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Genetic Control of Stress-Tolerant Extra-Early Quality Protein Maize Inbreds for Resistance to Northern Corn Leaf Blight Disease in the Tropics

By

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Abstract Extra-early maturing quality protein maize (QPM) cultivars combining disease resistance with high grain yield and quality potentials could enhance nourishment and food security in the drought prone savanna agro-ecologies. A diallel cross of five stress-tolerant extra-early QPM inbreds was conducted with the aim of identifying northern corn leaf blight disease (NCLB) resistant genotypes with superior grain yield, lysine and tryptophan contents using artificial inoculation. The trial was evaluated at the Lower Niger River Basin Authority, Oke-Oyi, Nigeria in 2016 and 2017 cropping seasons. Significant general (GCA) and specific combining ability (SCA) effects were obtained for all the traits, indicating the necessity to screen for resistance to occurring diseases either in the dependable hot-spots or applying artificial inoculation. The Baker's ratios of GCA/SCA nearest to unity for all the traits revealed additive gene action controlling the inheritance of the traits. The inbreds 99 TZEF-W STR QPM C₀ and 99 TZEE-W STR QPM and their resultant hybrids were NCBD resistance with high grain yield, lysine and tryptophan contents. These two inbreds could be used for breeding NCBD resistance genotypes not only for drought escape, high grain yielding and quality protein potentials, but also adaptable to savanna agro-ecology to reduce malnutrition.

Keywords: Artificial inoculations, blight, diallel, grain quality, yield.

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Introduction

Normal endosperm maize is consumed by adult and infants in the rural poor in Nigeria. It is usually prepared as porridge without protein supplements (beans, meat or eggs) because they are relatively expensive (Yusuf, 2010.). Normal maize has poor nutritional quality with 10% protein based on their inadequate essential amino acid levels of lysine and tryptophan. These two amino acids need to be supplemented, as these cannot be synthesized by humans (Mbuya et al. 2010). Thus the rural poor are prone to essential amino acid deficiencies resulting to health problems such as kwashiorkor, underweight, weakened resistance to infections and impaired intellectual development (Mbuya et al., 2010). However,, Quality protein maize (QPM) varieties discovered in 1964 using Opapue-2 mutant gene produced twice the lysine and tryptophan amino acids levels, enhance manufacture of complete proteins in the body and produced more than 10% increase in grain yield than the normal maize (Mbuya et al., 2010).. QPM also offers 90% of the nutritional value of skim milk (Upadhyay et al., 2009).

Northern Corn Leaf Blight (NCLB) caused by the heterothallic ascomycete fungus *Exserohilum turcicum* (Pass.) Leonard and Suggs (syn. *Helminthosporium turcicum* Pass.) is one of the major foliar wilt maize diseases in temperate and tropical environments (Galiano-Carneiro et al. 2017). The humid tropics had prevalence of 95 to 100% and 70% loss of grain yield in susceptible varieties (Wang et al. 2012). Heavily infection also causes decline in grain quality by reducing sugar contents and decrease seed germination. Its severity on crop stands defoliation during grain-filling stage can dispose to stalk rot (Muiru et al. 2015).

Statement of the Problem

Currently, the NCLB disease incidence and severity is threatening maize production in savanna of Nigeria. Factors related with the disease outbreak include alternative hosts, host susceptibility, new races, new pathotypes emergence, host-pathogen interactions and probable breakdown of resistance. The symptom of NCLB emerged on the surface of the leaves as tiny grayish green elliptical lesions with narrowed ends spreading from the leaves to the husks, resulting to leaf necrosis and premature foliage death (Kutawa et al. 2017). This infection is usually visible on the plants at every growth stage during and after anthesis, decreasing maize grain yield and fodder value considerably in endemic agro-ecological zones. However, the control of the disease is very difficult because of unpredictable weather conditions with high relative humidity and low temperature which increase its occurrence and damage (Vivek et al. 2010). Most of the small-holding farmers can't afford the control of the disease because of limited access to pesticides. Though, various methods of chemical control, ranging from seed dressing to foliar spraying appeared decreasing the prevalence and severity of several diseases, but resistance pathogens could lead to a substantial injury on the germinating maize (Sibiya et al. 2013). Again, other control measures adopted include crop rotation, crop residues elimination, adequate plant density, spacing and fertilization (Bergamin and Amorim 2011). Didactically, the development of varietal resistance not only offers efficient and economical management strategy to control the disease, but also environmentally responsive and reduction of production cost (Ayiga-Aluba et al. 2014,). NCLB, however, has remained a foremost challenge in the world despite all concerted efforts by research thrusts in curbing the

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menace of the disease (Ribeiro et al. 2016). Thus, detection of resistant cultivars and integrating the disease resistance into desirable genotypes is very important. Meanwhile knowledge of disease resistance nature and performance is necessary to transfer stable and durable resistance sources in diverse genetic base.

