

Phenotyping and Prediction of Maize (*Zea mays* L.) Yield using Physiological Traits

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Abstract

The use of physiological traits as an indirect selection is important in augmenting yield – based selection procedures. Field experiment was conducted at the Research and Teaching Farm of Faculty of Agriculture, Bayero University, Kano to study physiological responses of different maturity groups of maize in Sudan savanna, determine the association between physiological traits and grain yield as well as predict grain yield of maize using physiological traits. The genetic materials used were twenty two maize genotypes laid out in a randomized incomplete block design (RCBD) with three replications. The results obtained revealed no significant difference between the genotypes. However the genotypes showed a good response to some physiological traits that can be used to improve maize response in developing tolerant genotypes. Differences were also observed in anthesis-silking interval, plant height, days to tasseling and days to silking respectively. Significant correlation was observed between days to tasseling with harvest index. There was a lack of fit in prediction of grain yield using physiological traits because of low R² (0.19) and high RMSE (480.871kg yield/ha).

Keywords: Correlation, Maize, Physiological trait, PLSR, Prediction.



Introduction

Population growth and climate change, combined with the degradation and scarcity of natural resources and recurrent food price crises, threaten food security and the livelihoods of millions of resource-poor people. In many regions of the sub-Saharan Africa (SSA), maize is the principal crop accounting for up to 51% of consumed calories. Yield levels in SSA remain low and highly variable across years at less than 2 t/ha in most countries (FAO, 2011), which is insufficient to meet future demands. Increasing temperatures, changing precipitation patterns, and extreme weather events are likely to further exacerbate the ability to meet future demands within maize growing regions (IPCC, 2007).

Many studies have reported a reduction in growth that was related to chemical signals resulting from water deficits (Ismail et al., 1994; Ismail and Davies, 1998; Hurley and Rowarth, 1999). A major effect is a reduction in photosynthesis, which is caused by decreased leaf expansion and impaired photosynthetic machinery (Wahid et al., 2005). In addition, drought can affect the photosynthetic pigments (Anjum et al., 2003) and reduce the relative water content (RWC), which has been noted in a wide variety of plants (Nayyar and Gupta, 2006). Improving crops yield under water - limited conditions is the most daunting challenge faced by breeders. To this end, accurate, relevant phenotyping plays an increasingly pivotal role for the selection of drought resilient genotypes and, more in general, for a meaningful dissection of the quantitative genetic landscape that underscores the adaptive response of crops to drought (Roberto, 2012). The genetic improvement of yield and its component depend upon the nature and the magnitude of variability present in the genotypes. Most of the characters that were of breeders' interest are complex and polygenically controlled. A successful selection program depends not only on heritability of desirable characters but also on the

information on association among various physiological characters and their association with grain yield (Beleke and Nageshwar Rao, 2013). The use of physiological traits as an indirect selection would be important in augmenting yield – based selection procedures (Shaibu *et al.*, 2015b). Selection efficiency could be improved if particular physiological attributes related to yield under a stress environment could be identified and employed as selection criteria for complementing traditional plant breeding (Acevedo, 1991).

Secondary traits can help improve the precision with which drought tolerant genotypes are identified, compared with measuring only grain yield under drought stress. Secondary traits such as canopy temperature, stomata conductance, ears per plant and anthesis silking interval have been found to possess strong correlations with grain yield (Shaibu et al., 2015c) and have been used previously to select for higher levels of tolerance to drought (Badu-Apraku et al., 2011). Different maturity groups of maize have been evaluated for prediction, association and contribution to grain yield. However, the genotypes used were few and the assessment may not be accurate (Shaibu et al., 2015a; b; c). There is therefore a need to evaluate for differences in physiological traits of different maturity groups of maize using large numbers of genotypes comprising both hybrids and open pollinated varieties (OPVs). Each maturity group have has its unique merits and demerits with regard to climatic conditions. The objectives of this study was to therefore, determine the association between physiological traits and grain yield as well as predict grain yield of maize using physiological traits.

Materials and Methods

The experiment was conducted at the Research and Teaching Farm of Faculty of Faculty of Agriculture, Bayero University, Kano (Lat 11°58'N, Long 8°25'E and 475m above sea level). The materials used for the experiment were



twenty two (22) maize genotypes obtained from IITA. These were laid out in an 11×2 randomized incomplete block design with three replications. Six ridges of 5m length were used to represent a plot and 2 seeds were sown manually at interval of 75 x 25cm inter and intra row spacing, respectively. Fertilizer was applied at the rate of 120kg N, 60kg P and 60kg of K per ha at 2 weeks after sowing (WAS) with the N applied in two splits. Data were recorded on days to tasseling, days to silking, plant height, relative water content, leaf area index, chlorophyll content and grain yield. Chlorophyll content was measured using SPAD 502 PLUS Chlorophyll meter.

