Original Research Article

AJAB

Line × tester analysis across equatorial environments to study combining ability of Indonesian maize inbred

N.N. Andayani[1], M. Aqil[2]*, Roy Efendi[2] and M. Azrai[1]
[1]Department of Plant Breeding, Indonesian Cereals Research Institute, Maros, Indonesia
[2]Department of Agronomy, Indonesian Cereals Research Institute, Maros, Indonesia

Abstract

Selection of optimal combination in hybrid development is crucial to successful breeding program and key determining factor for generating superior variety. Knowledge of gene combination system of maize traits under equatorial environments has not been extensively studied. It is the aim of this study to assess the performance of maize inbred lines across equatorial environments in Indonesia. Twelve test crosses (MAL01 × MYL10, MR14 × MYL10, MAL01 × MYL12, MR14 × MYL12, MAL01 × MYL15, MR14 × MYL15, MAL01 × MYL16, MR14 × MYL16, MAL01 × MYL2, MR14 × MYL2, MAL01 × MYL7 and MR14 × MYL7) and three commercial hybrids (NK 33, DK979 and Bima 11) were investigated for six agronomic components in randomized complete block design across six locations in Indonesia. The results revealed that interaction of crosses versus environment was significant for grain yield, maturity and other agronomic components. The estimates of GCA exhibited that lines MYL10 (L3), MYL15 (L5) and tester MR14 (T2) were a good general combiner, hence MYL10 (L3), MYL15 (L5) and tester MR14 (T2) can be used for generating superior maize hybrid. Combined analysis of SCA effects showed that the crosses MYL 10 (L3) × MR 14 (T2) gave the highest yield of 10.73 t/ha and significantly superior to the best check DK979 (10.17). The hybrid from this cross has to be evaluated in advance to determine the prospect for release as a new commercial hybrid in Indonesia.

Corresponding author email:
acchmad@yahoo.com

Introduction

Recently, Indonesia has made significant advances in hybrid maize research and development. Government and private sector have released new and superior maize hybrid on a continuous basis. In the last 10 years maize production in Indonesia has nearly doubled, but cultivated area averaging 3.6 million ha have changed little (CBS, 2016). Approximately more than 35 hybrids are planted on more than 85% of the total maize area. Hybrid use and a consequent increase of germplasm exploration of maize has been the major driving factor in the maize yield increase recorded in Indonesia in the last two decades.

Among food crops species, hybrid crossing in maize crop has been the most extensively studied. Various methods have been applied to improve the selection of genes controlling the desired agronomic characters. A common approach for assessing the expression of genetic aspects of traits is line × tester analysis (Kempthorne, 1957). Estimation of combining ability can be used to determine the usefulness of the inbred lines in hybrid combinations and to develop superior hybrid adaptable to the wider environments (Sprague and Tatum, 1942).

Information on GCA enabled to explore and distinguish variability among breeding materials, to identify desirable individual genotypes and to describe

the closeness of each inbred (Vacaro et al., 2002). Furthermore, SCA helps in determining the pattern of heterotic group among genotypes, selecting candidates for generating hybrid particularly single cross hybrid and stratifying the heterotic pair among genotypes (Parentoni et al., 2001; Melania and Carena, 2005). Various quantitative estimation of GCA and SCA among maize inbreeds have been performed by many researchers. Application of GCA and SCA will enhance the opportunity for getting best combination among maize populations (Vassal et al., 1992). In addition, the effectivity of SCA parameter for identifying the tolerance of maize inbreds to the MRC (Mal de Rio Cuarto) disease caused by virus has reported in Argentina (Borghi et al., 2012). Study on highland maize top crossed with local East Africa maize population indicated that genetic aspect exhibit more action in regulating agronomic components of maize (Assefa et al, 2017). Furthermore, GCA/SCA based selection would increase the possibility of selecting maize inbreds associated with heat stress tolerance in order to avoid yield losses due to the high temperature and extreme heat waves (Akula et al., 2016). Significant role of GCA for regulating various agronomic components of maize inbreds viz., seed rows per ear, but vice versa for grain yield and seeds per row have been investigated by Dehghanpour and Ehdaie (2013). Viana and Pina (2003) also investigated the greater contribution of dominance effects in regulating agronomic components of white corn genotypes.