Review of Relevant Literature

A reliable approach of detecting superiority performance of progenies for disease resistant is the use of diallel analysis. NCBBD-resistant cultivars can be evaluated using diallel analyses for estimating combining ability to ascertain the most dependable hybrid combinations. Combining ability helps the breeders in selecting promising plant breeding materials to be exploited and the suitable breeding programme to be adopted to enhance success against variety of stresses (Kiyoy and Kusolwa 2017)). Further, combining ability assists in predicting heterotic groups and assessing genetic diversity (Bello and Olawuyi 2015). Many researchers revealed different types of gene actions (additive and nonadditive effects) controlling the conventional maize grain yield under NCBBD evaluations with varied levels of the disease resistance. Significant additive over non-additive gene action additive genetic effects over non-additive effects found to be controlling quantitative inheritance of NCBBD (Sibiya et al. 2013,). Conversely, preponderance dominance effects were also reported, which relied on the types of germplasm used and growth phases of the plant (Welz and Geiger 2000). Epistatic genetic effect, however, was not significant (Schechert et al. 1997). It is therefore pertinent to study genetic control of QPM inbreds for NCBBD resistance in order to identify promising genotypes in formulating a suitable breeding strategy.

Objectives of the Study

Presently, there seems a dearth of literature on resistance to NCBBD using diallel analysis in QPM cultivars. In line with these aforesaid, this study was conducted to:

1. Compare the newly developed stress-tolerant extra-early QPM inbred lines with their F₁ crosses for resistance to NCLB disease by artificial field inoculation.
2. Carried out the diallel analyses to test for relative importance of general (GCA) and specific combining ability (SCA) to the disease resistance.
3. Thirdly, a test of correlation of the characters among the genotypes was performed. Finally, this study is of the view of identifying NCLB resistant QPM inbreds and hybrids with superior grain yield and quality for further improvement adaptable to savanna agroecology of SSA.

Materials and Methods

Field Evaluations

Five extra-early QPM inbred lines of 85 days to maturity were obtained from International Institute of Tropical agriculture (IITA), Ibadan, Nigeria and crossed in a 5 x 5 partial-diallel fashion excluding reciprocals $[n(n-1)/2]$. The trials consist of 5 QPM inbreds, their 10 F₁ hybrids and 2 commercial hybrids used as checks. They were evaluated under NCBBD artificial inoculation at the Lower Niger River Basin Authority, Oke-Oyi, Nigeria (8° 30'N and 8° 36'E) in 2016 and 2017 cropping seasons. The description of the 5 extra-early QPM inbred lines and 2 commercial hybrid checks are shown in Table 1.

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Table 1 Description of 5 extra-early QPM inbred lines and 2 commercial hybrid checks

Inbreds	Endosperm colour	Reaction to drought	Reaction to <i>Striga</i> infestation
99 TZEF-W STR QPM C ₀	White	Tolerant	Resistant
99 TZEE-W STR QPM	White	Tolerant	Resistant
TZEE-W POP STR QPM C ₂	White	Moderately tolerant	Resistant
2000 SYN EE-W STR QPM	White	Susceptible	Resistant
2000 SYN EE-W QPM C ₀	White	Drought escaping	Resistant
Commercial hybrid checks			
Oba Super 9	White	Susceptible	Susceptible
Oba 98	White QPM	Susceptible	Susceptible

