academicJournals

Vol. 12(19), pp. 1674-1677, 11 May, 2017
DOI: 10.5897/AJAR2016.11872
Article Number: 4EEB76F64160
ISSN 1991-637X

http://www.academicjournals.org/AJAR

African Journal of Agricultural Research

Full Length Research Paper

Classification of selected white tropical maize inbred lines into heterotic groups using yield combining ability effects

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Received 26 October, 2016; Accepted 1 February, 2017

A line x tester mating design involving sixteen white maize inbred lines as females and two testers as males generated thirty-two single crosses. These hybrids plus three checks were evaluated using a 5 x 7 alpha lattice design replicated twice at the University of Ghana, WACCI research farm during 2015/16 offseason using drip irrigation. The objective of the study was to: assign the tropical inbred lines into heterotic groups. Based on the SCA effect for grain yield, the lines were separated into two heterotic groups. The lines L1, L3, L4, L8, L11 and L14 belonged to tester group 1368, while L2, L5, L6, L7, L9, L10, L12, L13, L15 and L16 belonged to heterotic group of CML 444. This is useful for the development of hybrids and synthetic varieties. Thus, the information generated in the present study will be useful for breeders who want to improve yield and yield-contributing traits of maize.

Key words: Hybrids, heterotic group, line x tester (LxT), maize, yield.

INTRODUCTION

Knowledge on the genetic heterogeneity and progeny performance, are significant for deciding breeding schemes, assigning the parental lines, defining heterotic groups, and predicting future hybrid performance. Thus, information on genetic diversity among genetic materials has an utmost importance for hybrid maize breeding programmes for development of lines, the assigning of lines into different heterotic groups and the preference of testers for hybrid combinations (Xia et al., 2004). Thus, assigning of maize lines into different heterotic group is very vital for hybrid breeding programmes in giving information about the germplasms (Hallauer et al., 2010). Melchinger (1999) proposed that, when a large number of inbred lines is available and proven testers exist, the relative performance of the lines in testcrosses with proven testers can be used as a main criterion for grouping of the lines. Vasal et al. (1992a, b) used this approach to evaluate the performance of testcrosses of 92 tropical and 88 subtropical maize inbred lines with two dent and two flint tester lines. In developing countries, use of available genetic materials and application of available crop improvement methods to improve yield

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and yield stability are required to meet the increasing demand of improved maize hybrids (Dhliwayo et al., 2009; Morris et al., 1999).

Heterotic effects of the maize lines and their allocation into well-known heterotic groups is the secret for the success of a maize breeding programme, which would give utmost exploitation of heterosis. The objective of the study was to: classify the tropical inbred lines into heterotic groups.

MATERIALS AND METHODS

Description of experimental area

The experiment was carried out during 2015/16 offseason using drip irrigation at, West Africa Centre for Crop Improvement Research Field, University of Ghana. The University is located at 5.6508° N, latitude and 0.1869° W longitude and an altitude 97 m above sea level (m.a.s.l).

Genetic materials used for the study

Eighteen white tropical maize inbred lines with diverse genetic backgrounds were selected from the pool of inbred lines at the West Africa Centre for Crop Improvement (WACCI). This comprises of ten lines from the International Institute for Tropical Agriculture (IITA), six from International Maize and Wheat improvement Center (CIMMYT) and the two testers 1368 from IITA and CML 444 from CIMMYT maize breeding programmes. The 16 inbred lines were crossed to the two testers using the line by tester method (Table 1) and it generated 32 (16 x 2) cross combinations.

Experimental design and field evaluation

The 32 F_1 crosses including the hybrids between the two testers, one popular open pollinated variety and a standard hybrid checks were evaluated for their agronomical performance using a 5 x 7 alpha lattice design at WACCI Research Field, the University of Ghana under irrigation system during 2015/2016. The genotypes were planted in two- rows plots, 5 m long with spacing of 0.75 m between rows and 0.5 m spacing between plants within a row. Three seeds were planted per hill, and then thinned to two plants per hill after three weeks of planting, giving 22 plants per row or 44 plants $plot^{-1}$, to get a total plant density of 53333 plants ha^{-1}. The experiment was managed using normal agronomic practices (planting, irrigation, thinning, fertilization, weeding and insect controls) from sowing to maturity.