Although genetic studies of maize have been widely conducted, little efforts have been made for combined environments of equatorial agro-ecologies such as Indonesia. The objectives of the research were to assess the possibility of generating maize test crosses suitable to the equatorial agro-ecologies of Indonesia and to determine the prospect for releasing a new commercial hybrid to fulfill the increasing demand of hybrid maize variety in Indonesia.

Material and Methods

Plant Materials and Experimental Design

The material for present study were developed at six diverse locations in Indonesia i.e. Bone, Bajeng, Donggala, Konawe Selatan, NTB, and Probolinggo Regency during rainy and dry seasons 2016. Six maize inbred lines i.e. MYL2, MYL7, MYL10, MYL12, MYL15, MYL16 were crossed to two testers MR14 and MAL01 in a line x tester mating design. Site information (Soil type, altitude, and rainfall) is given in Table 1. The tester genotypes were developed at Indonesian Cereals Research Station, Maros. The inbred testers MR 14 and MAL 01 were elite inbred lines with good combining ability. The crosses were evaluated according to the desired criteria of agronomic components and suitability to the tropical agro-ecologies of Indonesia. Three commercial varieties i.e. DK979, NK33 and Bima11 were used as check varieties for evaluating the performance of the test hybrid.

All inbreds along with the commercial check varieties were investigated for six agronomic components in randomized complete block design across six locations in Indonesia. Each genotype was represented by two rows with five meter length at each site. Planting spacing used in the experiment was 70×20 cm with one plant per hill. Fertilizer application in each site were N, P_2O_5 and K_2O with a split dose of 138 kg N ha^{-1} each just before sowing and 30 days after sowing, P_2O_5 and K_2O fertilizers were applied just after sowing with 72 and 64 kg ha^{-1} respectively. Data were collected on six agronomic parameters viz., ear length (cm), ear height (cm), plant height (cm), grain yield (t/ha), ear diameter (cm) and days to silking (days).

Table 1. Experimental sites

Location	Altitude	Soil type	Land type	Rainfall
Bone, South Sulawesi Province	100 masl	Alfisol	Dry land	2485 mm
Bajeng, South Sulawesi Province	49 masl	Ultisol	Irrigated land	2163 mm
Donggala, Central Sulawesi Province	60 masl	Latosol	Rainfed land	1263 mm
Konawe, Southeast Sulawesi Province	80 masl	Alfisol	Rainfed land	1850 mm
Lombok, West Nusatenggara Province	75 masl	Regosol	Rainfed land	1557 mm
Probolinggo, East Java Province	10 masl	Inceptisol	Dry land	1929 mm

The line × tester analysis was performed for all environments by using SAS and AGD-R (Analysis of Genetic Design in R) Version 3.0 (Rodrigues, 2015) softwares. Each of six sites were analyzed twice i.e. analysis for each site and followed by combined analysis. The location effects were treated as random for variance calculation of dependent variable and cross effects treated as fixed (under our control). Line by tester analysis was performed for each environment using the method described by Kempthorne (1957) and Arunachalam (1974). The statistical model used to obtain the different effects was as follows:

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + e_{ijk}$$

Where Y_{ijk} is the performance of the cross between the ith and j^{th} genotypes in the kth replication; μ is the overall mean; g_i and g_j are GCA effects for the ith and j^{th} parents respectively; s_{ij} is the SCA effect for the cross between the ith and j^{th} genotypes; and e_{ijk} is the error term associated with the cross evaluated.

