

Multiple Trait-Based Selection of Maize Accessions for Resistance to Armyworm, *Spodoptera Frugiperda*

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Abstract

Maize is perhaps the most popular component of diets in sub-Saharan Africa. Armyworm (*Spodoptera frugiperda*) constitutes huge economic losses to maize growers in SSA, due to devastating grain yield losses and/or increased production costs arising from its control. It is essential to identify useful genetic materials for development of resistant cultivars. The aim of this study was to identify armyworm-resistant maize accessions for cultivation and further improvement. Twenty-seven maize accessions were evaluated under natural infestation in 2019. Randomized Complete Block Design was used with three replications. Data collected on numbers of days to anthesis and silking, anthesis-silking interval, plant and ear heights, number of ears per plant, plant and ear aspects, and grain yield were subjected to analysis of variance. Significantly ($p < 0.05$ or $p < 0.01$) different means were separated using Duncan's Multiple Range Test. A genotype \times yield*trait (GYT) biplot was employed to identify resistant genotypes based on multiple trait. There were significant ($p < 0.05$ or $p < 0.01$) genotype mean squares for most of the measured traits, indicating scope of selection. There was correspondence between estimates of phenotypic and genotypic coefficients of variation meaning that environmental influence on observations was limited. From the GYT biplot analysis, the trait profiles of TZM 51 and TZM 87 composed of plant and ear aspects, suggesting resistance to the armyworm, while TZM 16 was the closest to the ideal cultivar. The accessions TZM 51 and TZM 87 are useful for further improvement and extraction of inbred lines to develop high-yielding armyworm-resistant maize hybrids.

Keywords— armyworm; biplot; maize; resistance; selection.

1. Introduction

Maize (*Zea mays* L.), also known as corn, is a member of the Poaceae family. It is regarded as one of the most important cereal crops in Sub-Saharan and Saharan Africa as well as in the humid and sub-humid savannas of West and Central Africa (Batiano and Mokwunye, 2001). Maize is a staple food with high levels of starch, valuable proteins and oils. Depending on the variety, it may contain a number of important B vitamins, folic acid, Vitamin C, and beta-carotene, the precursor of vitamin A. The crop is also rich in phosphorus, magnesium, manganese, zinc, copper, iron and selenium, and has small amounts of potassium and calcium. The kernels are of various colors: blackish, bluish-gray, red, white and yellow. When ground into flour, maize yields more flour, with much less bran, than wheat does. The kernels are processed into a number of products which create an extra source of income to maize farmers, processors, and distributors. Some of the products that can be gotten from maize include corn starch, corn oil and ethanol.

The armyworm (*Spodoptera frugiperda*) is a lepidopteran pest that feeds in large numbers on leaves and stems of more than 80 plant species, causing major damage to maize, rice, sugarcane and vegetable crops and cotton (FAO, 2019).

The pest is of immense concern among agricultural experts, due to the huge amount of damage it causes to African food crops. The armyworm's life cycle is completed within 30 to 60 days. The adults live for about 10 days, and sometimes up to 21 days, with the female laying most of her eggs early in life. Adult armyworms are nocturnal and fare best during warm and humid nights (Smith, 2005). Armyworm has been a major insect pest of maize, and it is a major problem recently faced by African maize farmers due to increased cost of production through control measures, reduction in yield and abandonment of farmland due to high infestation (FAO, 2019).

The control of armyworm has been achieved mainly using chemical insecticides that have an adverse effect on the environment and may promote the build-up of resistant insects. The use of host-plant resistance (HPR) has the potential for use as a strategy to control armyworm on crops, and is a desirable strategy because it is compatible with other control measures and often exhibits synergistic effects with insecticides and natural enemies of the pest (Nagoshi, 2009). Utilizing diverse crop genetic resources that confer insect and disease resistance in crop breeding has been one of the most effective strategies for integrated pest management programs on maize and other crops for decades. However, maize germplasm that confers native resistance to biotic stresses (insects and diseases) often suffers from poor agronomic traits (e.g. low yield potential and lodging). Although, several studies have been conducted to examine multiple insect resistance in maize germplasms (Abel et al., 2000; Ni et al., 2008) the agronomic traits influencing resistance in maize genetic resources could be further improved.

Farmers prefer high-yielding maize cultivars to any others irrespective of other qualities they may possess. However, the effect of other traits in determining the yield levels of crop cultivars is established. Breeders have effectively employed the genotype \times trait (GT) biplot procedure to study the relationships among traits, including yield (Kendal, 2019; Oral et al., 2018; Akcura et al., 2016). Essentially, the GT biplot is useful for defining genotypes, as well as for comparison of crop genotypes based on measured traits. Yan and Fréreau-Reid (2018) pointed out a limitation of the GT biplot in that it is not able to determine the effect of trait combinations on yield. The GYT biplot technique was thus developed to overcome this limitation. The effectiveness of the GYT biplot technique to provide information on the usefulness of crop genotypes for trait improvement through a comprehensive trait profiling (via the polygon view) has been described and reported (Yan and Fréreau-Reid, 2018; Kendal, 2019). Nevertheless, there is limited information on the use of the technique to evaluate, compare and make selections among crop genotypes (Kendal, 2019). As stated earlier, a high-yielding maize genotype that is poor in other traits may not meet the selection benchmark of the breeder. For instance, a maize genotype with good grain yield per se that is overly tall may be predisposed to lodging while one that has poor ear appeal may be neglected. The value of a high-yielding cultivar is enhanced by its good agronomic and quality traits. Yield-trait combinations are thus more meaningful than the effects of the traits singly. Therefore, this study employed genotype \times yield-trait combinations to identify maize accessions with good agronomic and yield potentials under infestation by the armyworm (*Spodoptera frugiperda*) in the study area for further improvement.

2. Materials and methods

2.1 Experimental materials and land preparation

Twenty-seven maize accessions obtained from the Genetic Resources Centre of International Institute of Tropical Agriculture (IITA) were used in this study. The experiment was conducted during the main season of 2019 at the Teaching and Research Farm of the Department of Crop Production and Horticulture, Lagos State Polytechnic, Ikorodu, Nigeria. The experimental site is located between Lat. 5°10' N and Long. 3°16' E and has altitude of 50 m above sea level. The experimental land has been under continuous cultivation for maize for over three years. To encourage the build-up of the eggs of the insects, the experimental field was initially grown to maize without insecticide or herbicide use. Thereafter, the land was ploughed twice and harrowed to a fine tilth.