Data analysis and procedures

Analysis of variance for all agronomic parameters studied was calculated using the PROC GLM procedure and test for significant differences among the genotypes was performed using SAS software (SAS, 2002). Traits that showed significant differences among genotypes were further partitioned into crosses, checks and check vs. crosses using (SAS, 2002). Traits that showed significant differences among crosses were partitioned into three components, namely females in crosses, males in crosses and female x male in crosses (Kempthrone, 1957; Singh and Chaudhary, 1985). The crosses means were adjusted for block effects as analyzed according to lattice design (Singh and Chaudhary, 1985) and used to perform combining ability analysis.

Table 1. List of parents and testers used for the study.

Code no.	Female parents	Male parents	
		1368 (T1)	CML 444 (T2)
L1	TZMI 763	X	X
L2	TZMI746	X	X
L3	TZMI749	X	X
L4	CML15	X	X
L5	CML 24	X	X
L6	TZMI740	X	X
L7	CML16	X	X
L8	TZMI-Unknown	X	X
L9	TZ-STR-133	X	X
L10	TZIL41	X	X
L11	CML10	X	X
L12	9006	X	X
L13	CML 05	X	X
L14	TZIL 39	X	X
L15	CML12	X	X
L16	TZMI760	X	X

RESULTS

Genetic variability of genotypes, crosses, crosses vs check, lines, testers and line x testers and heterotic grouping of tropical white inbred lines are given in Table 2 and Table 3, respectively.

The result showed that genetic variability of GCA for lines were highly significant at $P \leq 0.001$, for days to 50% anthesis and silking, plant height, ear height, plant aspect, ear length, number of kernel rows ear^{-1} and number of kernels row^{-1}. Highly significant differences at $P \leq 0.01$ were detected for anthesis-silking interval, maize streak virus disease, ear rot and grain yield. In addition, significant differences ($P \leq 0.05$) were observed for husk cover.

The mean squares due to GCA for testers were significant $P \leq 0.001$, for days to 50% anthesis and ear length, significant at $P \leq 0.01$ were mean squares for anthesis-silking interval, plant aspect and number of kernel rows ear^{-1}, and significant at $P < 0.05$ were days to 50% silking, plant and ear height. The GCA mean squares for testers were not significant for husk cover, ear rot and number of kernels row^{-1}.

The line x tester (SCA) mean squares showed significant differences at $P \leq 0.001$ for plant height, ear length and number of kernels row^{-1}, and significant differences at $P \leq 0.05$ for days to 50% silking, ear height, number of kernel rows ear^{-1} and grain yield. No significant differences was observed for days to 50% anthesis, anthesis-silking interval, plant aspect, maize streak virus disease score, husk cover and ear rot.

Table 2. Genetic variability of genotypes, crosses, crosses vs check, lines, testers and line x testers for grain yield and yield contributed traits of maize at university of Ghana, WACCI research farm in 2015/16.

Source of variation	DF	MS						
		AD	SD	ASI	MSD	PH	EH	PLASP
Rep	1	2.41*	0.91	0.23	0.32	73.64	10.73	0.13
B(rep)	12	2.97***	2.70***	0.18	0.08	185.38***	75.13*	0.39
Lines (L)	15	7.03***	6.23***	1.10*	0.35**	268.68***	153.84***	1.00***
Testers (T)	1	12.60***	2.11*	4.71**	0.02	199.12*	184.63*	1.91**
L x T	15	0.57	0.94*	0.18	0.16	154.15***	78.38*	0.40

Source of variation	DF	MS					
		HC%	E rot%	EL	NKRE	NKR	Yld (kg ha^{-1})
Rep	1	0.53	1390.45***	2.41	0.06	10.4	219.73
B(rep)	12	30.87	80.53	0.96	1.10	6.36	484481.53*
Lines (L)	15	303.97***	301.19***	7.31***	6.07***	28.1***	958743.06***
Testers (T)	1	0.67	189.95	18.0***	8.05**	5.86	1558855.12**
L x T	15	128.40*	109.63	3.85***	2.39*	25.9 ***	466294.02*

*, ** and ***=Mean squares significant at P ≤ 0.05, P ≤ 0.01 and P ≤ 0.001, respectively. MS= mean squares, DF= degree of freedom, Rep = replications, B(rep) = block within replications, AD = days to anthesis, SD = days to silking, ASI = anthesis- silking interval, MSD = maize streak disease, PH = plant height, EH = ear height, plAsp = plant aspect, HC% = husk cover, RL%= root lodging, SL%= shoot lodging, E rot= number ear rot, EL =ear length, NKRE =number of rows ear-1, NKR =number of kernels row-1 and Yld = grain yield.