General combining ability (GCA) and specific combining ability (SCA) were computed for characters that showed significant differences among crosses following Line × Tester analysis Kempthorne (1957) and Arunachalam (1974). Estimation of GCA of line and tester and SCA of crosses was performed using the following expression:

$$\text{Lines} = \text{GCA (line)} = g_i = \frac{X_i}{tr} - \frac{X}{ltr}$$
$$\text{Tester} = \text{GCA (line)} = g_j = \frac{X_j}{tr} - \frac{X}{ltr}$$
$$\text{SCA effect} = S_{ij} = \frac{X_{ij}}{r} - \frac{X_i}{tr} - \frac{X_j}{lr} + \frac{X}{ltr}$$

Where x_i is the total of the ith line, x_j is the total of the jth tester; x_{ij} is the crossing of the ith line and jth tester; x is grand total; r is the number of replications, l is number of lines; t is number of tester. The significant of GCA and SCA effects were tested by dividing the corresponding GCA and SCA values by their respective standard error and comparing the obtained t with tabular t-value at error degree of freedom.

The estimate of GCA and SCA for agronomic parameters indicated significant or highly significant differences among six lines, two testers and twelve genotypes (crosses). In order to test the significant effects of lines, testers and crosses, the corresponding GCA and SCA values were divided by the calculated standard error and the resulting values were compared

with tabular t-value at certain degree of freedom (Sprague and Tatum, 1942).

Results and Discussion

Analysis of variances
Combining analysis was carried out according to Kempthorne (19570 at the six locations (Bone, Bajeng, Donggala, Konawe Selatan, NTB, and Probolinggo) on six agronomic parameters including grain yield. Results of pooled analysis of the sites is shown in Table 2. Results indicated that estimated mean squares of lines (L), testers (T) and crosses for the six agronomic parameters (DS, EH, PH, EL, ED and Y) were highly significant. Significant mean square for lines were observed for ear length (3.56*), ear diameter (0.19**), days to silking (3.57**), ear height (460.42**) and yield (3.14**). As for testers, significant values were observed for ear length (111.26**), ear diameter (1.01*), days to silking (24**), ear height (1241.28**) and yield (78.12**). Moreover, mean square for line × tester were observed for ear length (2.65*), ear diameter (0.07**), days to silking (9.82**), ear height (190.79**), plant height (315.12*) and yield (1.59*). The results indicated that pattern of appropriate line combinations may be varying depending on the tester mode. Higher magnitude of the mean squaren of testers indicating greater diversity among the testers and these testers can be pursued for developing maize heterotic groups with high combining ability (Aly et al, 2014; Chandel and Mankotta, 2014; Shiri et al, 2010). Therefore, the choice of appropriate tester is crucial in developing high yielding hybrid maize.

Furthermore, mean squares of genotypes × environment interaction exhibit significant results for ear length (2.12**), ear diameter (0.06**), days to silking (5.18**), ear height (157.09**), plant height (285.55**) and yield (1.45**). This phenomenon indicated that inbred lines performed differently as reflected in their respective test crosses from one environment to another. Although means squares of line × tester × environment interaction indicated non-significant values for grain yield and ear diameter, several agronomic parameters still exhibit significant effect viz., for ear length (1.97**), days to silking (3.89**), ear height (86.91**), and plant height (271.75**). These results are in general agreement with the finding of Chandel and Mankotta (2014) who conducted study on cross evaluation of maize inbreds for generating maize hybrid adaptable to multi

environments. Furthermore, Mosa (2010) suggested that line and/or tester interactions with multi environments affect the agronomic performance of maize inbreds. It indicated that environment may exhibit different response to the the agronomic components during the crossing trials, thus different results may be obtained for each location/environment. Aly (2013) reported that variation of agronomic performance of inbreds were influenced by locations and growing seasons. Thus, phenotypic evaluation may be applied to identify the pavorable inbred combiners.