2.2 Experimental design and field evaluation

The accessions were laid out in Randomized Complete Block Design with three replications. Each accession was planted in a 2.5-meter row. Two seeds were sown per hole and thinned to one at establishment. Sowing was done at a spacing of 0.25 m and 0.75 m within and between rows respectively to give a population density of 53,333 plants per hectare. Weeds were controlled manually subject to field inspection. A compound fertilizer, NPK 15:15:15, was applied at the rate of 60 kg N per hectare at three weeks after sowing weeks after sowing (WAS) and top-dressed with 60 kg N per hectare of urea at five WAS. No insecticide application was carried out throughout the experiment. Cobs were harvested at twelve weeks after planting.

2.3 Data Collection

All eleven plants in each row were involved in data collection. Number of leaves per plant, stem diameter (mm) and plant height (cm) were recorded at 2, 4, and 6 weeks after sowing (WAS). Data were also recorded on numbers of days to anthesis and silking, anthesis-silking interval, final plant height (cm), ear height (cm), plant and ear aspects, number of ears per plant, and grain yield (ton/Ha).

Plant height at 2, 4, and 6 WAS were measured as the plants average height measured from ground level to the node bearing the flag leaf while final plant height was taken as the height of the plant from ground level to the first tassel branch. Numbers of days to anthesis and silking were recorded as the numbers of days from planting to the day when 50% of the plants in each row had anthesized and emerged silk respectively. Anthesis-silking interval was calculated as the absolute difference between numbers of days to anthesis and silking. Ear height was taken as the height from ground level to the node bearing the uppermost ear. Plant aspect (which incorporated observable damage on the plants' leaves, silk and tassel, due to feeding by the armyworm) was rated based on overall appeal of the plants per plot, and rated on a scale of 1-9, where 1= excellent and most desirable plants while 9 = plants with poor physical appearance. Ear aspect was also rated based on overall appeal of the harvested ears, incorporating extent/freedom from insect damage, size and uniformity of ears, and level of grain filling, also on a scale of 1-9 where 1 and 9 had the same interpretations as for plant aspect. Harvested ears were shelled and the moisture content and grain weights were determined using XYZ and ABC respectively. Grain yield (kg per hectare) was calculated and adjusted to 15% MC according to the formula used by Oyetunde (2019).

2.4 Data Analysis

Scored data of PASP and EASP were transformed using logarithm transformation prior to analysis. Plot means of grain yield and other traits were subjected to analysis of variance using proc glm in SAS (SAS Institute, 2012). Means, when significantly different at 95% level of confidence, were separated using Duncan's Multiple Range Test. Estimates of genetic, phenotypic, and environmental variances, genotypic and phenotypic coefficients of variation, broad-sense heritability, and genetic advance (as per cent of mean) were determined as described by Oyetunde and Ariyo (2015). Genotypes were ranked for selection by using the genotype \times yield-trait (GYT) biplot procedure described by Yan and Frégeau-Reid (2018). To create the GYT biplot dataset, DYA, DYS, ASI, PASP, and EASP which had negative correlation with grain yield (data not presented), thus for which larger values would not favour increased grain yield, were converted to the corresponding yield-trait combinations by dividing the grain yield value with the trait value for each genotype. For plant and ear heights which shared positive correlation with grain yield, the grain yield values were multiplied by the corresponding trait values. Hence, a larger value is always preferable in the GYT dataset. The resulting data were standardized (mean of 0 and standard deviation of 1) before it was subjected to GYT biplot analysis. The GYT biplot was constructed using the GGEBiplotGUI package in R version 3.4.2 (R Core Team, 2013).

3. Results

Table 1 shows that performance of the seedlings of the maize accessions with respect to number of leaves per plant, plant height and stem girth at 2, 4 and 6 weeks after sowing (WAS). Numbers of leaves of the maize accessions were significantly ($p < 0.05$) different at 2 and 4 WAS. Accession TZM 61 and TZM 1118 had the highest numbers of leaves of 6.35 and 8.42 at 2 and 4 WAS respectively while the least numbers of leaves were observed for accessions TZM 1200 and 6.00 at 2 and 4 WAS respectively. Also, statistically significant ($p < 0.05$) differences were observed in the plant height of the maize seedlings at 2 and 4 WAS. AT 2 WAS, TZM 128 had the tallest plants with an average height of 47.44 cm while TZM 236 plants were the tallest at 4 WAS with a height of 62.70. Accessions TZM 333 and TZM 32 had the shortest plants at 2 and 4 WAS respectively. In the same vein, the average stem girth of the seedlings of the maize accessions differed at 4 and 6 WAS, with accessions TZM 87, TZM 228 and TZM 1200 having the thickest stems at 4 WAS while TZM 16 plants had the thickest stems at 6 WAS.

Significant ($P < 0.05$ or $P < 0.01$) accession mean squares were revealed for all the measured traits except plant and ear heights as well as number of ears per plant (Table 2). Accession TZM 1147 was the latest to anthesize while TZM 1118 and TZM 1148 were the earliest. Accession TZM 1096 had the highest anthesis-silking interval and number of day to silking of 7 and 60.33 days respectively while accessions TZM 1148 and TZM 93 had the least numbers of days for the two traits respectively.

The least signs of damage due to infestation were observed in the plants and ears of accession TZM 51 while accession TZM 1147 plants showed the highest signs of damage, and accessions TZM 1121, TZM 1128, TZM 1148, and TZM 333 had the worst ear aspect. Accession TZM 56 had the highest grain yield of 4.83 tons per hectare while TZM 1148 produced the lowest grain yield of 0.47 ton per hectare.

