at two locations Makurdi and Wukari. The experiment was carried out in the 2015 cropping season between the months of June to November at the Teaching and Research Farm of the University of Agriculture Makurdi (lat. 7.73°N, long. 8.53°E). The location falls within the southern Guinea agro-ecological zone of Nigeria, and Wukari (lat. 7. 88°N, long. 9.78E). This location falls within the north-east agro-ecological zone of Nigeria. Ten lines of soybean were planted out in a randomized complete block design with three replications on 30th June 2015 and 7th July, 2015 in Makurdi and Wukari respectively. The size of each plot was 32m². Each plot consisted of 4 ridges of 4m length, spaced 0.75m apart. Harvesting was carried out in November and the following parameters were measured. Days to flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, 100 seed weight, seed weight per plant and yield per plot. Resistance to soybean rust, A scale of 1-5 adopted from Iqbal et al. (2004) was used for the disease rating where 1= highly resistant, 2= resistant, 3=moderately resistant, 4= susceptible and 5= highly susceptible.

Statistical analysis

Analysis of variance was performed initially for each of the parameters measured above in the different locations. Using the general linear model of SAS (2007) Yield data were analyzed using GGE models to determine GEI, genotype stability and winning cultivars in the locations using GENSTAT 13th Edition.

Experiment 2;

Assessing Soybean for Resistance to Bulk Isolates of Rust (*Phakopsora pachyrhizi*).

A set of three soybean plants for each of the 10 genotypes were planted in 10 litre buckets in the University of Agriculture screen house in Makurdi and arranged in a completely randomized design. Two weeks later, soybean rust isolates were collected from the field for inoculation. Soybean rust isolates were harvested using a handheld Liliput® vacuum from random soybean leaves at the R6 stage from two locations that represent the major soybean growing areas in this study (Makurdi and Wukari). These locations are described above. Rust isolates, were selected from about five to twelve leaves and bulked. The bulked rust isolates were then inoculated on the 10 advance soybean lines using the detached leaf technique at the second Vegetative growth stage within 48 hours of collection from the field Obua. (2012, Twizeyimana et al. (2010) For each isolate, freshly harvested field spores were mixed with distilled deionised water containing the surfactant Tween-20 at 0.5ml/l. Urediniospore suspensions were diluted to a concentration of 50 000 spores per milliliter using a haemocytometer. Leaves at two trifoliate stages were detached from the seedlings and artificially inoculated with 1.5 ml of spore suspension on the abaxial leaf surface using a hand sprayer. Each of the inoculated detached leaves was carefully placed in 9-cm-diameter Petri dish with the adaxial side placed on the moist filter paper. After inoculation, the leaves were covered with black polythene bags for 24 hours at 22°C-24°C to maintain high relative humidity, necessary for infection. After 24 hours, the polythene bags were removed for the rest of the experimental period.

The data recorded from the study includes;

Reaction type: immune (I), Reddish-Brown (RB), Tan colored (TAN), Mixed reaction with both RB and TAN (MX), Lesion number and Frequency of lesions with uredinia. This was done using ×10 magnification lenses. Data were collected after five days of inoculation on a three day interval up to the 16th day after inoculation and subjected to analysis

of variance in GENSTAT 13th Edition.

III. RESULT

Genotype Reaction to Soybean Rust Disease

Mean rust severity scores on soybean genotypes for the locations are presented in Table 1. Genotype with lowest rust severity scores includes TGX-1835-10E (3.13) and TGX-1945-4F (3.07). On the other hand, TGX-1485-1D had the highest mean score from both location; Rust severities were significantly different across the different genotypes within locations ($p < 0.01$). makurdi had the lowest mean scores of 3.17 while wukari had higher mean score of 3.50.