Table 3. Heterotic grouping of tropical white inbred lines based on SCA values with two testers: 1368 and CML 444.

Lines	GCA	SCA of grain yield		Heterotic grouping
		1368 (A)	CML444 (B)	
L1	595.33*	-491.32*	491.32*	A
L2	295.72	163.38	-163.38	B
L3	-594.96*	-620.53**	620.53**	A
L4	11.22	-214.33	214.33	A
L5	181.44	108.63	-108.63	B
L6	-522.95*	423.92	-423.92	B
L7	105.30	108.63	-108.63	B
L8	549.73*	-902.78***	902.78***	A
L9	246.73	476.46*	-476.46*	B
L10	- 996.23***	173.86	-173.86	B
L11	- 201.23	-137.35	137.35	A
L12	- 268.84	175.99	-175.99	B
L13	260.87	233.12	-233.12	B
L14	-817.39***	-722.69**	722.69**	A
L15	288.31	322.19	-322.19	B
L16	866.95***	568.98*	-568.98*	B
SE	**223.39**	**223.39**		

Heterotic group A= tester 1368 and heterotic group B = tester CML 444.

Clustering of tropical white maize inbred lines into heterotic groups

Assigning inbred lines into heterotic groups is a vital step in a hybrid-breeding programme, which can provide maximum heterosis exploitation. The relative performance of inbred lines in crosses with divergent testers of known origin has been commonly used to assign maize inbred lines into heterotic groups (Hallauer et al., 1988). Significant GCA and SCA effects for grain yield were detected among the tropical white maize inbred lines. The SCA effect for grain yield was

considered to be a major criterion for classifying the inbred lines. The testers were able to classify 16 of tested inbred lines into two heterotic groups based on SCA effects. Therefore, inbred lines under this study were assigned into two heterotic groups based on SCA effects of mean grain yield (Menkir et al., 2004; Vasal et al., 1992a,b). An inbred line, which had negative SCA effect with tester 1368, was assigned to heterotic group A (1368) whereas, an inbred line which had negative SCA effect with tester CML 444 was assigned to heterotic group B (CML 444). All the inbred lines under study were assigned to two heterotic groups. Among the sixteen tropical white inbred lines, six inbred lines L1, L3, L4, L8, L11 and L14 were grouped into heterotic group A (1368) while ten inbred lines L2, L5, L6, L7, L9, L10, L12, L13, L15 and L16 were grouped into heterotic group B (CML 444). Thus, in order to exploit genetic diversity and then heterosis during hybrid variety development when using these inbred lines, one parent should come from the six inbred lines belonging to tester heterotic group A while the other parent should come from the ten inbred lines belonging to tester heterotic group B. Therefore, inbred lines with same heterotic groups and positive GCA effects can be used in the development of synthetic varieties while those in different heterotic groups can be used in the development of hybrid varieties to maximize on heterosis.

Conclusions

The two testers included in the study separated effectively inbred lines into two heterotic groups. Among sixteen inbred lines included in the study, six were assigned into tester heterotic group 1368, while ten were assigned to tester heterotic group CML 444. This will be useful for developing hybrids and synthetic varieties in future breeding. Breeding programmes can take advantage of this information on combining ability to find best breeding strategy for developing high yielding lines and hybrids.

RECOMMENDATION

Inbred lines assigned into two opposite heterotic groups should be used as parental lines for researchers who want to develop hybrid varieties and inbred lines with same heterotic group with positive GCA should be used for synthetic variety development.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

ACKNOWLEDGEMENTS

The first author is thankful for the scholarship award from Crop Scientist for African Agriculture (SCAA) project for this work to be done. A special thanks to Mr. Amos Rutherford Azinu and the field workers at West African for Crop Improvement Centre for the support rendered during field evaluation.

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