As displayed in Table 3, genotypic component of variation ranged from 0.003 to 9.533 for numbers of ears per plant and days to anthesis respectively while phenotypic variance values ranged from a minimum 0.046 to 44.27 for number of ears per plant and plant height respectively. Genotypic variances were higher than environmental component of variation for numbers of days to anthesis and silking, plant and ear aspects, and grain yield. There was close correspondence between genotypic and phenotypic variance estimates for all the measured traits except plant and ear heights, and number of ears per plant. Estimates of PCV were higher than the corresponding GCV values for all the measured traits. Values of GCV and PCV ranged from low to high, with GCV ranging from 1.424 for plant height to 26.962% for grain yield while PCV estimates ranged from 4.739 for ear height to 34.951 for grain yield. There was also, close correspondence between GCV and PCV estimates for all the measured traits except number of ears per plant. Broad-sense heritability ranged from 4.676% for plant height to 82.924% for number of days to anthesis while genetic advance (as percent of mean) ranged from 0.662% to 44.717% for plant height and grain yield respectively. The genetic advance values associated with the high broad-sense heritability estimates of numbers of days to anthesis and silking were not as high as those of anthesis-silking interval (34.578%), plant aspect (25.374), ear aspect (27.623%), and grain yield (44.717%) which had much lower heritability estimates.

The principal component axes 1 (PC1) and 2 (PC2) jointly explained 89.91% of yield-trait combinations; with PCs 1 and 2 individually explaining 73.84 and 16.07% respectively. Figure 1 is a graphical representation of the relationship among the measured traits. As expected since they all have yield incorporated, all the yield-trait combinations appear to be positively correlated. The magnitude of angle between a pair of traits is an indication of the strength and direction of association between the traits. Thus, there was positive association among numbers of days to anthesis and silking and ear height as well as plant height and number of ears per plant while the relationship among number of ears per plant and plant and ear aspects. The polygon view (Figure 2) of the GYT biplot, representing the trait profiles of the maize genotypes, revealed five sectors with accessions TZM 56, TZM 51, TZM 299, TZM 61, and TZM 128 as the vertex cultivars (counterclockwise orientation). The polygon view also classified the yield-trait into two mega groups: mega group 1 composed of number of ears per plant, plant and ear heights, and numbers of days to anthesis and silking while mega group 2 consisted of plant and ear aspect with anthesis-silking interval (counterclockwise orientation). The sector to which a genotype belonged on the GYT biplot describes the trait profile of that genotype. Thus, the vertex genotype in each sector of the polygon represents the genotype that is most associated with the yield-trait combinations defining that sector. It follows that TZM 56 was the most associated with the yield-trait combinations defining mega yield-trait group 1 while accessions TZM 16 and TZM 1284 are other genotypes associated with the mega yield-trait group.

In the same vein, TZM 51 had the strongest association with the yield-trait combinations of mega yield-trait group 2 while TZM 87 is another accession with association to the same yield-trait combinations. Other vertex accessions, TZM 299, TZM 61, and TZM 128, with other accessions in their respective sectors are associated with other yield-trait combinations that were not considered in this study. Figure 3 showed the mean performance and stability of 10 maize accessions for the yield-trait combinations under natural attack by the armyworm. The average-tester ordinate separates entries with below average means from those with above average means. The overall performance of a genotype is approximated by the projections of its marker on the average-tester axis (ATA) (horizontal line with single arrow) while the stability of the genotypes is measured by their projection onto the average-tester coordinate y axis (the ATC abscissa) (vertical line). Genotypes with short projections (i.e. placed close to the ATA) are more stable, and have a more balance trait profile than those with longer projections (i.e. placed far from the ATA). The overall best-performing accession was TZM 56, followed by TZM 16, TZM 51, TZM 1284, and TZM 87 in that order while TZM 299 was the worst among the selected 10 genotypes. A function of the ATA is to rank genotypes based on superiority. Thus, based on yield-trait combinations, the accessions were ranked as follows: 1 > 2 > 6 > 3 > 5 > 4 > 7 > 9 > 8 > 10. Yan *et al.* (2007) described an ideal genotype (genotype of which performance has large contribution from genotype and a small contribution from GYT components) identifiable from the GYT biplot as a genotype with high grain yield and high stability across

the GYT means. Therefore, based on the GYT mean values (Figure 4), the accessions TZM 56, TZM 16 and TZM 1284 were closest to the ideal cultivar (represented by the innermost circle in the figure). Again from Figure 4, it was found that TZM 56, TZM 16, TZM 1284, TZM 87, and TZM 51 performed higher than the average yield-trait combination mean while TZM 128, TZM 1202, TZM 61, TZM 1118, and TZM 299 performed below average.

4. Discussion

The observed significant difference among the accessions for agronomic traits at the seedling stage is an indication of the existence of useful level of variability for early selection. Thus, TZM 61, TZM 128, and TZM 228 which had highest height, number of leaves per plant, and the thickest stems respectively could be useful genetic resources for developing maize genotypes with vigorous growth. Similar results have been reported by Ruswandi et al. (2015) and Kamara et al. (2014). The significant observed for all the measured traits implied that there was inherent genetic variability among the genotypes used. There is thus scope for selection for numbers of days to anthesis and silking, anthesis-silking interval, plant and ear aspects, and grain yield. Several earlier workers have also reported genetic differences among maize germplasm lines under natural infestation by the armyworm. For instance, Alvarez and Miranda Filho (2002) observed significant genotype differences for grain field, plant height and resistance to armyworm among 180 diallel crosses of maize evaluated under natural infestation. Abel et al. (2019) observed significant genotype differences in scored data of damage by armyworm among 13 maize genotypes of USA origin grown under artificial infestation. Also, Brooks et al. (2007) identified quantitative trait loci contributing to reduced damage due to the armyworm infestation in a population of 427 individual maize genotypes. These results underscore the importance of genetic background in development of resistance to the armyworm in maize. The significant differences in flowering synchronization and numbers of days to flowering (silking and anthesis) indicated the possibility of improvement of flowering synchronization and earliness respectively among the accessions. The significant difference among the accessions for numbers of days to silking and anthesis, as well as anthesis-silking interval under natural infestation by armyworm was generally due to varietal differences among the examined genotypes. This is an indication of abundant genetic variability amongst the genotypes. Comparables results have been reported by Shahrokhi and Khorsani (2013). Also, Badji et al. (2017) attributed differences in the performance of maize genotypes under insect infestation to their different levels of resistance to the insect. The accessions TZM 1148 and TZM 93 that were earliest to flower and/or had the most synchronized flowering pattern could be useful for producing maize genotypes with desirable flowering pattern under armyworm attack. Significant mean squares due to accession were also observed for plant and ear aspects, and grain yield. Thus, there is a possibility of improvement in plant and ear aspects using TZM 51 while grain yield of maize under infestation can be improved through TZM 56. Abel et al. (2019) had earlier reported that genetics had major influence in determining the reaction maize to natural infestation by the insect while Castro Lourenco et al. (2017) and Alvarez and Miranda Filho (2002) observed genetic differences in grain yields of maize genotypes.