Table.1: Mean Number of Rust Disease Reaction to Genotypes

Genotypes	Makurdi	Wukari
TGX-1949-10F	3.80	3.90
TGX-1987-10F	3.23	3.53
TGX-1448-2E	3.50	3.67
TGX-1485-1D	4.13	4.09
TGX-1835-10E	3.13	3.23
TGX-1904-6F	3.67	3.63
TGX-1935-3F	3.33	3.27
TGX-1945-1F	3.67	3.09
TGX-1945-4F	3.47	3.07
TGX-1951-4F	3.53	3.43
Mean	3.17	3.50
Cv%	5.46	6.32
Lsd	0.33	0.3

key; 1.0-1.9=highly resistant 2.0-2.9= resistant 3.0-3.9=moderately resistant 4.0-4.9=susceptible 5.0->=highly susceptible a scale of 1-5 (iqbalet al. 2004).

Number of Lesions per Leaf

Analysis of variance for number of lesions per leaf showed that location effect was significant ($p=0.02$) while genotypes were not significant for lesion number per leaf; this implies that isolates from different locations infected all genotypes differently. Genotypes TGX 1935-3F had a mean of 21 lesions; followed by TGX 1904-6F (15). On the other hand, TGX 1985-10F showed the lowest mean number of (12) lesions; followed by TGX 1949-10F (27), TGX 1485-1D(20) and TGX-1951-4F(25) as summarized in Table 2.

Table.2: Mean of Lesion Number per Leaf of 10 Soybean Lines after inoculation with Rust Bulk Isolates from two study locations

Genotypes	Makurdi	Wukari	Mean
TGX-1949 10F	40	14	27
TGX-1987-10F	25	13	18
TGX-1448-2E	28	20	24
TGX-1485-1D	55	15	35
TGX-1835-10E	11	12	13
TGX-1904-6F	14	6	15
TGX-1935-3F	38	14	21
TGX-1945-1F	25	21	23
TGX-1945-4E	29	11	20
TGX-1951-4F	32	16	24
Mean	30.2	14.4	20.8
LSD	1.76	3.11	3.47

Effects of Genotypes on Yield and Yield Component

The result in Table 3 show that the effects of genotypes on yield and yield component at different locations were significant ($P < 0.05$) confirming the previous studies of Lymon et al (2017) in Tanzania

In this study, the genotypes TGX 1835-10E and TGX 1987-10F outperformed the local check in all the two locations with the average mean performance of 799.51 and 766.75 kg/ha respectively, while TGX-1485-1D had the lowest (254.23kg/ha) yield in all locations. Alongside TGX 1945-4E, TGX 1904-6F and TGX 1448-2E yield performance were significantly high than the control (TGX-1485-1D) in all locations. The low yielding ability of TGX-1485-1D variety was previously reported by (Ojo et al. 2010) for the southern Guinea Savanna. The mean performance of the genotypes across the location revealed that TGX 1835-10E had the highest number of seed per plant (1.87), followed by TGX1904-6F (1.71) and TGX-1485-1D showed the lowest (1.11). TGX1835-10E and TGX 1904-6F had the largest number of pods per plant with 50.10 and 43.60 respectively, and TGX-1485-1D revealed the lower value (26.28). Similarly, the genotype TGX1835-3F and TGX 1904-6F had the highest plant height with 49.15 and 47.58cm respectively while TGX-1485-1D recorded the least (36.45cm). High yields attained by TGX 1835-10E and TGX 1935-3F genotypes could be explained by the high performance of agronomic variables such as the number of pods per plant and number of seeds per plant which featured high in these genotypes compared to others (Table 2).