Source: International Institute of Tropical agriculture (IITA), Ibadan, Nigeria

Experimental Design and Cultural Practices

According to agronomic standard of maize production in the savanna agro-ecosystems of Nigeria, the tested field was plowed, harrowed and ridged. Thereafter, pre-emergence (a.i. 3kg/l Metolachlor and 170g/l Atrazine ha⁻¹) and post-emergence (a.i. 3kg/l Paraquat ha⁻¹) herbicides were sprayed to ensure a weed-free trial. A layout of randomized complete block design (RCBD) with four replications comprised of each plot planted with four rows of 5 m length, 0.5 m spacing within row and 0.75 m between the ridges, resulting in a density of 53,333 plants ha⁻¹. The 10 F₁ crosses, their 5 parents QPM inbred lines and 2 commercial hybrids used as controls were cultivated on 19th and 18th July, 2016 and 2017 cropping seasons under rain-fed environments, respectively, with artificially infested NCLB. To prevent seed borne diseases, the maize grains were seed-dressed with Apron-plus. Three kernels were planted per hill and thinned to two at two weeks after planting (WAP). Complementary hand weeding was carried out at four WAP prior to fertilizer application. A basal application of fertilizer was applied at the rate of 80 kg ha⁻¹ N (urea), 40 kg ha⁻¹ P (single superphosphate) and 40 kg ha⁻¹ K (muriate of potash). Subsequently, a supplemental urea of 60 kg ha⁻¹ N was top-dressed at eight WAP.

NCLB Inoculation and Disease Infection

According to Nwanosike et al. (2015) for the preparation of the inoculum, the lesion was scrapped from the leaves infected by the disease and deposited into moist chamber for two to three days in order to facilitate sporulation. Sterile microscope was used to pick the single spores from the lesions and transferred to the PDA plate for incubation at a room temperature. Each colony of the *E. turcicum* was further sub-cultured on new PDA plates. The sub-cultured inoculum were placed onto inoculate autoclaved sorghum kernels to allow colonization of the grains for almost ten days, and thereafter air dried. A range of 20 to 30 of colonized kernels were spread onto the plant leaf whorls. The inoculum, conidial suspensions were usually sprayed at 4th to 6th leaf stage in the evening to ensure effective infection when relative humidity was optimum. This process was followed by two supplementary inoculations at 1 to 2 weeks interval.

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NCLB Symptom Ratings

Data on disease evaluation were recorded immediately the symptoms appeared. Ten randomly chosen stands at the centre row per plot were tagged for the assessment of the disease. The infected plants were rated at ten days interval for disease severity by applying visual scales of 0 to 5 with slight modification. The disease severity rating was as follows; 0 = leaves free from infection, 1 = a few restricted lesions on the lower leaves ($\leq 5\%$), 2 = several small and large lesions on many leaves (5.1-10 %), 3 = numerous small and large lesions on many leaves (10.1-25 %), 4 = many enlarged and coalesced lesions on many leaves above the cob (25.1-50 %) and 5 = several coalesced lesions, leaf showing wilting, tearing and blotching typical blight symptoms ($> 50\%$) (Ribeiro et al. 2016).

Measurements of Maize Grain Yield

From ear weight per plot, grain yield was calculated with the assumption of 80% shelling percentage. The grain yield thereafter was transformed to tonnes per hectare ($t\ ha^{-1}$) after 12.5% moisture content adjustment.

Proximate Analysis of Lysine and Tryptophan

A single step papain hydrolysis method described by Hornandez et al. (1969) was applied for protein solubilization. Iron ions oxidized acetic acid to glyoxylic acid with the application of sulphuric acid. The indole ring of free tryptophan which bound in the soluble proteins reacted with glyoxylic acid and a violet-purple compound was generated. The intensity of the violet-purple color was measured at 545 nm with a spectrophotometer. The drawing of optical density standard curve against tryptophan concentration, the percentage of tryptophan in the sample was estimated as follows:

$$\% \text{ tryptophan in protein} = \frac{\% \text{ tryptophan in sample}}{\% \text{ protein in sample}}$$

The tryptophan was utilized as the factor for protein quality assessment while the value obtained was multiplied by 4 to attain lysine value (Sentayehu 2008).

Statistical Analyses

Data collected, excluding that of the checks, were firstly subjected to independence analyses of variance (ANOVA) for each year on plot means for the four measured characters (natural log transformations of NCLB percentage, grain yield, lysine and tryptophan) to assess the significant differences among the genotypes after verifying the homogeneity of variance with Levene's test. Thereafter, a combined ANOVA across the two years of evaluation was performed. Year and replicates were regarded as random effects while crosses as fixed factors. However, partial diallel analyses were carried out by employing Model I (fixed genotype effects); and Method II (parents and hybrids with no reciprocal crosses) as suggested by Griffing (1956). The mean squares for GCA and SCA were tested against their respective error variances inferred from the ANOVA. The total sums of squares were partitioned into year, crosses and crosses \times year interactions. GCA and SCA effects were determined through a linear model for ANOVA across years using PROC GLM in SAS (SAS 2012) program. Further the variation in the trait means was calculated using the least significant difference (LSD) test. Pearson's correlations coefficients were also computed to infer the relationship in studied characters applying PROC GLM in SAS (SAS, 2012).

