Genetic Analysis of Grain yield of Extra-early Provitamin A Maize Inbreds and Hybrid Performance under Multiple-stress and Non-stress Environments

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Introduction

Maize (*Zea mays* L.) is a major staple crop in sub-Saharan Africa (SSA) and provides most of the calories, protein, vitamins, and minerals in the diets of the people. Vitamin A is an essential micronutrient and its deficiency could result in night blindness, corneal blindness, reduced immunity, and stunted growth among affected children. Therefore, the development and commercialization of maize varieties and hybrids with elevated levels of pro-vitamin A carotenoids in the grain is the most cost effective and sustainable means of delivering micronutrients to maize consumers and hence, it is the most attractive option for alleviating vitamin A deficiency. Furthermore, maize production in SSA is constrained by the parasitic weed *Striga*, drought, and low soil nitrogen (low N).

A major focus of the IITA maize improvement program in SSA is to develop multiple-stress tolerant hybrids with improved nutritional value. To promote rapid development and the deployment of hybrids, it is important to determine the usefulness of available provitamin A inbred lines in hybrid combinations through combining ability studies. The objectives of the present study were to: (i) examine the general combining ability (GCA) and specific combining ability (SCA) effects of grain yield and other traits of extra-early maturing provitamin A inbreds, (ii) classify the inbreds into heterotic groups using the general combining ability of multiple traits (HGCAMT) method, (iii) identify provitamin A inbred testers, and (iv) assess the grain yield performance of the extra-early maturing provitamin A single-cross hybrids under multiple-stress and non-stress environments in Nigeria.

Materials and Methods

Thirty-three extra-early provitamin A S_7 inbred lines were crossed to four standard inbred testers, TZdEEI 7, TZdEEI 12, TZEEI 79, and TZEEI 95 to obtain 132 testcrosses using the line × tester design (Kempthorne 1955). The 132 testcrosses were evaluated using a 12 × 11 lattice design with two replications under four multiple-stress (terminal drought stress at Bagauda, 2015; induced drought stress at Ikenne, 2015/2016, *Striga* infestation at Mokwa, 2015 and low-N at Mokwa, 2015) and two non-stress environments (Mokwa and Zaria, 2015) where water and nitrogen (90 kg/ha) were not limiting and were also *Striga* free. The induced drought stress was achieved by withdrawing irrigation water 21 days after planting until maturity so that the maize plants relied on stored water in the soil. The experimental fields used for the low-N evaluations were depleted of N by planting maize and removing the biomass after each harvest for several years. Prior to planting, soil samples were taken in all the test environments and N content was determined in the laboratory in Ibadan. Fertilizer was applied to bring the total available N to 30 kg/ha for the low N based on the soil tests. Artificial *Striga* infestation at Mokwa was done according to the method of Kim (1991) and Kim and Winslow (1991).

Data recorded on grain yield and other agronomic traits of the testcrosses were subjected to statistical analysis and the effects of general combining ability (GCA) and specific combining ability (SCA) were computed using the line × tester model. Also, the relative importance of GCA and SCA was examined. The inbred lines were assigned to heterotic groups under multiple-stress, non-stress and across test environments based on GCA of the multiple traits (HGCAMT) grouping method proposed by Badu-Apraku et al. (2013). The additive main effects and multiplicative interaction (AMMI) analysis was used to decompose the G × E interactions and to assess the performance and yield stability of the single-cross hybrids across environments.

Results and Discussion

Results revealed a preponderance of additive genetic variance over the non-additive for grain yield and other measured traits under multiple-stress, non-stress and across environments (Fig. 1). The inbreds TZEEIOR 30, TZEEIOR 41, TZEEIOR 42, TZEEIOR 97, TZEEIOR 109 and TZEEIOR 140 possessed genes for multiple-stress tolerance and Provitamin A (Table 1) and could be used to develop stress-tolerant hybrids with high provitamin A and also introgressed into tropical maize populations to improve the levels of provitamin A. The HGCAMT method classified the inbreds into five groups under multiple-stress and three groups each under non-stress and across test environments. The inbreds TZEEIOR 197 and TZEEIOR 30 were identified as testers for heterotic groups 1 and 2, while no tester was identified for heterotic group 3 across environments (Table 2). The hybrids TZEIOR 197 × TZdEEI 12 and TZEIOR 123 × TZdEEI 7 were the most stable and high yielding across multiple-stress and non-stress environments (Fig. 2) and should be tested on-farm to confirm consistency of performance and commercialized in SSA.