The observed values of genotypic components variance for the measured traits implied that the genetic architecture influenced the performance of the maize accessions under the growth condition, and so there is possibility of selection among the maize accessions. The higher genotypic variances than the environmental counterparts for numbers of days to anthesis and silking, plant and ear heights, and grain yield implied that the differences observed among the accessions for these traits were mostly due to genetic causes rather than environmental causes while the reverse is the case for anthesis-silking interval, plant and ear heights, and number of ears per plant. These results are similar to the observations of Abe and Adelegan (2019). The fact that the estimates of genetic variance were lower than the phenotypic counterparts for all the measured traits means that the environment played a role in determining the observed phenotype. Thus, the accessions will likely perform differently given a different growth condition, with the largest variations possibly observable in plant and ear heights which had the highest estimates of environmental variation. Abe and Adelegan (2019) and Sandeep et al. (2015) have earlier observed the important role of environment in the phenotypic expression of traits in maize. The high correspondence between the genotypic and corresponding phenotypic variance estimates highlights the minimal environmental influence on the expression of the traits and thus put emphasis on the important role of genetics in the phenotypic expression of the measured traits.

Besides the use in comparing the relative amount of phenotypic and phenotypic variation in traits, estimates of genotypic (GCV) and phenotypic coefficients of variation (PCV) are useful to estimate the scope of improvement through selection. The difference between the GCV and PCV value of a trait provides an estimate of environmental influence on the trait. Albeit low GCV and PCV values indicate generally low variability among evaluated genotypes, high proportion of GCV to PCV is desirable to a breeder. There was substantial variability among the accessions, and subsequently, good scope for selection. The higher PCV values than GCV indicated that environment played a role in the expression of phenotype.

However, the close correspondence between the PCV and GCV estimates implied that environmental influence was minimal in phenotypic expression but largely determined number of ears per plant. Similar findings have been reported for maize by Abe and Adelegan (2019). The high GCV estimates obtained for grain yield and anthesis-silking interval followed by the moderate values for plant and ear aspects suggested that variability is high/moderate among the genotypes for these traits. Consequently, selection would be effective based on these traits rather than on traits with low GCV values. Meena et al. (2016) and Rafiq et al. (2010) also reported similar levels of variability for agronomic traits studied in maize.

Similar high broad-sense heritability estimates to the ones observed in this study have previously been reported in maize (Abe and Adelegan, 2019; Meena et al., 2016; Ogunniyan and Olakojo, 2015). High heritability estimates are more reliable when coupled with high genetic advance. Ogunniyan and Olakojo (2015) earlier reported poor correspondence between heritability and genetic advance values. The low genetic gain values for numbers of days to anthesis and silking were however sufficiently compensated for by the high heritability estimates. Both broad-sense heritability and genetic advance (as a percentage of mean) were high for anthesis-silking interval, plant and ear aspects, and grain yield suggesting the possibility of better performance of progenies derived from the accessions in future breeding programmes. Meena et al. (2016) and Rafiq et al. (2010) reported similar observations in maize. The high heritability but low genetic advance values observed for numbers of days to anthesis and silking meant that these traits were not reliable.

Yan and Fregeau-Reid (2018) proposed and described a genotype \times yield-trait (GYT) biplot procedure for describing the relationships among measured traits, and to achieve a multi-trait-based ranking for selection among genotypes. The substantial percentage of variation controlled by the PCs indicated that the GYT biplot adequately approximated the data based on the yield-trait combinations, and the results obtained were reliable. The existence of interrelationship among the measured traits provided the possibility of simultaneous improvement of maize for resistance to armyworm. The classification of the yield-trait combinations into two mega-groups by the GYT biplot implied that the yield-trait combinations in one mega-group were distinct from those in the other. The fact that some maize accessions were associated (vertex and sector genotypes) with each mega-group indicated that the maize accessions used in this study had different trait profiles and that different accessions could be selected for improvement of desirable traits. The traits anthesis-silking interval, and plant and ear aspects (which have incorporated the level of observable damage by the armyworm on the plants and on the cobs) are key traits in determining grain yield and resistance of maize to the insect. These traits belonged to the same mega-group, and the associated accessions, TZM 51 and TZM 87, would likely be useful genetic materials for developing maize with resistance to the armyworm. Similarly, TZM 56, TZM 16 and TZM 1284 which are associated with the other traits could be important genetic resources for maize programs with focus on developing armyworm-resistant maize cultivars. Also, inbred lines could be extracted from these accessions for combining ability studies to identify the mode of inheritance of resistance to the insect. Comparable findings were reported by Musvosvi and Wali (2017) who used the GT biplot to identify maize inbreds for improvement of drought tolerance traits in maize. The short vector lengths of TZM 1202, TZM 1118, and TZM 16 compared to other accessions implied that these accessions were the most stable across the various yield-trait combinations as described by Kendal (2019) and Yan and Frégeau-Reid (2018). Inbreds can be extracted from TZM 56, TZM 16 and TZM 1284 which and crossed to inbreds from TZM 51 and TZM 87 to develop maize hybrids with potentials to enhance food security if areas where the armyworm is endemic.

5. Conclusion

There was sufficient genetic variability among the maize accessions to permit selection. Those accessions that silked and anthesized early will be useful for producing early maturing maize varieties. Accessions TZM 56, TZM 16, and TZM 1284 that were highest-yielding and moderately stable for the yield-trait combinations means

will be useful genetic materials for improvement of maize yield under infestation by the armyworm. Accessions TZM 87 and TZM 51 which were associated with resistance traits on the GYT biplot will be useful resources to develop armyworm-resistant maize cultivars. Maize inbreds can be extracted from the five accessions, for planned crosses to develop high-yielding armyworm-resistant maize hybrids for areas endemic with the insect.