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Results and Discussion

Grain Yield

Grain yield evaluated across the two cropping seasons varied significantly among the genotypes (Table 2). Significant difference ($p < 0.05$) in the inbred parents for yield was also observed. Most of the QPM hybrids had significant grain yield than the inbreds. Among the inbreds, highest yield was observed on 99 TZE-F-W STR QPM C₀ (5.79 t ha⁻¹) followed by TZE-E-W POP STR QPM C₂ (5.71 t ha⁻¹), while 2000 SYN EE-W QPM C₀ attained low yield of 4.99 t ha⁻¹. In the hybrids, 99 TZE-F-W STR QPM C₀ x 99 TZE-E-W STR QPM (7.11 t ha⁻¹) was superior for grain yield followed by 99 TZE-F-W STR QPM C₀ x TZE-E-W POP STR QPM C₂ with 2000 SYN EE-W STR QPM x 2000 SYN EE-W QPM C₀ (5.51) exhibiting inferior performance. Inbreds 99 TZE-F-W STR QPM C₀ and 99 TZE-E-W STR QPM were better combiners for high grain yield among the studied hybrids. Nonetheless, inbred 2000 SYN EE-W QPM C₀ was a common inbred with lower yield in the hybrids. The two commercial hybrids (Oba Super 9 and Oba 98) that served as checks had abysmal grain yield compared to the inbreds and their hybrids.

NCBD Rating

For the NCBD rating, inbreds 99 TZE-F-W STR QPM C₀ and 99 TZE-E-W STR QPM followed the same trend with grain yield revealing low disease resistance. These inbreds also feature as superior combiners for NCBD tolerant. Hybrid 99 TZE-F-W STR QPM C₀ x 99 TZE-E-W STR QPM had high tolerant to the disease with a rating of 2.0 representing 50% advantage over Oba 98, the commercial QPM hybrid. All the hybrids were tolerant to the disease, except 2000 SYN EE-W STR QPM x 2000 SYN EE-W QPM C₀ with a rating of 3.42. It is noteworthy that despite the appearance of the NCBD symptoms on the maize crops in the field, this significantly not influences their productivity. The two checks were vulnerable to the disease with a score of 4.0 on the average were also inferior for grain yield and quality protein contents. The susceptibility of the two checks to NCBD rating not only shows that the magnitude of pathogen virulence but also the application of the virus inoculum on the field was very efficient.

Quality Protein Potentials

For quality protein contents, significant difference was recorded among the inbreds. The variation noted in the QPM inbreds indicates that they were of diverse sources and possessed resistant characteristics for improved quality protein and grain yield potential that are suitable for adaption in the tropical regions. High Tryptophan and Lysine were realized among the hybrids, followed by the inbreds and commercial checks. Generally, inbreds 99 TZE-F-W STR QPM C₀ and 99 TZE-E-W STR QPM appeared promising for high quality protein potentials, albeit with high grain yield and NCBD resistance. They combined favorably with all the inbreds to produce hybrids with appreciable performance in all the studied traits. It seems that these two inbreds not only possess NCBD resistance gene pool for introgression into other varieties but also proven alleles for higher quality protein contents and grain yield.

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Table 2 Genotypic performance of 5 extra-early QPM inbreds, their 10 hybrids and 2 commercial checks evaluated for NCBD rating, grain yield and quality protein in 2016 and 2017 cropping seasons