Table.3: Effect of Genotype on yield and yield component

GENOTYPES	DDF	DYSM	PLT(m)	NOB	NPPLT	SPPLT	HSW	YIELD(kg/ha)
TGX-1949-10F	43.16 ^a	88.00 ^{de}	37.58 ^d	1.91 ^c	30.76 ^{bc}	1.18 ^{dc}	7.65 ^c	404.30 ^{bc}
TGX-1987-10F	40.66 ^{ba}	85.50 ^e	40.67 ^{dc}	1.88 ^c	36.63 ^c	1.53 ^{bac}	9.77 ^{bac}	766.75 ^{ba}
TGX-1448-2E	41.33 ^{ba}	101.33 ^a	45.13 ^{ba}	2.63 ^{ba}	31.43 ^{bc}	1.71 ^{ba}	11.95 ^a	690.26 ^a
TGX-1485-1D	41.66 ^{ba}	94.83 ^{bc}	34.45 ^{bc}	2.15 ^{bc}	26.28 ^{qbac}	1.11 ^d	7.80 ^c	254.23 ^c
TGX-1835-10E	40.50 ^b	85.50 ^e	49.15 ^{bc}	2.10 ^{bc}	50.10 ^{bc}	1.87 ^a	11.03 ^{ba}	799.51^a
TGX-1904-6F	42.00 ^{bac}	99.16 ^{ba}	47.58 ^{bc}	2.06 ^{bc}	43.60 ^{bac}	1.70 ^{ba}	11.71 ^{ba}	750.68 ^a
TGX-1935-3F	41.83 ^{ba}	92.16 ^{dc}	51.46 ^a	2.93 ^a	39.43 ^{bac}	1.31 ^{bdc}	8.68 ^{bc}	585.40 ^{ba}
TGX-1945-1F	43.00 ^{ba}	97.83 ^{ba}	41.93 ^{bcd}	2.10 ^{bc}	37.46 ^{ba}	1.58 ^{ba}	10.53 ^{bac}	652.21 ^{ba}
TGX-1945-4E	41.33 ^{ba}	91.66 ^{dc}	47.36 ^{ba}	2.53 ^{ba}	33.23 ^a	1.65 ^{ebdac}	11.26 ^{ba}	742.63 ^{ba}
TGX-1951-4F	41.66 ^{bac}	94.33 ^{dc}	36.96 ^d	1.61 ^c	36.16 ^{bac}	1.60 ^{ba}	11.00 ^{ba}	559.65 ^a
Mean	41.61	93.03	43.08	2.19	35.61	10.14	1.52	775.35
SE	0.55	1.70	1.89	0.20	4.51	0.14	1.06	110.01
Cv(%)	2.60	4.48	10.71	22.73	31.33	23.26	25.62	34.71

Means with the same letter are not significantly different at the 0.05 probability level based on Tukey's Studentized Range Test; Bolded values are highest genotype grain yield at each test environment, and highest yielding genotype across environments and the highest yielding environment; DFF: Days to flowering, DYSM: Days to maturity, PLT; Plant height, NOB; number of branches, NPPLT; number of pods per plant, SPPLT; number of seed pod per plant, HSW; hundred seed weight per plant.

Best Performing Soybean Genotypes

From The different environments best performing genotypes were visualized using a polygon view in Figure 1. This polygon view was drawn by joining five soybean genotypes at the furthest corners from the origin of the biplot. These were TGX-1987-10F, TGX-1485-1D, TGX-1935-3F, TGX-1945-4F; TGX-1835-10E from which five perpendicular lines were drawn to each of the polygon side passing through the origin of the biplot dividing the biplot into five sectors. Environments 1 (Makurdi), and Environments 2 (Wukari), lines TGX-1987-10F was the best performed genotype in Environments 1, followed by TGX-1835-10E, performed best in Environment 2, while Other vertex genotypes like TGX-1485-1D, TGX-1935-3F, TGX-1945-4E did not fall under any of the test environments. The rest of the genotypes were located within the polygon, while TGX-1945-1F was located close to the biplot origin.