6. References

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Table 1. Seedling performance of maize accessions evaluated under natural infestation by the armyworm at Ikorodu, in 2019

Accession	Number of leaves per plant			Plant height			Stem girth		
	2	4	6	2	4	6	2	4	6
TZM 100	5.33abc	6.58ab	10.41	36.07a-g	54.00abc	79.33	4.73	8.43ab	11.70abc
TZM 1096	5.27abc	7.58ab	11.85	46.51ab	53.70abc	83.57	5.37	9.90ab	13.57abc
TZM 1118	5.93ab	8.42a	9.50	42.62a-e	53.43abc	72.57	5.97	9.87ab	11.77abc
TZM 1121	5.17abc	6.60ab	9.77	34.22c-g	48.50abc	78.17	4.60	6.97bc	10.13c
TZM 1128	5.28abc	7.45ab	11.95	34.74b-g	52.40abc	86.73	4.77	7.93abc	11.57abc
TZM 1135	4.93abc	7.35ab	12.17	34.08c-g	50.73abc	77.80	4.93	7.8abc	13.43abc
TZM 1147	5.28abc	7.62ab	13.03	37.80a-g	42.73bc	72.47	5.23	7.93abc	12.23abc
TZM 1148	5.50ab	6.78ab	10.45	39.98a-g	50.07abc	83.33	5.57	8.23abc	11.17bc
TZM 1180	5.52ab	7.68ab	11.50	37.57a-g	45.90abc	72.63	5.83	7.60abc	12.4abc
TZM 1200	4.78bc	6.65ab	11.25	37.47a-g	53.70abc	85.75	4.83	11.35a	14.85ab
TZM 1202	5.75ab	6.87ab	11.77	41.03a-g	55.57abc	82.30	5.25	9.23ab	13.33abc
TZM 1277	4.85bc	6.92ab	10.83	29.27fg	39.90c	66.40	5.33	7.77abc	13.07abc
TZM 128	5.70ab	8.03ab	11.62	47.44a	54.00abc	89.40	4.73	10.47ab	13.17abc
TZM 1284	5.68ab	7.43ab	12.52	40.42a-g	54.03abc	82.93	6.17	8.70ab	13.33abc
TZM 16	5.78ab	8.18ab	12.53	41.70a-e	60.63ab	89.57	5.20	10.37ab	15.90a
TZM 228	5.95ab	7.75ab	11.93	40.40a-g	59.70ab	85.23	6.07	11.23a	15.00ab
TZM 236	5.37abc	6.90ab	10.93	40.58a-g	62.70a	86.27	5.77	8.97ab	11.47abc
TZM 299	5.02abc	7.67ab	10.87	35.61a-g	49.47abc	88.50	5.37	8.63ab	12.1abc
TZM 32	6.17ab	6.00b	9.43	43.21a-d	39.00c	66.73	4.93	9.27ab	12.83abc
TZM 328	5.28abc	7.23ab	10.12	30.65efg	47.47abc	79.37	6.03	7.07bc	10.37c
TZM 333	5.45ab	7.20ab	10.27	29.02g	48.10abc	74.47	4.90	8.50ab	13.53abc
TZM 51	5.33abc	7.25ab	11.77	41.57a-e	54.03abc	89.93	4.70	8.90ab	12.5abc
TZM 56	5.27abc	8.35a	11.60	45.44abc	55.00abc	87.33	5.63	10.33ab	13.47abc
TZM 61	6.35a	7.50ab	10.60	38.23a-g	51.57abc	83.07	5.60	10.17ab	12.33abc
TZM 7	4.92abc	7.92ab	12.02	39.87a-g	57.57abc	81.07	5.93	10.53ab	14.13abc
TZM 87	5.68ab	8.28ab	11.18	42.88a-e	54.90abc	85.33	5.80	11.13a	14.80ab
TZM 93	5.37abc	7.68ab	13.35	41.38a-f	52.23abc	78.63	6.10	8.43ab	12.37abc

Means followed by the same letter(s) in a column are not significantly different using Duncan's Multiple Range Test at 95% confidence level.

Table 2. Agronomic and yield performance of 27 maize accessions evaluated under natural infestation by the armyworm at Ikorodu in 2019