Parents	Grain yield (t ha ⁻¹)	NCBD rating (No)	Tryptophan (%)	Lysine (%)
99 TZEF-W STR QPM C ₀	5.79	2.12	3.99	0.97
99 TZEE-W STR QPM	5.61	2.22	3.67	0.81
TZEE-W POP STR QPM C ₂	5.49	3.44	3.78	0.90
2000 SYN EE-W STR QPM	5.71	3.65	3.79	0.89
2000 SYN EE-W QPM C ₀	4.99	3.39	3.87	0.89
Hybrids				
99 TZEF-W STR QPM C ₀ x 99 TZEE-W STR QPM	7.11	2.00	4.02	1.12
99 TZEF-W STR QPM C ₀ x TZEE-W POP STR QPM C ₂	6.90	2.11	4.0	0.99
99 TZEF-W STR QPM C ₀ x 2000 SYN EE-W STR QPM	6.89	2.13	3.90	0.89
99 TZEF-W STR QPM C ₀ x 2000 SYN EE-W QPM C ₀	5.43	2.46	3.67	0.77
99 TZEE-W STR QPM x TZEE-W POP STR QPM C ₂	6.88	2.21	3.92	0.81
99 TZEE-W STR QPM x 2000 SYN EE-W STR QPM	6.83	2.01	3.84	0.89
99 TZEE-W STR QPM x 2000 SYN EE-W QPM C ₀	5.54	2.41	3.89	0.91
TZEE-W POP STR QPM C ₂ x 2000 SYN EE-W STR QPM	6.82	3.22	3.86	0.91
TZEE-W POP STR QPM C ₂ x 2000 SYN EE-W QPM C ₀	5.49	3.40	3.84	0.86
2000 SYN EE-W STR QPM x 2000 SYN EE-W QPM C ₀	5.51	3.42	3.79	0.92
Oba Super 9	4.10	3.97	2.84	0.56
Oba 98	4.00	4.02	3.77	0.84
SE	0.011	0.065	0.079	0.053
LSD (0.05)	0.72	0.56	0.7	0.31
CV (%)	8.63	6.11	5.64	4.51

Source: Field trials in 2016 and 2017 cropping seasons

Combined Analysis of Variance

Table 3 shows the combined analysis of variance of the parental lines and their resultant hybrids for NCBD rating, quality protein content and grain yield assessed across two years. Mean squares for year that was nonsignificant for all traits show that all the genotypes had the same performance in both two years. Significant hybrids mean squares were obtained from all studied traits, including NCBD rating with highly significance ($p < 0.01$). This indicates that there were adequate variations that could enable appreciable selection in the genotypes for this trait. This also denotes that heritable variation can be increased in most of the procedures

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of selection at crop improvement schemes. Nonsignificant mean squares of crosses by years interaction detected among all the traits signify that in the two years, the crosses performances were similar.

Significant GCA and SCA mean squares were recorded for all the traits connoting that both additive and non-additive genetic effects controlled the traits. These therefore indicate that the inbreds varied in genic frequencies distribution. These further highlight that the production of improved hybrids through accession diversity could result to effective productivity. It also revealed progress from selection of promising alleles for widening genetic base of the inbreds and maintained genetic gain for hybrid productivity. Significant mean squares due to GCA by year and SCA by year interactions achieved in all traits implies that both genetic variance (additive and nonadditive) were the same in the two years of cropping. The Baker's ratio of GCA/SCA obtained which is nearest to unity for all the measured traits indicates that additive gene action controlled the inheritance of the traits, similar to the results of many workers (Bello 2017, Bello and Olawuyi 2015,). Therefore, recurrent selection breeding methods among these two inbreds could be effective for the production of improved the genotypes.

Table 3 Mean squares from combined analysis of variance for NCBD rating, grain yield and quality protein of 10 extra-early QPM inbreds diallel evaluated in 2016 and 2017 cropping seasons

Source of variation	Mean squares			
	NCBD rating (No)	Grain yield (t ha ⁻¹)	Tryptophan (%)	Lysine (%)
Year	0.94	0.53	0.46	0.72
Rep (Year)	1.23	0.74	1.54	1.03
Hybrids	113.45**	9.56*	7.87*	12.11*
Hybrids * Year	2.82	1.27	1.81	0.97
GCA	63.68*	22.53*	4.59*	6.34*
SCA	39.72*	19.01*	12.32*	7.87*
GCA* Year	1.91	1.56	1.68	1.11
SCA* Year	1.75	0.89	1.54	1.35
Pool Error	0.97	1.28	0.98	0.75
GCA/SCA (Baker's ratio) %	0.89	0.95	0.87	0.84
CV %	12.67	14.72	8.34	6.58