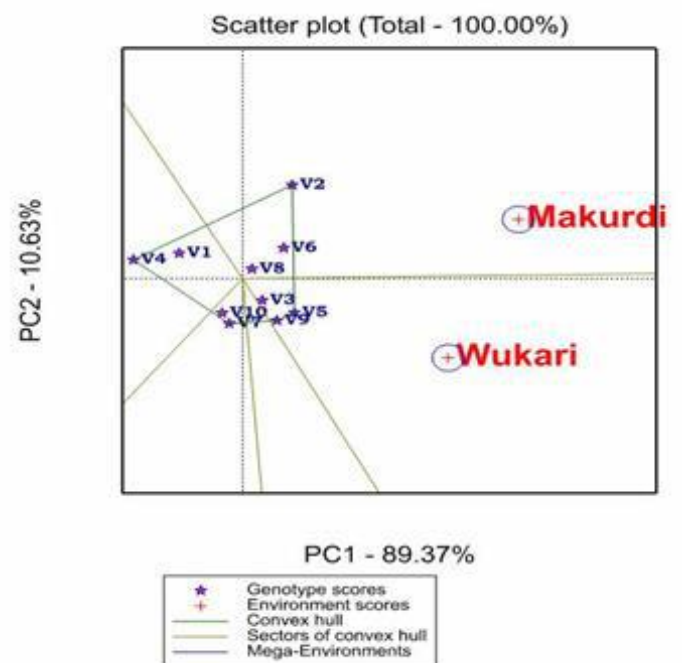


Fig.1: Polygon view of GGE biplot based on symmetrical scaling for 10 genotypes in two environments. PC1 and PC2 are the first and second principal components, respectively.

KEY VI= TGX-1949-10F, V2=TGX-1987-10F, V3=TGX-1448-2E, V4=TGX-1485-1D, V5=TGX1835-10E, V6=TGX-1904-6F, V7=TGX-1935-3F, V8=TGX-1945-1F, V9=TGX-1945-4F, V10=TGX1951-4F.,

Soybean Yield Performance and Stability

Below shows a GGE biplot for soybean yield performance and stability based on average environment coordination (AEC) procedure Figure 2. A straight line passing through the origin of the biplot and the average environment is represented by a small circle. A

perpendicular line to AEC axis passing through the biplot origin separates the genotypes with more than the grand mean yield from those with less than grand mean yields. Therefore, genotypes with more than grand means and are located near the AEC line and are genetically desirable. To this regard, genotypes TGX-1448-2E (V3), and TGX-1945-4E (V9) had yields above the grand means, and the yield were stable because they were not far from the AEC line. Conversely, genotypes TGX-1835-10E (V5) and TGX-1945-1F (V10) were among the high yielding genotypes but their yields were unstable because they were located far from the AEC line. Other genotypes had yields below the grand mean but their yields were stable. These included; TGX-1904-6F (V6). On the other hand, genotypes, TGX-1485-1D (V4) and TGX-1949-10F (V1), recorded the lowest yields and were position far away from AEC line.

A comparison biplot that is genotype focused (Figure 3) showed that genotype TGX-1448-2E(V3) is the most stable genotype while TGX-1945-4E(V9) is the most ideal genotype, followed by TGX-1835-10E(V5) and TGX-1945-1F(V8) TGX-1951-4F(V10),TGX-1935-3F(V7)others were far from the AEC line which are TGX-1904-6F(V6),TGX-1949-10F(V1),TGX-1485-1D(V4) and the least is TGX-1987-10F(V2)

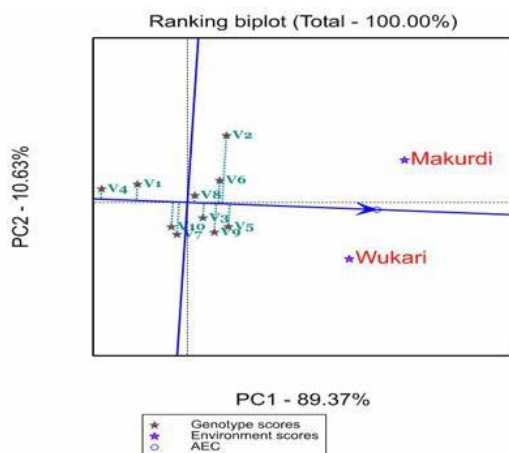


Fig.2: GGEBiplot for ranking for Yield Performance and Genotype Stability Based on Average Environment Coordination (AEC). PC1 and PC2 are the first and second principal components, respectively Where V1–V10 are codes for soybean genotypes.