Accession	DYA	DYS	ASI	PHT	EHT	EPP	PASP	EASP	YIELD	
	Mean performance									
TZM 100	56.00abc	58.33a-e	2.33de	99.33	50.00ab	1.14a	5.33abc	7.33abc	1.92b-g	
TZM 1096	53.33a-f	60.33a	7.00a	103.57	52.93ab	0.48ab	5.67abc	7.67ab	1.54c-g	
TZM 1118	46.67i	51.67g-j	5.00a-e	92.57	53.27ab	0.85ab	3.67b-e	4.67de	2.98a-f	
TZM 1121	58.00a	59.67ab	2.33de	98.17	56.03a	0.90ab	5.67abc	8.00a	0.54fg	
TZM 1128	57.33ab	60.00ab	2.67cde	106.73	50.47ab	0.44ab	6.00ab	8.00a	1.90c-g	
TZM 1135	49.67f-i	53.33f-i	3.67b-e	97.8	52.30ab	0.73ab	5.00a-d	5.67a-e	2.49a-g	
TZM 1147	47.00i	51.00hij	4.00a-e	92.47	51.17ab	0.33b	7.00a	7.00a-d	0.93efg	
TZM 1148	46.67i	49.00j	2.33de	103.33	57.90a	0.25b	5.33abc	8.00a	0.47fg	
TZM 1180	53.00b-f	57.33a-f	4.33a-e	92.63	51.90ab	0.71ab	4.67a-d	6.67a-d	2.09b-g	
TZM 1200	55.33a-d	58.33a-e	3.00b-e	104.03	58.55a	0.37b	5.00a-d	7.67ab	2.41a-g	
TZM 1202	50.00f-i	53.67e-i	3.67b-e	102.3	51.00ab	0.8ab	3.67b-e	5.67a-e	3.25a-e	
TZM 1277	55.00a-e	59.00a-d	4.00a-e	86.4	55.03ab	0.83ab	4.33b-e	6.67a-d	2.02b-g	
TZM 128	52.67b-g	58.67a-d	6.00ab	109.4	56.43a	0.78ab	4.67a-d	6.00a-e	3.77abc	
TZM 1284	50.00f-i	54.67c-h	4.67a-e	102.93	52.83ab	0.98ab	3.33cde	4.67de	3.93abc	
TZM 16	50.67d-i	54.67c-h	4.00a-e	109.57	55.43a	0.77ab	4.00b-e	4.67de	4.43ab	
TZM 228	52.00c-h	55.33b-h	3.33b-e	105.23	48.47ab	1.10a	4.00b-e	5.00cde	2.76a-g	
TZM 236	48.00ghi	53.67e-i	5.67abc	106.27	55.10ab	0.57ab	4.67a-d	7.00a-d	1.70c-g	
TZM 299	50.33e-i	53.67e-i	3.33b-e	108.5	52.63ab	0.67ab	3.67b-e	5.00cde	2.78a-g	
TZM 32	55.00a-e	59.00a-d	4.00a-e	86.73	50.30ab	0.87ab	5.00a-d	7.33abc	2.55a-g	
TZM 328	50.67d-i	54.33d-i	3.67be	99.37	50.80ab	0.73ab	4.33b-e	5.67a-e	2.20b-g	
TZM 333	50.00f-i	55.67a-g	5.67abc	94.47	55.07ab	0.81ab	4.67a-d	8.00a	1.12d-g	
TZM 51	47.67hi	50.00ij	2.33de	109.93	51.00ab	0.72ab	2.00e	4.00e	3.60a-d	
TZM 56	56.33abc	59.33abc	3.00b-e	107.33	56.73a	0.71ab	5.67abc	6.33a-e	4.83a	
TZM 61	54.00a-f	59.33abc	5.33a-d	103.07	49.83ab	0.88ab	4.33b-e	5.67a-e	3.06a-e	
TZM 7	55.00a-e	58.00a-e	3.00b-e	101.07	50.13ab	0.72ab	5.00a-d	7.00a-d	2.20b-g	
TZM 87	54.00a-f	57.00a-f	3.00b-e	105.33	50.83ab	0.78ab	2.67ed	5.33b-e	3.73abc	
TZM 93	55.33a-d	57.33a-f	2.00e	98.63	50.93ab	0.74ab	4.33b-e	6.67a-d	2.72a-g	
SOV	DF	Mean square								
Block	2	29.42*	13.86	3.42	729.26*	41.64	0.32	6.27*	1.12	1.37
Accession	26	34.49**	31.63**	4.98*	132.81	18.82	0.14	3.30*	4.45**	2.32**
Error	52	5.92	5.57	2.6	126.6	17.05	0.13	1.6	1.47	0.94

Means followed by the same letter(s) in a column are not significantly different using Duncan's Multiple Range Test at 95% confidence level

* and **, significant at 95 and 99% confidence levels respectively; DYS, number of days to silking; DYA, number of days to anthesis; PHT, plant height; EHT, ear height; EPP, number of ears per plant; PASP, plant aspect; EASP, ear aspect.

Table 3. Mean squares and genetic components of grain yield and agronomic traits of maize evaluated under natural infestation by the armyworm at Ikorodu, in 2019

Component	DYA	DYS	ASI	PHT	EHT	EPP	PASP	EASP	GY
σ^2_g	9.533	8.687	0.793	2.070	0.590	0.003	0.567	0.993	0.460
σ^2_p	11.496	10.544	1.660	44.270	6.273	0.046	1.100	1.483	0.773
σ^2_e	1.963	1.857	0.867	42.200	5.683	0.043	0.533	0.490	0.313
Hb (%)	82.924	82.388	47.771	4.676	9.405	6.522	51.545	66.959	59.508
GCV (%)	5.914	5.262	23.269	1.424	1.453	7.522	16.438	15.701	26.962
PCV (%)	6.494	5.797	33.666	6.587	4.739	29.455	22.896	19.188	34.951
GA (%mean)	11.578	10.269	34.578	0.662	0.958	4.130	25.374	27.623	44.717

* and **, significant at 95 and 99% confidence levels respectively; DYS, number of days to silking; DYA, number of days to anthesis; PHT, plant height; EHT, ear height; EPP, number of ears per plant; PASP, plant aspect; EASP, ear aspect; σ^2_g , genotypic variance; σ^2_p , phenotypic variance; σ^2_e , environmental variance; Hb, broad-sense heritability; GCV, genotypic coefficient of variation; PCV, phenotypic coefficient of variation; GA (% mean), genetic advance (as percent of mean).