Relative water content

A sample consisting of five flag leaves were taken from each sub plot and the fresh weights were recorded. Leaves were immersed in distilled water for 14 - 16 hours, and saturated weights were recorded after blotting off the excess water. Then the dry weights of the same leaves were recorded after drying in an oven at 80°C for forty eight hours. The relative water contents were calculated using the formula (Waraich and Ahmad, 2005):

$$RWC = \frac{FRESHWEIGHT - DRYWEIGHT}{SATURATEDWEIGHT - DRYWEIGHT} \times 100$$

Leaf area index

Leaf area index was computed using leaf area measured by using leaf area meter instrument and ground area using the following formula:

$$LAI = \frac{LA}{GA}$$

Where:

LAI = Leaf area index LA = Leaf area GA = Ground Area

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Data collected were analyzed using the PROC MIXED statement. The analysis was done using SAS (SAS, 2015). Replication and block were considered as random effect and the genotypes were considered as fixed effect. Simple correlation among trait was calculated using PROC CORR statement.

Partial least square (PLS) regression was carried out using the PLS module of the XLSTAT software (Addinsoft, 2009) as also applied by Shaibu *et al.* (2015b) to predict grain yield using physiological traits. The performance of the model was measured by coefficient of determination of the model (R^2) and the root mean square error (RMSE) that is an indicator of the average error in the analysis expressed in original measurement unit (Kvalheim, 1987)..

Results

Descriptive statistics of some traits of Maize

The descriptive statistics of the maize traits measured is presented in Table 1. The descriptive statistics shows the mean, minimum, maximum and p levels of traits measured. There was no significant difference (P>0.05) between the genotypes for the physiological traits measured (chlorophyll content, relative water content, leaf area and leaf area index). Significant difference was observed (P<0.05) for anthesissilking interval and plant height and there is highly significant difference for days to tasseling and days to silking.

The mean relative water content was 49.98 SPAD with minimum, maximum, variation and standard error of 30.57 SPAD, 73.27 SPAD, 18.16 SPAD and 1.117 SPAD respectively. The mean of leaf area index was 0.19 with minimum, maximum, variation and standard error 0.14, 0.28, 14.84 and 0.004 respectively. The mean of grain yield was 4197.05 Kg/ha with minimum, maximum, variation and standard error of 2927.00 Kg/ha, 5600.00 Kg/ha, 17.07 Kg/ha and 88.163 Kg/ha respectively.



Correlation between some physiological and agronomic traits of the genotype is presented in Table 2. Most of the correlation between the traits shows no significant association (P>0.05). There was positive and highly significant (P<0.01) correlation between anthesis-silking interval with harvest index. Negative correlation exists between grain yield and harvest index.

The Prediction of grain yield of maize using chlorophyll content, relative water content, leaf area and leaf area index traits are presented in Table 3. The R^2 value was low (0.195) with a relatively high RMSE (480.871) indicating a poor fit for yield prediction using physiological traits. This is also evident in Figure 1. Chlorophyll content and leaf area have negative contribution in the model. Leaf area index have the highest positive value (45040.495).

Discussion

The non-significant difference in the agronomic traits of genotypes measured could be due to differences in the maturity group of the genotype. The mean plant height is within reasonable range compared with the report of Menkir and Akintunde (2001) and Shaibu et al., (2015a) for plant height (163 - 172 cm). The shortened ASI observed in these cultivars is desirable because it has been reported that low ASI enhance maize tolerance to stresses during flowering and it ensures good grain filling (Edmeades et al., 1993; Bolanos and Edmeades 1996). The lack of significant difference observed in the physiological traits of the genotypes measured was an indication that irrespective of the differences in the maturity group the physiological response of the maize genotypes are the same (Shaibu et al., 2015a). This also confirms that physiological variability in the traits does not exist between the different maturity groups of the maize genotypes. The maize genotypes showed a good response in terms of improving them towards becoming drought tolerant genotypes.

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Positive correlation between anthesis-silking intervals with harvest index was found. Negative correlation exists between grain yield and harvest index. The relationship among these traits will cause them to respond similarly during improvement (Shaibu *et al.*, 2015a).