Mean Performance

Mean estimates of agronomic parameters of the 15 crosses (12 test crosses + 3 check hybrids) crossed over six locations in Indonesia are presented in Table 3. The pooled grain yield (GY) mean ranged from 8.60 to 10.73 t/ha. The coefficient of variance (CV) of six combined locations was 8.40%, comparatively lower than the allowable CV (under 20%). This indicated that consistency/stability of the data across locations is quite measurable. Mean performance analysis indicated that MYL10 (L3) × MR 14 (T2) produce the highest yield of 10.73 t/ha and significantly superior to the hybrids checks i.e. DK 979 (10.17t/ha), NK 33 (9.03 t/ha) and Bima 11 (8.08 t/ha). Results also indicated that MYL10 (L3) × MR 14 (T2) test crosses for ear length and ear diameter were significantly superior to the best check DK 979. As for plant height trait, test crosses ranged from 211.37 cm for test cross MYL15 (L5) × MR 14 (T2) to 229.62 cm for test cross MYL12 (L4) × MAL 01 (T1). Only three test crosses i.e. MYL15 (L5) × MR 14 (T2), MYL10 (L3) × MR 14 (T2) and MYL15 (L5) × MAL 01 (T1) showed lower performance than check variety Bima 11 in plant height. As for ear height (EH), three test crosses i.e. MYL15 (L5) × MR 14 (T2), MYL10 (L3) × MR 14 (T2) and MYL15 (L5) × MAL 01 (T1) were significantly different than the standard check hybrid, NK 33. Ear height is among essential characters for breeding double ear and maize lodging resistance particularly in windy areas. Higher ear position may accelerate the growth of the second ear in the lower nodes. However, too high location of the ear may increase the risks of stalk or break in maize plant particularly during ripening period. Zsubori et al. (2002) reported that although shorter ear position may contribute to the decrease of grain yield, it has an advantage of preventing the plant from stalk due to excessive burden.

Estimation of GCA and SCA components

The GCA values of agronomic components of the 12 crosses evaluated at six different sites are presented in Table 4. Two lines viz., MYL10 (0.278*) and MYL15 (0.342*) indicated significant positive values for yield parameter. The results exhibited that lines MYL10 (L3), MYL15 (L5) and tester MR14 (T2) were a good general combiner, hence MYL10 (L3), MYL15 (L5) and tester MR14 (T2) can be utilized further as additive gene sources to get favorable grain yield (Darrigues et al., 2005). Inbreds MYL2 (L1), MYL 12 (L4) and MAL01 (T1) indicated significant negative values over pooled locations for grain yield (Table 4), suggesting that those lines were unsuitable/poor combiner for developing high yielding maize. Positive and significant GCA values among maize lines are desirable parent for maize hybridization development and involvement in the maize breeding program as they provide good alleles in the process of varietal development (Rawi, 2016).

GCA calculation for days to silking showed MYL 12 (L4) line and MAL 01 (T1) tester were an ideal combiner as these inbreds lines had gene combinations that enhance early maturity. Significant and negative GCA effect is desirable for breeding early maturity maize particularly for short rainy season and dry areas (Pswarayi and Vivek, 2007). High yield and early maturity are also among the most important characteristics for choosing a maize variety in Indonesia (Azrai, 2013). Such early types of varieties are appropriate in area with short rainy season so as to escape the depletion of moisture at stages of crop growth particularly grain filling period or late in the season. Estimates of GCA for plant height and ear height showed MYL 15 (L5) line and MR 14 (T2) were good combiners for both plant and ear heights. Plant and ear heights are among essential agronomic parameters in maize selection breeding. Shorter plant height and medium ear placement is desirable for lodging resistance and mechanized agriculture (Rawi, 2016; Ali et al, 2012).