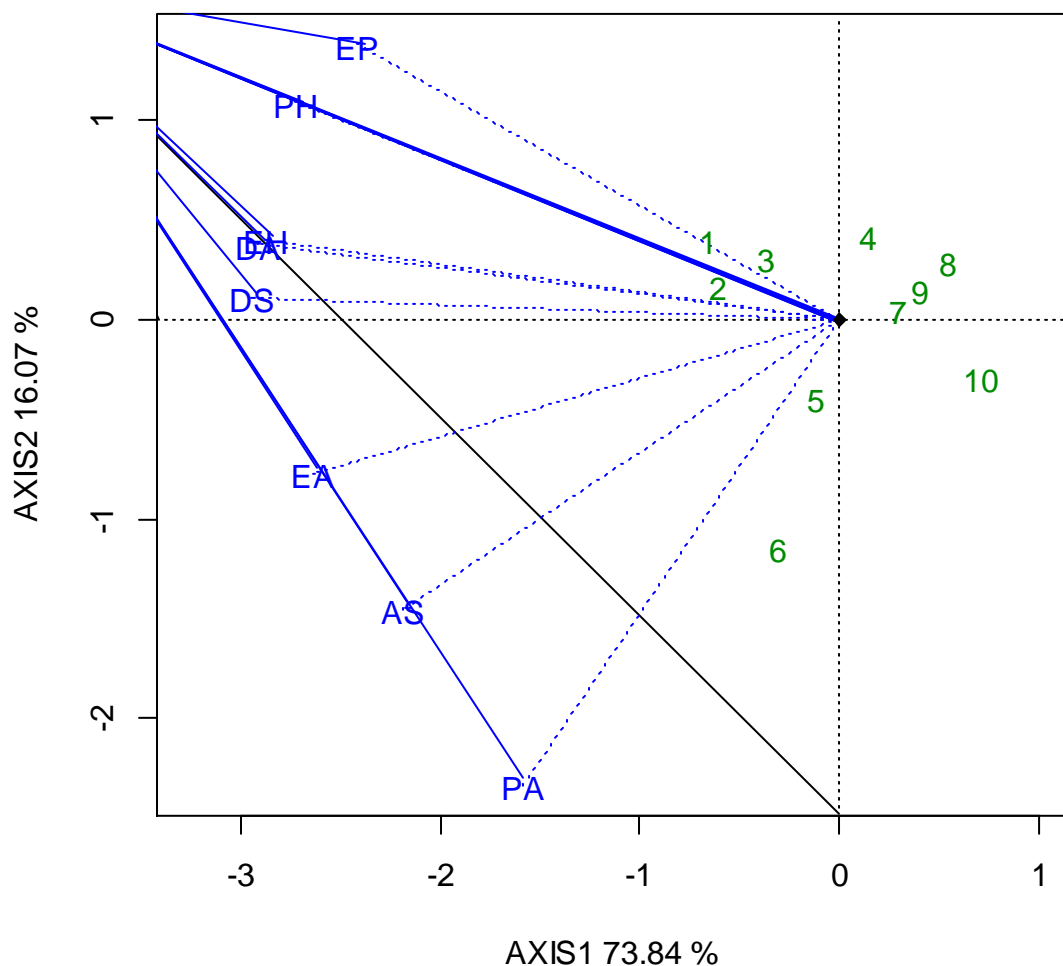


Figure 1: The GYT biplot of the relationship among measured traits of maize under natural infestation by the fall armyworm

Key

ID	Accession	Grain yield (ton/Ha)
1	TZM 56	4.83
2	TZM 16	4.43
3	TZM 1284	3.93
4	TZM 128	3.77
5	TZM 87	3.73
6	TZM 51	3.60
7	TZM 1202	3.25
8	TZM 61	3.06
9	TZM 1118	2.98
10	TZM 299	2.78

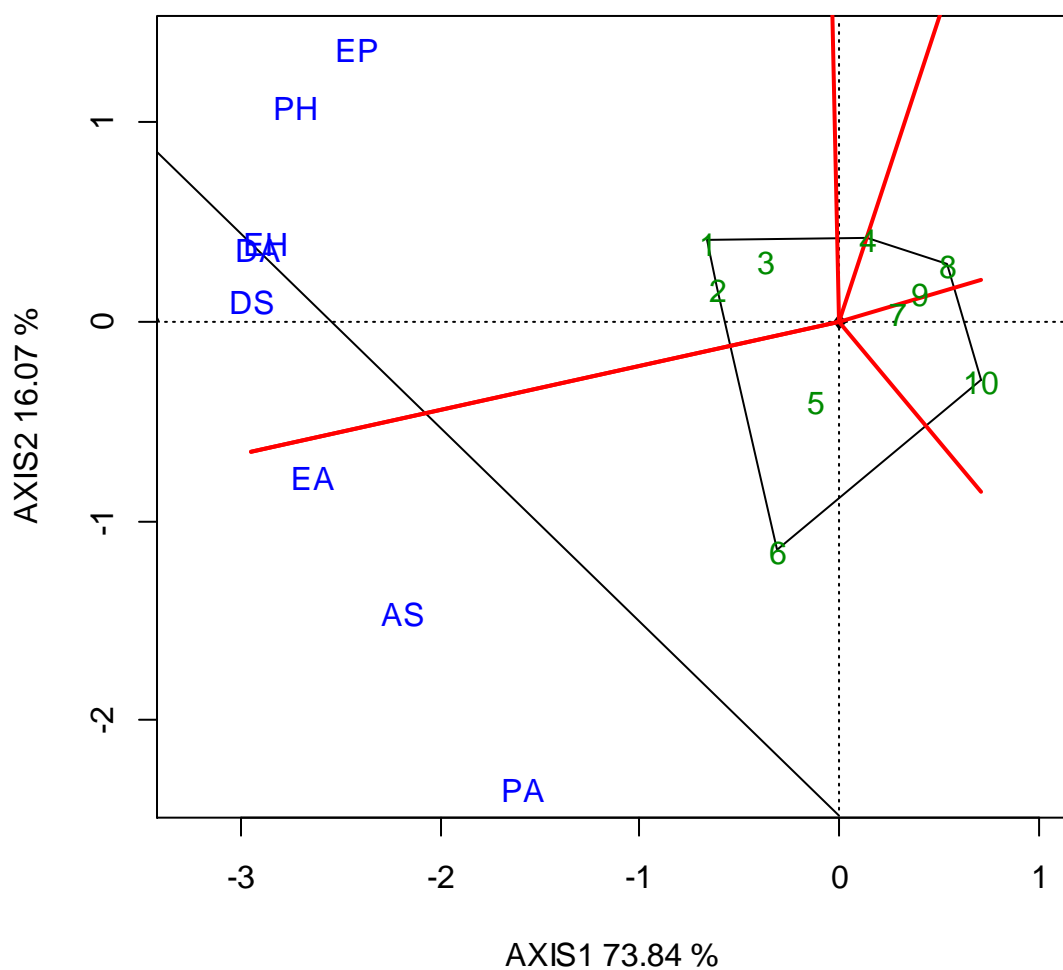


Figure 2: The polygon view of the GYT biplot to identify genotypes with outstanding trait profiles.