Generally, there was a lack of fit for predictions using physiological traits. This finding is in contrast to the report of Nguyen and Lee (2006), Li *et al.* (2014), Shaibu *et al.*, (2015b) who reported a good fit for prediction of rice leaf growth, canopy nitrogen of wheat and maize yield, respectively using PLSR. The lack of fit of the prediction might be as a result of the fewer physiological traits observed as compared to the findings of Shaibu *et al.* (2015b). Vargas *et al.* (1998) used the PLSR in interpreting the genotype by environment interaction of wheat and observed that the PLS was effective in detecting environmental and cultivar explanatory variables associated with factors that explained large portions of the interaction.

Improving crops yield under water – limited conditions is the most daunting challenge faced by breeders. To this end, accurate, relevant phenotyping plays an increasingly pivotal role for the selection of drought resilient genotypes and, more in general, for a meaningful dissection of the quantitative genetic landscape that underscores the adaptive response of crops to drought. Improvement of the physiological traits of maize genotypes can lead to improvement in level of maize production in Sudan savanna. The genotypes used in this study shows a good response to drought and no difference was observed between the genotypes for physiological traits observed.

The lack of significant difference in the physiological traitsof the genotypes which included drought tolerant genotypes(2009TZEEWDTSTR,2013TZEEWDTSTR,2013DTEYSTR,2013TZEEWPOPDTSTR,DTSTRW,DTSTRY,EVDTW99STR,EVDTY2000STR,



IWDC2,TZEYPOPDTSTRC4 x TZEEI13 and TZLCOMP4DTC2) shows that these genotypes can also be improved to become drought tolerance genotypes.

Conclusion

Predicting the performance of maize under drought before yield stage will enhance breeding activities and selection. Partial least square regression (PLSR) can be used to achieve this objective and reported in our previous studies. However, in this study, the PLSR analysis revealed a poor fit in predicting maize grain yield but can be improved by increasing the physiological traits evaluated and increasing the number of environments. Also the genotypes used in this study showed good response to drought in terms of their physiological traits indicating that physiological breeding can be targeted in this genotype to improve their drought tolerant instead of using some agronomic traits such as stay green characteristics which is measured towards physiological maturity.

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Variable	Mean	Minimum	Maximum	Variation	Std Error	P level
DTT	53.18	48.00	58.00	5.62	0.368	<.0001
DTS	56.77	50.00	62.00	5.70	0.399	<.0001
ASI	3.61	1.00	6.00	28.73	0.128	0.0316
PH	166.22	131.90	213.00	9.44	1.932	0.0063
CHL	49.98	30.57	73.27	18.16	1.117	0.1560
RWC	51.64	39.34	63.44	10.69	0.680	0.9882
LA	362.35	256.39	524.37	14.72	6.565	0.4298
LAI	0.19	0.14	0.28	14.84	0.004	0.5308
GYD	4197.05	2927.00	5600.00	17.07	88.163	<.0001
HI	0.25	0.11	0.44	29.28	0.009	0.0138

 Table 1: Descriptive Statistics of different Maturity group of Maize Traits evaluated at BUK

DTT, DTS,ASI, PH,SPAD.,RWC, LA,LAI, GYD and HI = Days to tasseling, days to silking, anthesis silking interval, plant height, chlorophyll content, relative water content, leaf area, leaf area index, grain yield and harvest index respectively.

Table 2: Correlation Matrix of some physiological and agronomic traits of maize

Variables	DTT	DTS	ASI	PH	SPAD	RWC	LA	LAI	GYD	HI
DTT	1.00									
DTS	0.88**	1.00								
ASI	-0.29*	0.20	1.00							
PH	0.33**	0.44**	0.20	1.00						
CHL	0.05	0.17	0.25*	0.18	1.00					
RWC	0.06	0.07	0.02	-0.01	0.10	1.00				
LA	-0.12	-0.19	-0.13	-0.15	-0.15	-0.15	1.00			
LAI	-0.17	-0.22	-0.09	-0.18	-0.15	-0.15	0.99**	1.00		
GYD	0.21	0.17	-0.09	-0.04	-0.01	-0.06	-0.18	-0.17	1.00	
HI	-0.12	0.06	0.35**	-0.14	0.14	0.14	0.10	0.13	-0.04	1.00

*, ** = Significant at 5% and 1% level of probability, respectively. And DTT, DTS, ASI, PH, SPAD., RWC, LA, LAI, GYD and

HI = Days to tasseling, days to silking, anthesis silking interval, plant height, chlorophyll content, relative water content, leaf area, leaf area index, grain yield and harvest index respectively.

Table 3: Prediction grain yield of maize using physiological traits.



Variables	Yield
Intercept	5336.837
CHL	-4.590
RWC	21.337
LA	-29.566
LAI	45040.495
R ²	0.195
RMSE	480.871



Figure 1. Predicted vs. actual grain yield of maize

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