Calculation of SCA among twelve tests crosses (MAL01 × MYL10, MR14 × MYL10, MAL01× MYL12, MR14 × MYL12, MAL01 × MYL15, MR14 × MYL15, MAL01 × MYL16, MR14 × MYL16, MAL01 × MYL2, MR14 × MYL2, MAL01 × MYL7 and MR14 × MYL7) for the agronomic components across six locations are given in Table 5. Combined analysis of SCA effects showed that most of the test crosses performed non-significantly for the most of the agronomic components. MYL 10 (L3)/ MR 14 (T2)

was the only cross showing significant (positive) SCA value for maize yield parameter, suggesting that MYL 10 line possibly reveal superior heterotic prevalence and give higher grain yield when crossed with MR 14 tester. Contrarily, MYL 10 x MAL 01 was poor combiner with statistically negative significant SCA effect for grain yield. Falconer (1988) reported that excellent GCA value is derived from diverse parents such as pools, population, and composite. On the other hand, excellent SCA is manifested by the tendency to a narrow source of parents during maize crossing.

With respect to days to silking, the crosses MYL 10/MR 14 and MYL 15/MAL 01 showed significant (negative) SCA values. Similar phenomenon was found for the plant height and ear height for MYL 10/MR 14 cross. Moreover, MYL 7/MAL 01 produced significant (positive) SCA value for ear length. The crosses MYL 10/MR 14 was good specific combiner for the plant and ear height, silking days and maize yield. Vacaro et al. (2002) reported that higher SCA values are generally derived from hybrids having at least one parental line with high GCA. The results also indicated that although GCA between inbred and tester is not significantly different, the combination of crossing can produce significant SCA effect. Therefore, in the estimation of SCA effect, the number of location/environment should be taken into consideration. Azrai et al. (2006) reported that testing on larger number of location and season can reduce the subsequent effect of environments/locations on crossing performance. Thus, the combination of crossing with inbred lines having significant SCA or tester with significant GCA should be considered as the best combination in selection intended to improve grain yield of maize.

Estimation of pooled GCA, SCA, dominance and additive variance components is presented in Table 6. Higher σ^2 GCA magnitudes were observed for several agronomic components viz., yield, 1000 seed weight, and ear diameter. This phenomenon suggested that the prevalence of additive gene was comparatively larger than dominance gene in regulating those agronomic components particularly grain yield. Furthermore, higher σ^2 SCA magnitude were observed for silking date, plant and ear heights, and ear length, indicated that dominance effect played a more significant role in regulating the inheritance of those agronomic components. This finding suggest that population improvement is needed through the application of appropriate breeding selection method to produce superior inbreds (Mousa and Aly, 2012; Chandel and Mankotta, 2014 and Joshi et al, 1998).

The proportional contribution of line, tester, and line x tester interaction to the total variances is presented in Table 6. Maize testers played a significant contribution for several agronomic components viz., ear length and maize yield. In addition, the contributions of the lines were found vital for several parameters such as plant height, ear height, diameters, and days to silking. Proportional contribution of line x tester interaction was higher than tester contribution for days of silking parameter.

Table 2. Analysis of variance pooled over environments of all the studied traits.

Source	Df	DS	EH	PH	EL	ED	Y
Site (E)	5	97.26**	5024.81**	14296.62**	30.85**	0.36**	14.44**
Rep(site)	12	3.51**	106.78*	188.29	2.36*	0.07**	1.17*
Crosses (C)	11	12.82**	408.85**	556.93**	12.94**	0.21**	9.25**
Line (L)	5	13.57**	460.42**	555.35**	3.56*	0.19**	3.138**
Tester (T)	1	24**	1241.28**	1773.89**	111.26**	1.01*	78.12**
L x T	5	9.82**	190.79**	315.12*	2.65*	0.07**	1.59*
C x E	55	5.18**	157.09**	285.55**	2.12**	0.06**	1.45**
L x E	25	6.66**	224.4**	261.17**	2.33**	0.07*	1.59**
T x E	5	4.18**	171.38**	476.42**	1.78	0.06**	4.14**
L x T x E	25	3.89**	86.91*	271.75**	1.97*	0.06	0.78
Residuals	132	1.00	51.99	121.16	1.15	0.02	0.62

*, ** Significant at 1 and 5% level of probability, respectively. Df = degree of freedom, DS = days to silking , EH = ear height, PH = plant height, EL = ear length, ED = ear diameter, Y = yield (t/ha).