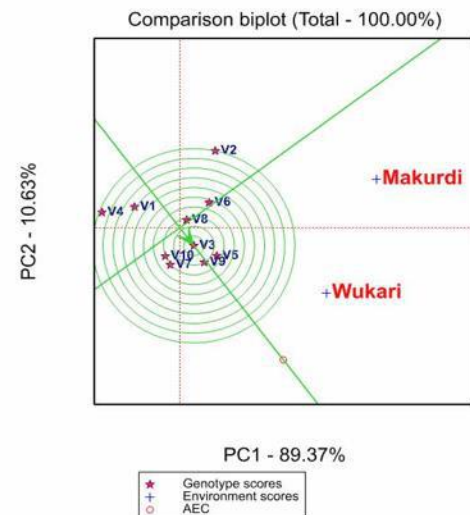


Fig.3: Genotype focused comparison biplot showing PC2 versus PC1 for 10 soybean genotypes and two environments, where V1–V10 are codes for soybean genotypes.

Soybean Yield Performance and Stability

A GGE biplot based on environment-focused scaling was used to estimate the relationship of the test environments (Figure 4.) The line from the origin of the biplot to the marker of the environment is the environment vector. Environments with longer vectors (PC1 scores) and PC2 scores close to zero are desirable for discriminating genotypes and representative environments, respectively. In regard to this, Environment 1 had the longest vector (largest PC1 scores) and PC2 scores close to zero. Then Environment 2 with relatively low PC2 scores close to zero, and moderately low PC1 scores.

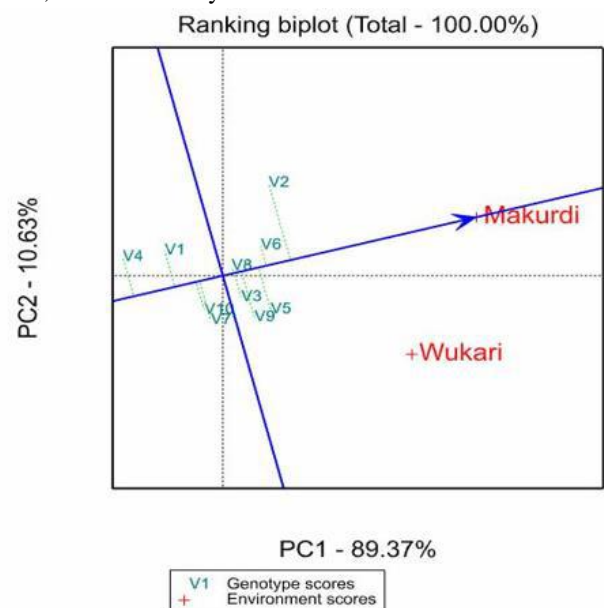


Fig.4: GGE Biplot based on environment focused scaling for 10 varieties. PC1 and PC2 are the first and second principal components, respectively. Where V1–V10 are codes for soybean genotypes.

IV. DISCUSSION

Rust disease symptoms, in this study, started to appear since 6 to 7 days after inoculation. The incubation period in the present study was consistent when compared with the results of other researches in Africa. Twizeyimana et al. (2007) found that in Nigeria it took 5 to 7 days after inoculation to lesion of rust disease appear on the surface of leaves. Meanwhile, Maphosa et al. (2013) reported that the incubation period of rust disease in Uganda began to be seen since 4 to 5 days after inoculation. This means that the isolates of rust fungus from Nigeria are more virulent compared with isolates and or soybean genotypes from other places are more resistant than soybean genotypes from Makurdi and Wukari.