Table 1. Reaction to stresses and provitamin A content of inbreds used for line × tester study

		Reaction to stresses		Provitamin A content (µg/g)
S/N	Pedigree	DT	STR	
1	TZEEIOR 11	S	T	6.48
2	TZEEIOR 30	T	S	10.19
3	TZEEIOR 35	S	S	6.67
4	TZEEIOR 41	S	T	11.57
5	TZEEIOR 42	T	T	10.48
6	TZEEIOR 47	S	S	9.17
7	TZEEIOR 76	S	S	7.77
8	TZEEIOR 92	S	T	7.83
9	TZEEIOR 97	T	T	10.44
10	TZEEIOR 99	T	S	8.77
11	TZEEIOR 102	T	T	4.85
12	TZEEIOR 109	S	T	10.24
13	TZEEIOR 123	T	S	6.25
14	TZEEIOR 125	T	T	4.95
15	TZEEIOR 139	T	T	7.68
16	TZEEIOR 140	T	T	10.32
17	TZEEIOR 146	T	T	7.78
18	TZEEIOR 161	T	S	5.93
19	TZEEIOR 197	S	T	8.45
20	TZEEIOR 249	T	T	6.43
21	TZEEIOR 251	S	T	7.94
22	TZdEEI 9	S	S	4.93
23	TZdEEI 13	-	-	6.29
24	TZEEI 58	S	S	0.97
25	TZEEI 63	S	T	0.86
26	TZEEI 64	T	T	2.45
27	TZEEI 68	T	S	1.63
28	TZEEI 69	T	S	-
29	TZEEI 73	S	T	1.02
30	TZEEI 76	T	S	-
31	TZEEI 81	T	S	1.86
32	TZEEI 82	T	S	1.39
33	TZEEI 96	S	S	1.84
34	TZdEEI 7 (Tester 1)	T	T	6.49
35	TZdEEI 12 (Tester 2)	T	S	5.68
36	TZEEI 79 (Tester 3)	S	S	1.12
37	TZEEI 95 (Tester 4)	T	S	3.94

Table 2. Heterotic groups of thirty-three pro-vitamin A inbred lines plus four testers under multiple-stress, non-stress and across environments in Nigeria, 2015–2016.

Research condition	Group 1	Group 2	Group 3	Group 4	Group 5
Multiple-Stress	TZEEIOR 11, TZEEI 76, TZEEI 81, TZEEIOR 92, TZEEIOR 197, TZEEIOR 249, and TZEEIOR 251	TZEEIOR 35, TZEEIOR 42, TZEEI 79, TZEEIOR 109, TZEEIOR 139, TZEEIOR 140, and TZEEIOR 146	TZdEEI 13, TZEEI 58, TZEEI 69, TZEEI 82, and TZEEI 96	TZEEI 63, TZEEI 64, TZEEI 68, TZEEI 73, TZEEI 95, and TZEEIOR 102	TZdEEI 7, TZdEEI 9, TZdEEI 12, TZEEIOR 30, TZEEIOR 41, TZEEIOR 47, TZEEIOR 76, TZEEIOR 97, TZEEIOR 99, TZEEIOR 123, TZEEIOR 125, and TZEEIOR 161
Non-stress	TZdEEI 9, TZEEIOR 11, TZEEIOR 92, TZEEIOR 97, TZEEIOR 99, TZEEIOR 102, TZEEIOR 125, TZEEIOR 139, TZEEIOR 249, and TZEEIOR 251	TZdEEI 7, TZdEEI 12, TZEEIOR 30, TZEEIOR 35, TZEEIOR 41, TZEEIOR 42, TZEEIOR 47, TZEEIOR 76, TZEEI 79, TZEEI 81, TZEEIOR 109, TZEEIOR 123, TZEEIOR 140, TZEEIOR 146, TZEEIOR 161, and TZEEIOR 197	TZdEEI 13, TZEEI 58, TZEEI 63, TZEEI 64, TZEEI 68, TZEEI 69, TZEEI 73, TZEEI 76, TZEEI 82, TZEEI 95, and TZEEI 96		
Across Environments	TZdEEI 7, TZdEEI 9, TZEEIOR 11, TZEEI 81, TZEEIOR 92, TZEEIOR 97, TZEEIOR 99, TZEEIOR 102, TZEEIOR 197, TZEEIOR 249, and TZEEIOR 251	TZdEEI 12, TZEEIOR 30, TZEEIOR 41, TZEEIOR 42, TZEEIOR 47, TZEEIOR 76, TZEEI 79, TZEEIOR 109, TZEEIOR 123, TZEEIOR 125, TZEEIOR 139, TZEEIOR 140, TZEEIOR 146, and TZEEIOR 161	TZdEEI 13, TZEEIOR 35, TZEEI 58, TZEEI 63, TZEEI 64, TZEEI 68, TZEEI 69, TZEEI 73, TZEEI 76, TZEEI 82, TZEEI 95, and TZEEI 96		