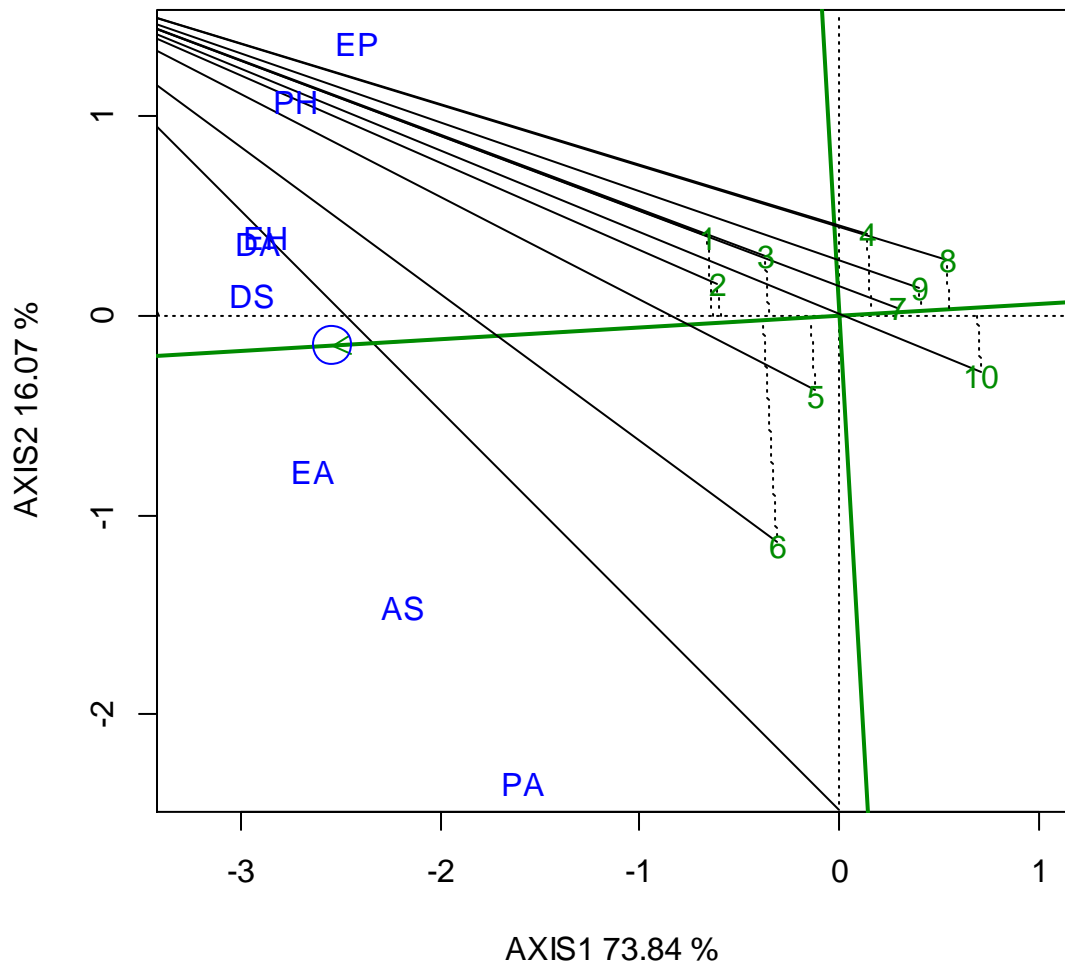


Figure 3: The Average Tester Coordination view of the GYT biplot ranking the accessions based on overall superiority

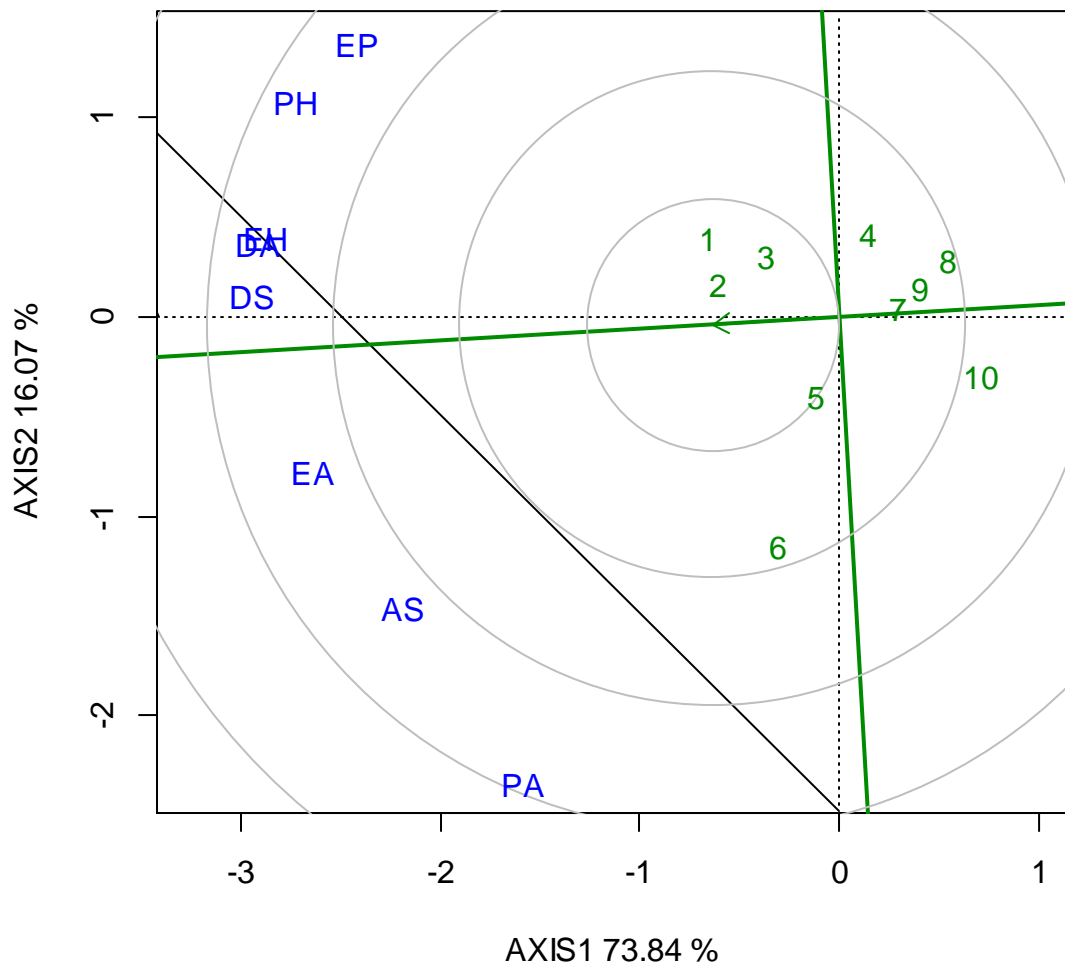


Figure 4: The Average Tester Coordination view of the GYT biplot showing the accessions in relation to the based on overall superiority and their strengths and weaknesses.