* and **significant at 0.05 and 0.01 levels of probability, respectively

Source: Field trials in 2016 and 2017 cropping seasons

Percent contribution of GCA and SCA sums of squares

Percentage contribution of GCA sums of squares to the total sums of squares was 79% for NCBD and 67% for grain yield indicating the predominance of additive genetic effects governing the disease resistance and yield (Table 4). This suggests that efficient methods for developing maize conferring resistance to diseases require selecting resistant inbreds and their hybrids by applying artificial inoculation or hot spot nursery methods. Thereafter, there testing at different locations and years to detect the inbreds that possess better combining ability for grain yield and disease resistance will be adopted. Again, percent contributions of GCA sums of squares to the total sums of squares were 73% and 76% for Tryptophan and Lysine, revealing preponderance of additive gene effects controlling the quality protein

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contents. Negative GCA effects that are of interest to the breeders were also noted for NCBD reaction among all the inbreds. In contrary to negative GCA effects required for disease trait, highly positive GCA effects are essential for grain yield, because allelic complementation effects are important for notable genotypes generations.

Most of the GCA effects were positive and significant among the lines except inbreds 2000 SYN EE-W QPM C₀ and 99 TZEE-W STR QPM. These two inbreds could be selected for further breeding to produce segregants resistance to NCBD as they stood out in conferring resistance. On the other hand, nonsignificant GCA effects were obtained in all the lines for both tryptophan and lysine contents. It is noteworthy that hybridization featured as most favorable option in attaining genetic gains in NCBD resistance, grain yield and quality. Earlier researchers reported preponderance of additive genetic action than non-additive genetic effects in NCBD. For instance, many researchers recorded additive genetic effects governing the manifestation of resistance to NCBD (Abera et al 2016, Kim et al. 2013, Vivek et al. 2010). Thompson et al. (1987) and Ulrich et al. (1990) also noted 100% contribution of GCA for grey leaf spot disease in maize and Menkir and Ayodele (2005) observed 70%. Contrarily, Nihei and Ferreira (2012) obtained nonadditive genetic control in inheritance of NCBD resistance. It can be suggested that genetic effects governing this trait could differ across where the resistance cultivars were sourced.

Table 4 Percent contribution of GCA sums of squares to the total sums of squares and estimates of GCA for 5 extra-early QPM inbreds evaluated for NCBD rating, grain yield and quality protein in 2016 and 2017 cropping seasons

Parent	NCBD rating (No)	Grain yield (t ha ⁻¹)	Tryptophan (%)	Lysine (%)
Percent contribution of GCA sums of squares to the total sums of squares				
GCA	79	67	73	76
SCA	21	23	27	24
GCA effects evaluated for NCBD, grain yield and quality protein				
99 TZEF-W STR QPM C ₀	-0.31	0.72*	0.91	0.93
99 TZEE-W STR QPM	-0.36	0.46*	0.86	0.87
TZEE-W POP STR QPM C ₂	-0.59	0.39*	0.82	0.80
2000 SYN EE-W STR QPM	-0.79	0.87*	0.74	0.69
2000 SYN EE-W QPM C ₀	-0.81	0.05	0.71	0.64
SE	0.12	0.23	0.06	0.13

* and **significant at 0.05 and 0.01 levels of probability, respectively

Source: Field trials in 2016 and 2017 cropping seasons

The SCA effects for NCBD rating for ten F₁ progenies are depicted in Table 5. The SCA effects followed the same trend of GCA where the entire hybrids had significant negative SCA effects for NCBD. They also exhibited significant positive SCA effects for grain yield. Besides, all the hybrids demonstrated significant positive SCA effects for both tryptophan and lysine. In this context, the crop breeders need to characterize the resistance sources to maximize genetic gains in the process of selection. It has also been accentuated that sources of quantitative and qualitative resistance genes are available and diverse, but that of qualitative trait are usually erratic (Chandrashekara et al, 2014). Instability resistance genes can break down by occurrence of new virulent pathogens or responsive expression to harsh climatic conditions (Abera et al 2016, Hooda et al. 2017). It is therefore necessary to monitor

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quality protein potentials in QPM genotypes when breeding for NCBD resistance or making selection.