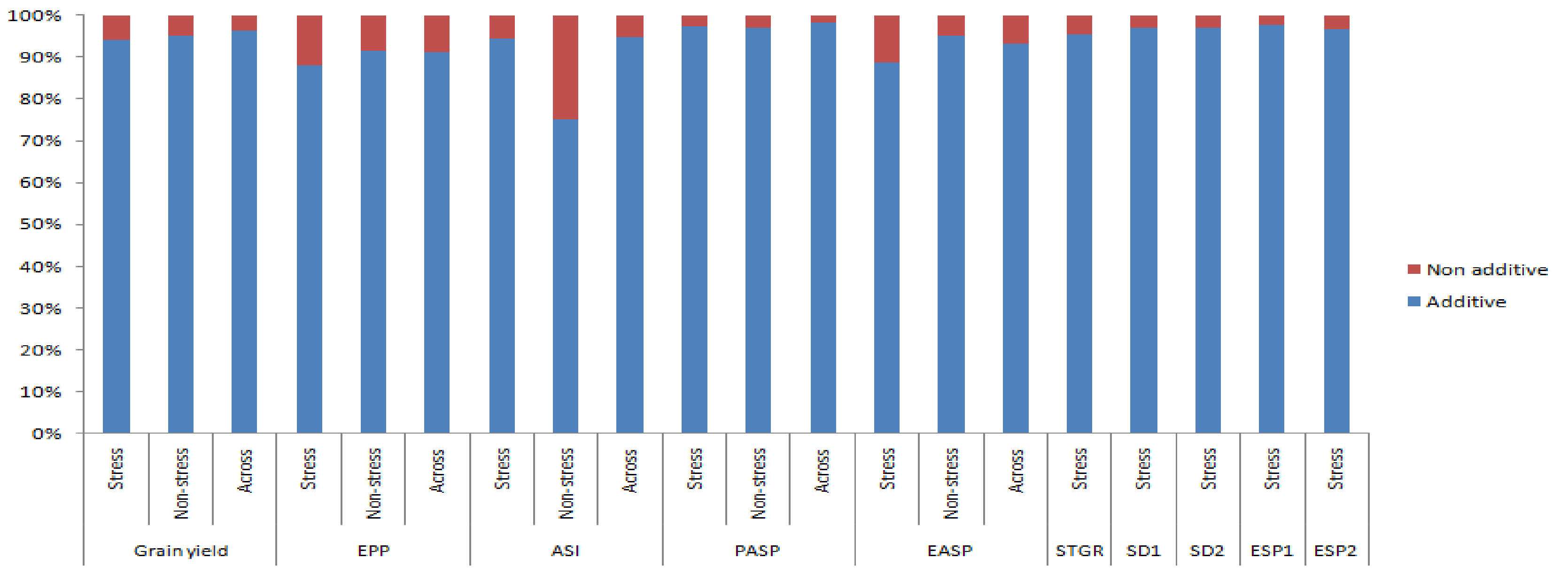

Figure 1. Proportion of additive (lower bar) and non-additive (upper bar) genetic variance for grain yield and other agronomic traits under multiple stress and non-stress and across test environments in testcrosses involving 33 extra-early provitamin A lines and four testers.