Table 3. Mean performance of the test crosses and 3- checks for all studied traits combined over the six environments

Crosses	DS	PH	EH	EL	ED	Y
L1/T1	53.89	226.29bc	112.07b	15.28	11.39	8.71c
L2/T1	54.78	223.52	111.69b	15.69	11.36	8.88c
L3/T1	54.89	226.48bc	115.07bc	15.45	11.42	8.73c
L4/T1	52.44	229.62bc	109.38b	15.09	11.07	8.60c
L5/T1	52.89	217.44	101.46	15.98	11.05	9.29c
L6/T1	54.06	219.72	107.44b	15.34	10.17	8.88c
L1/T2	55	223.13	105.72	16.66b	11.74	9.52bc
L2/T2	55.17	220.17	107.27b	16.09	11.84b	10.02bc
L3/T2	54.06	211.64	102.66	17.28b	12.00ab	10.73abc
L4/T2	53.94	220.24	105.07	16.82b	11.4	9.59bc
L5/T2	54.83	211.37	98.52	17.43ab	11.39	10.29bc
L6/T2	53.94	222.13	109.11b	17.17b	11.28	10.15bc
Check						
DK979	57.56	227.91	112.76	16.99	11.52	10.17
NK33	57.89	220.52	103.66	16.23	11.42	9.03
Bima 11	56.11	219.83	110.6	17.1	11.78	8.08
SE	0.24	2.5	1.67	0.26	0.2	0.18
LSI 5%	0.4	4.08	2.72	0.42	0.32	0.3
CV %	1.9	4.8	6.6	6.8	7.4	8.4

a = significantly higher than DK979 variety; b = significantly higher than NK 33 variety; c = significantly higher than Bima 11 variety

Table 4. General combining ability effects of lines and testers for yield and yield components in Maize inbreds.

Genotype	GCA effects						
	DS	PH	EH	EL	ED	TSW	Y
Line							
MYL2 (L1)	0.287	3.73*	1.774	-0.218	0.22	-6.837	-0.336*
MYL7 (L2)	0.815**	0.863	2.36	-0.3	0.259*	-4.02	0.003
MYL10 (L3)	0.315	-1.92	1.744	0.175	0.367**	-10.109	0.278*
MYL12 (L4)	-0.963**	3.952*	0.105	-0.238	-0.11	9.069	-0.352**
MYL15 (L5)	-0.296	-6.57**	-7.131**	0.516**	-0.122	6.633	0.342*
MYL16 (L6)	-0.157	-0.054	1.149	0.066	-0.614	5.263	0.064
SE line	0.167	1.835	1.202	0.179	0.13	5.761	0.132
Tester							
MAL01 (T1)	-0.333**	2.866**	2.397**	-0.718**	-0.266**	-7.497*	-0.601**
MR14 (T2)	0.333**	-2.866**	-2.397**	0.718**	0.266**	7.497*	0.601**
SE tester	0.096	1.059	0.694	0.103	0.075	3.326	0.076

*: significant at 5% level; **: significant at 1% level. DS = days to silking , EH = ear height, PH = plant height, EL = ear length, ED = ear diameter, TSW = 1000-seed weight, Y = yield (t/ha).

Table 5. Specific combining ability effects for yield and yield components traits in maize.