Table 5 Estimates of SCA of 10 extra-early QPM hybrids and percentage contribution of SCA sums of squares to the total sums of squares for NCBD rating, grain yield and quality protein evaluated in 2016 and 2017 cropping seasons

Hybrid	NCBD rating (No)	Grain yield (t ha ⁻¹)	Tryptophan (%)	Lysine (%)
SCA effects for NCBD rating, grain yield and quality protein				
99 TZEF-W STR QPM C ₀ x 99 TZEE-W STR QPM	-0.27	0.97*	0.42*	0.51*
99 TZEF-W STR QPM C ₀ x TZEE-W POP STR QPM C ₂	-0.33	0.55*	0.57*	0.62*
99 TZEF-W STR QPM C ₀ x 2000 SYN EE-W STR QPM	-0.41	0.60*	0.91*	0.87*
99 TZEF-W STR QPM C ₀ x 2000 SYN EE-W QPM C ₀	-0.56	0.73*	0.82*	0.65*
99 TZEE-W STR QPM x TZEE-W POP STR QPM C ₂	-0.58	0.56*	0.67*	0.79*
99 TZEE-W STR QPM x 2000 SYN EE-W STR QPM	-0.71	0.79*	0.77*	0.81*
99 TZEE-W STR QPM x 2000 SYN EE-W QPM C ₀	-0.86	0.56*	0.88*	0.92*
TZEE-W POP STR QPM C ₂ x 2000 SYN EE-W STR QPM	-0.97	0.61*	0.91*	0.77*
TZEE-W POP STR QPM C ₂ x 2000 SYN EE-W QPM C ₀	-0.93	0.54*	0.59*	0.69*
2000 SYN EE-W STR QPM x 2000 SYN EE-W QPM C ₀	-0.87	0.67*	0.91*	0.75*
SE	0.11	0.07	0.14	0.09

* and **significant at 0.05 and 0.01 levels of probability, respectively

Source: Field trials in 2016 and 2017 cropping seasons

Pearson's correlations

Pearson's correlations (r) among NCBD rating, grain yield and quality protein contents of the studied the QPM parents indicate that NCBD rating was exceedingly negatively variable ($r = -0.93^*$) with grain yield, but not significantly associated with tryptophan and lysine with coefficients of $r = 0.32$, and 0.56 , respectively (Table 6). This is probably due to differential responses of the tested inbreds and hybrids in this study. On the other hand, grain yield was non-significantly interrelated with tryptophan ($r = 0.43$) and lysine ($r = 0.43$). The correlation of tryptophan and lysine was positive and markedly varied with coefficients of $r = 0.72^{**}$. Similarly, among hybrids, grain yield was negative and decidedly significant, with NCBD whereas, non-significant was recorded for tryptophan and lysine. Tryptophan and lysine was also non-significantly correlated. The non-significant relationship among the traits studied with NCBD corroborates the existence of diversity among the genotypes. This enables selecting favorable NCBD tolerant cultivars that displayed superior grain yield potential regardless of their NCBD severity level.

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Table 6 Pearson correlation coefficients among inbreds (below diagonal) and hybrids (above diagonal) for NCBD rating, grain yield and quality protein of 5 extra-early QPM inbreds

	NCBD rating	Grain yield	Tryptophan	Lysine
NCBD rating	1	-1.45*	0.27	0.49
Grain yield	-0.93*	1	0.66	0.52
Tryptophan	0.32	0.43	1	0.81**
Lysine	0.56	0.52	0.72**	1

* and **, significant at 5 and 1% of the probability, respectively

Source: Field trials in 2016 and 2017 cropping seasons

Conclusion

There are immense potentials in bi-parental QPM breeding for resistance to NCBD pathogens with elevated grain yield, tryptophan and lysine contents in this study. Also, maize population improvement and hybrid breeding employing hybridization could allow for favorable gene manipulation, as all the traits studied are controlled by additive genetic effects. Inbred parents 99 TZEF-W STR QPM C₀ and 99 TZEE-W STR QPM are better combiners for high quality protein potentials, albeit with high grain yield and NCBD resistance. This affirms that breeders of maize in this ecological zone are regularly transferring disease resistance/tolerance genes into recently developed genotypes even if targets of breeding were not due to disease resistances.

Recommendations

The two outstanding inbreds (99 TZEF-W STR QPM C₀ and 99 TZEE-W STR QPM) could be used as inbreds germplasm for evolving elite synthetic varieties and hybrids adapted to different agro-ecological zones or be exploited to enhance genetic base at the breeding schemes. The superior six hybrids that perform favorably for all the studied traits are suggested to be cultivated at varied cropping years and locations to affirm their potential performances or grown directly for commercial purposes in the savanna agroecology to reduce malnutrition. Since NCBD resistance alleles numbers contained in the inbreds have not been established, genome-wide analysis that can guide future allelic pyramiding is essential.

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