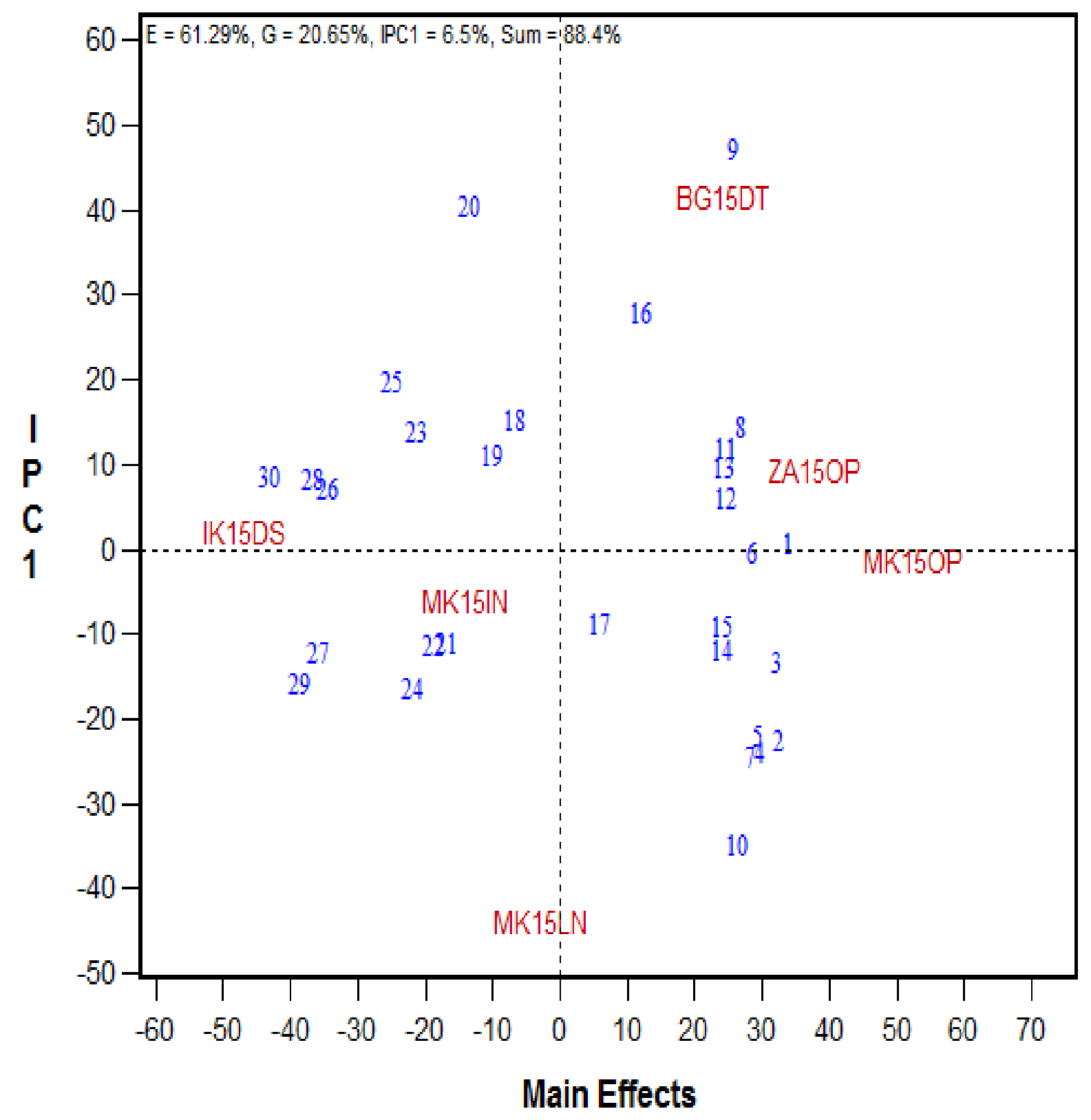

Figure 2. AMMI biplot of top 15, middle 10, and worst 5 pro-vitamin A hybrids evaluated across four multiple-stress and two non-stress environments in Nigeria, 2015-2016.

CODE	HYBRID
1	TZEEIOR 197 x TZdEEI 12
2	TZEEIOR 11 x TZdEEI 7
3	TZEEIOR 251 x TZEEI 79
4	TZEEI 81 x TZdEEI 12
5	TZEEIOR 30 x TZEEI 79
6	TZEEIOR 123 x TZdEEI 7
7	TZEEIOR 97 x TZdEEI 12
8	TZEEIOR 123 x TZEEI 79
9	TZEEIOR 99 x TZdEEI 12
10	TZEEIOR 97 x TZdEEI 7
11	TZEEIOR 249 x TZdEEI 7
12	TZEEIOR 249 x TZEEI 79
13	TZEEIOR 139 x TZdEEI 7
14	TZEEIOR 30 x TZdEEI 7
15	TZEEIOR 125 x TZdEEI 7
16	TZEEIOR 109 x TZdEEI 7
17	TZEEIOR 251 x TZEEI 95
18	TZEEI 63 x TZdEEI 7
19	TZEEI 82 x TZEEI 79
20	TZEEIOR 35 x TZdEEI 12
21	TZEEIOR 109 x TZEEI 79
22	TZEEIOR 47 x TZEEI 79
23	TZEEIOR 35 x TZEEI 95
24	TZEEIOR 146 x TZEEI 95
25	TZEEI 82 x TZdEEI 7
26	TZEEI 69 x TZEEI 95
27	TZdEEI 13 x TZdEEI 12
28	TZEEI 68 x TZEEI 95
29	TZEEI 58 x TZEEI 95
30	TZEEI 96 x TZEEI 79


Striga susceptible genotype

Striga resistant genotype

Low-N susceptible genotype

Drought tolerant genotype

Drought susceptible genotype

Conclusions

The identified pro-vitamin A testers will be invaluable for the development of pro-vitamin A hybrids for commercialization in the sub-region. The promotion and adoption of the multiple-stress tolerant, high-yielding, pro-vitamin A, extra-early hybrids will contribute to improved food security and nutrition in SSA.

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