Although the incubation periods of rust disease in present study was not longer when compared with the results obtained from Ibadan (Twizeyimana et al 2007), the inoculation of rust disease that has been done is able to bring up the different reactions of soybean genotypes tested. The reaction differences seen in the number of lesions between one genotype to other genotype were observed. Lesions of rust disease that appears, varies between genotype and within genotype, ranging from 6 lesions cm² (TGX-1904-6F) to 55 lesions cm² (TGX-1485-1D) on observation as shown in table 2.

Differences in the reaction of genotypes tested are also found in other studies (Sulistyo et al 2016, Pham et al 2010, Twizeyimana et al. 2008) stated that genotypes with non-characterized genes for resistance may be useful for host plant resistance studies and breeding soybeans for rust resistance. The reaction of soybean genotypes with resistance against rust diseases showed that all of the genotypes classified as resistant on observation were the genotypes categorized as moderately resistant. The different resistance reaction between the assessments is caused by spores of the rust disease which require time to germinate and form the new spores. According to Yang (2002), after an infection has occurred, it takes 5 to 7 days to produce uredinia by urediniospores and 10 to 20 days to produce a new generation of spores. This difference gives guidance for soybean breeders to determine the appropriate time to conduct the selection. Sulistyo and Sumartini (2015) found that there are differences in heritability of rust disease severity on observation of one, two and three weeks after inoculation. The emergence of rust diseases on the various phases of the development of soybean will determine how much yield loss will occur. Kumudini et al. (2008) found that if the rust disease began to occur at the R2 growth stage (full flowering phase), it would cause yield losses up to 66-68%, meanwhile, when it started at the R5 growth stages (seed filling phase), it will cause yield losses reach 35-39%. In this research, a soybean genotype with early flowering can avoid a large

yield loss. The mechanism was shown by line TGX-1835-10E and TGX-1987-10F. Both of these soybean lines flowering at 40.50 and 40.66 Days after Planting (DAP), had the highest seed yield per plant (799.51k g/ha and 766.75K g/ha, respectively) compared with other lines. In contrast, the line TGX-1949-10F and TGX-1945-1F were flowering at about 43 DAP, had a weight of seeds per plant (585.40, and 404.3kg/ha, respectively) were significantly lower than the two previous line. Plant height in this study appears to be one of the factors that will determine differences in the severity of rust disease on soybean genotypes tested. Analysis showed that there is a significant association between plant heights with the number of rust lesions in the observation. It means that the higher a plant, then the fewer rust disease lesions as with TGX 1485-1D Which have lowest height of (34.25cm) to TGX-1935-3F (51.46cm) With similar result from Abayomi et al (2009) in the southern Guinea Savannah environment. This is not surprising because *Phakopsora pachyrhizoides* does not have an active mechanism for spreading the spores. According to Isard et al. (2005), wind seems to be critical factors for spreading out spores and lifting them out of the canopy. Thus, it takes quite much wind to spread the spores of rust on soybean genotypes with appearances tall plants. Rust disease in present research did not seem to affect the character of other yield components, such as the number of branches, the number of seed/plant and the number of pods. However, the three characters have an influence on seed yield per plant. According to Oz et al. (2009) number of pods per plant had significant correlations with seed yield and gave direct positive effect. Ojo et al. (2010), Valencia-Ramirez and Ligarreto-Moreno (2012) found a similar result. Malik et al. (2007) suggested that number of pods can be considered as selection criteria in improving the bean yield of soybean genotypes. The Genotype main effect and the genotype x Environment effect were the major sources of variation important for Genotype evaluation. The first two PCs of the biplot explained 100% of the total grain Yield variation which was adequate for soybean evaluation. These Findings are also supported by Yan et al. (2007), who reported that GGE Biplot analysis was effective in regard to mega environment yield. The GGE biplot aims to use the "which-won-where" pattern to facilitate Identification of the most responsive genotypes Yan et al (2000). In this study, the most responsive genotypes were five advanced lines TGX-1945-4F, TGX-1835-10E, TGX-1935-3F, TGX-1485-1D, TGX-1987-10F. Interestingly, These genotypes demonstrated either higher (sometimes the highest) or Lower yields compared to the other genotypes in all the environments Within the sector in which they fall figure 1 Other vertex genotypes including TGX-1935-