Genotype	SCA effects						
	DS	PH	EH	EL	ED	TSW	Y
L1/T1	-0.222	-1.285	0.778	0.031	0.091	1.622	0.199
L1/T2	0.222	1.285	-0.778	-0.031	-0.091	-1.622	-0.199
L2/T1	0.139	-1.191	-0.186	0.517*	0.026	1.75	0.032
L2/T2	-0.139	1.191	0.186	-0.517*	-0.026	-1.75	-0.032
L3/T1	0.750**	4.554	3.808*	-0.197	-0.025	1.605	-0.399*
L3/T2	-0.750**	-4.554	-3.808*	0.197	0.025	-1.605	0.399*
L4/T1	-0.417	1.826	-0.242	-0.15	0.101	-2.206	0.104
L4/T2	0.417	-1.826	0.242	0.15	-0.101	2.206	-0.104
L5/T1	-0.639**	0.17	-0.928	-0.005	0.097	2.002	0.099
L5/T2	0.639**	-0.17	0.928	0.005	-0.097	-2.002	-0.099
L6/T1	0.389	-4.074	-3.231	-0.197	-0.291	-4.773	-0.035
L6/T2	-0.389	4.074	3.231	0.197	0.291	4.773	0.035
SE	0.3	2.508	1.418	0.214	0.145	5.006	0.134

DS = days to silking , EH = ear height, PH = plant height, EL = ear length, ED = ear diameter, TSW = 1000-seed weight, Y = yield (t/ha). L1 = MYL2, L2 = MYL7, L3 = MYL10, L4 = MYL12, L5 = MYL15, L6 = MYL16; T1 = MAL01, T2 = MR14

Table 5. Estimation of pooled GCA, SCA, dominance and additive variance components and their interaction with environment.

Traits	σ^2 GCA	σ^2 SCA	σ^2 Additive	σ^2 Dominacet	Contribution		
					L (%)	T (%)	L x T (%)
DS	0.014	0.49	0.056	0.49	48.1	17	34.8
PH	1.137	10.776	4.547	10.776	45.3	29	25.7
EH	1.025	7.711	4.1	7.711	51.2	27.6	21.2
EL	0.048	0.084	0.193	0.084	12.5	78.2	9.3
ED	0.015	0.012	0.058	0.012	54.9	35.6	9.5
TSW	9.359	-50.4	37.436	-50.4	45.8	48.4	5.7
Y	0.036	0.054	0.144	0.054	15.4	76.8	7.8

DS = days to silking , EH = ear height, PH = plant height, EL = ear length, ED = ear diameter, TSW = 1000-seed weight, Y = yield (t/ha).

Conclusion

This study demonstrated the combining ability of maize inbreds in diverse equatorial environments in Indonesia. Twelve test crosses were generated through line × tester analysis for each environment, along with three commercial hybrids as check varieties. The estimates of GCA exhibited that lines MYL10 (L3), MYL15 (L5) and tester MR14 (T2) were a good general combiner, hence MYL10 (L3), MYL15 (L5) and tester MR14 (T2) can be pursued for hybrid maize generation. Furthermore, combined analysis of SCA effects showed that the crosses MYL 10 (L3) × MR 14 (T2) exhibited excellent SCA values for maize yield and can be advanced for the release of hybrid variety. MYL 12 (L4) line and MAL 01 (T1) tester was also a good specific combiner for early maturity hybrid as this inbreds visualize combination of genes that enhance early maturing maize.

Acknowledgment

References

Akula D, Patil A, Zaidi PH, Kuchanur PH, Vinayan MT and Seetharam K, 2016. Line x testers analysis of tropical maize inbred lines under heat stress for grain yield and secondary traits. Maydica. 61:1-4.

Ali Q, Ali A, Awan MF, Tariq M, Ali S, Samiullah TR and Hussain T, 2014. Combining ability analysis for various physiological, grain yield and quality traits of *Zea mays* L. Life. Sci. J. 11(8): 540-551.

Assefa T, Zeleke H, Afriye T and Otyama P, 2017. Line x tester analysis of tropical high land maize (*Zea mays* L.) inbred lines top crossed with three East African maize populations. Amer. J. Plant Sci. 8:126-136.

Azrai M, Mejaya MJ and Aswidinnoor H, 2013. Combining ability of QPM maize. J. Food Crops Res. 33(3): 137-147.