3F, TGX-1448-2E which expressed highly Responsive behaviour but they did not fall under any of the test environments, indicating that they were not high yielding genotypes in Any of the two environments. The test environments appeared in five sectors of the polygon view figure 1, a Sign of cross-over of GEI effects, suggesting the presence of two possible mega-environments in Central and north Eastern Nigeria. According to Yan and Rajcan(2002), a mega-environment refers to Cluster of environments having the same high performing genotype(s). For instance, the first sector had one environment with TGX-1987-10F as the winning genotype. The Second Environment had two sectors having TGX-1835-10E and TGX-1945-4F appearing unique and them Performing the best. Mega-environments help plant Breeders to select high yielding genotypes for a specific environment; Making better use of GEI. The other importance of mega-environments is that genotypes may be evaluated in a few Representative environments, which will provide informative data representing GEI trials to cross a much larger number of Environments. Therefore, figure 2, environments 1 may be used for evaluating soybean Genotype in Central Nigeria. Based on average environment coordination (AEC) yield performance and stability of 10 soybean genotypes were evaluated figure 2. Accordingly both yield performance (large PC1 scores) and stability (PC2 close to zero) should be considered for effective selection of genotypes. Thus, genotype TGX-1835-10E and TGX-1945-4F were high yielding and stable. Other stable genotypes included TGX-1448-2E, TGX-1945-1F, TGX-1485-1D, TGX-1949-10F but they were low yielding. Such Genotypes would require further breeding for high yields before they are released to the farmer's figure 2. Although genotype TGX-1987-10F, TGX-1945-4F And TGX-1935-3F recorded the highest grain yields, they were unstable across the test environments. They will be recommended for specific environments or selected for their yield performance to Improve low yielding genotypes in a soybean breeding programme. In figure 3, The GGE genotype focused comparison biplot also showed that early Maturing genotypes were also low yielding and unstable. Among the locations, Makurdi had the highest seed yield. The high seed yield could have been due to optimal supply of water to the crops. In Addition to the longest period to physiological maturity, Makurdi had the Highest mean seed yield (1339kg/ha). Wukari recorded the lowest Yield of 589kg/ha. These results seem to suggest that presence of moisture in the soil during the season delays maturity but increases seed yield of soybeans. Makurdi was the most ideal environment as earlier observed by Ojo and Bello.(2012) and is therefore recommended as a primary testing centre for new soybean genotypes figure 4.

According to Jandonget al.(2011) Environments with longer vectors (large PC1 scores) have the ability to discriminate (informative) between Genotypes for a given trait, while short vectors identifies environments With a poor ability to discriminate between genotypes figure 3 . On the other hand, small PC2 values (PC2 scores close to zero) are good representative of the target environments and vice versa. Therefore, any test environment with large PC1 scores and PC2 scores close to zero are desirable. In this study, among the two environments, Makurdi had the longest vector, And PC2 scores close to zero. It was, therefore, identified as the most useful environment in terms of discriminating between genotypes and was the most representative of all the test environments.

V. CONCLUSION

Four moderately resistant TGX-1835-10E, TGX-1987-10F, TGX-1904-6F and TGX-1945-4E of the ten lines produce seeds with the seed weight per plant heavier than susceptible TGX-1949-10F and TGX-1485-1D, this Characteristics show among others the performance of plants is high with lot of number of branches and number of pods and beneficial to soybean growth and grain yield. Genotypes TGX-1448-2E and TGX-1945-1F identified as high performing genotypes and stable in test environments can be used for commercial production. While genotypes TGX-1835-10E and TGX-1987-10E though highest yielding but highly responsive to the environments, can only be used for specific environments or be utilized to improve yields.

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