Borghi ML, Ibanez MA, Bonamico NC, Kandus MV, Gomar DA, Guilin EA, Salemo JC and Renzo MAD, 2012. Combining ability of flint corn inbred lines: Mal de Rio Cuarto disease tolerance and grain yield. J. Exp. Bor. 81:123-131.

CBS, 2016. Indonesian agricultural statistic update 2016/2017. Statistical book, Jakarta Indonesia.

Chandel U and Mankotta BS, 2014. Combining ability in tropical and CIMMYT inbred lines of maize for grain yield and yield components using line x tester analysis. Sabrao J. Breed. Gen. 46(2):256-264.

Darrigues A, Buffard G, Lamkey KR and Scott MP, 2005. Variability and genetic effects for tryptophan and methionine in commercial maize germplasm. Maydica. 50: 147-156.

Dehghanpour Z and Ehdaie B, 2013. Stability of general and specific combining ability effects for grain yield in elite Iranian maize inbred lines. J. Crop. Impr. 27(2): 137-152.

Falconer DS and Mackan TEC, 1998. Introduction to quantitative genetics. 4th ed. Longman group Ltd. Essex, England.

Kempthorne O, 1957. An introduction to genetics statistics, 1st ed, John Wiley and sons, New York.

Melania MD and Carena MJ, 2005. Alternative maize heterotic patterns for the northern corn belt. Crop Sci. 45: 2186-2194.

Mosa HE, 2010. Estimation of combining ability of maize inbred lines using top crosses mating design. J. Agric. Res. 36:1-15

Mousa STM and Aly RSH, 2012. Estimation of combining ability effects of new white maize inbred lines (*Zea mays* L.) via line x tester analysis. Egy. J. Agric. Res. 90(4): 77-90.

Parentoni SN, Magalhaes JV, Pacheco CAP, Santos MX, Abadie T, Gamap EEG, Guimares EO, Weirelles MF, Lopes MA, Vvasconcelos MJV and Paiva E, 2001. Heterotic groupings based on yield-specific combining ability data and phylogenetic relationship determined by rapid markers for 28 tropical maize open pollinated varieties. Euphytica. 121: 197-208.

Pswarayi A and Vivek BS, 2007. Combining ability amongst CIMMYT's early maturing maize (*Zea mays* L.) germplasm under stress and non-stress conditions and identification of testers. Eupytica. 162:353-362.

Rawi, 2016. Relative performance and combining ability for yield and yield components in maize by using full dialel cross. Int. J. Current Res. 8(09): 37721-37728.

Revilla P, Malvar RA, Carea ME, Soengas P and Ordas A, 2002. Heterotic relationships among European maize inbreds. Euphytica. 126: 259-264.

Shiri M, Aliyev RT and Choukan R, 2010. Water stress effects on combining ability and gene action of yield and genetic properties of drought tolerance indices in maize. Res. J. Environ. Sci. 4: 75-84.

Sprague, GF and Tatum L A, 1942. General vs specific combining ability in single crosses of corn. J. Amer. Soc. Agron. 34(9): 23-32

Vacaro E, Neto JFB, Pegoraro DG, Nuss CN and Conceicao LD, 2002. Combining ability of twelve maize populations. Agropec. Bras. Brasilia. 37(1): 67-72.

Vassal S, Srinivasan G, Pandey S, Cordova HS, Han GC and Gonzales F, 1992. Heterotic patterns of ninety two white tropical CIMMYT maize lines. Maydica 37:259-270.

Viana JMS and Matta FDP, 2003. Analysis of general and specific combining abilities of popcorn populations including selfed parents. Genet. Mol. Biol. 26:465–471.

Zsubori Z, Gyenes-Hegyi Z, Ille´s O, Po´k I, Ra´cz F and Szoke C, 2002. Inheritance of plant and ear height in maize (Zea mays L.). J. Agric. Sci. Univer. Debrecen. 8:34–38.