



# Asian Journal of Crop Science

ISSN 1994-7879

**science**  
alert  
<http://www.scialert.net>

**ANSI***net*  
an open access publisher  
<http://ansinet.com>

## GGE Biplot Analysis for Combining Ability of Grain Yield and Early Maturity in Maize Mutant in Indonesia

<sup>1</sup>D. Ruswandi, <sup>1</sup>J. Supriatna, <sup>2</sup>B. Waluyo, <sup>3</sup>A.T. Makkulawu, <sup>4</sup>E. Suryadi, <sup>5</sup>Z.U. Chindy and <sup>1</sup>S. Ruswandi

<sup>1</sup>Faculty of Agriculture, Padjadjaran University, Bandung, 40600, Indonesia

<sup>2</sup>Faculty of Agriculture, Brawijaya University, Bandung, 40600, Indonesia

<sup>3</sup>Indonesian Cereals Research Institute, Maros, Bandung, 40600, Indonesia

<sup>4</sup>Faculty of Agriculture Engineering, Padjadjaran University, Bandung, 40600, Indonesia

<sup>5</sup>School of Life Sciences and Technology, Institute of Technology Bandung, Jl. Ganesha 10, Bandung 40132, Indonesia

*Corresponding Author: D. Ruswandi, Faculty of Agriculture, Padjadjaran University, Bandung, 40600, Indonesia*

### ABSTRACT

Determination of combining abilities and heterotic groupings of parental lines is very important in selecting the mutant lines and to decide breeding strategies for maize hybrid production. Fourty six new mutant lines used in maize breeding programs in Indonesia, were crossed to three tester lines in a lines×testers mating design. The 138 F1 hybrids, the 46 parental lines and 3 tester lines were evaluated at Arjasari, West Java, Indonesia for the following objectives: (i) to analyze line×tester data for maturity and grain yield using GGE for identifying genetic inter-relationships among parents and (ii) to identify the best combinations for maturity and grain yield in maize hybrids. The GGE biplot graphic allowed a rapid and effective overview of General Combining Ability (GCA) and Specific Combining Ability (SCA) effects of the inbred lines, best lines and tester, as well as their performance in crosses. High GCA effect for maturity and grain yield was determined based on Average Tester Coordination function of GGE Biplot. Thus, it was revealed that DR 4 is the best tester for early maturity and DR 6 for grain yield. The maximum best-parent heterosis values and the highest SCA effects resulted from mutants (10, 31, 32, 34, 36, 48) and mutants (5, 7, 10, 32, 34, 36, 37 and 48) crosses to testers (4, 6 and 8) for early maturity and grain yield, respectively. This is potentially useful in maize breeding programs to obtain high-yielding hybrids in areas with the same climate of Indonesia.

**Key words:** Early maturity, general combining ability, GGE biplot analysis, line×tester, maize, mutant, specific combining ability, yield

### INTRODUCTION

Improvement of new inbred lines adapted to global climate change is important stage in breeding program to sustain maize production in Indonesia. Ruswandi *et al.* (2014) developed new mutant lines for breeding program of maize in Indonesia using gamma irradiation. They reported some maize mutant lines showing early maturity and also drought tolerance. Furthermore, they identified some potential mutant lines and their cross combination for yield and yield component (Ruswandi *et al.*, 2015).

Information on combining abilities, including General Combining Ability (GCA) and Specific Combining Ability (SCA) are important indicators in assessing inbred lines in hybrid combinations as the step to develop hybrid varieties in maize (Abdel-Moneam *et al.*, 2014; Hallauer, 1990). Differences in GCA effects is attributed to additive and epistatic genetic effects in the base population, while differences in SCA effects is attributed to non-additive genetic variance, including dominance and epistatic genetic effects (Falconer, 1981). Diallel and line×tester analysis, provide an adequate information on the genetic identity of genotype especially on dominance-recessive relations and various types of gene effects (Singh and Chaudhary, 1977). These methods could be used to determine the inheritance of agronomically important trait among a set of genotypes and to estimate combining abilities to make decision whether to include it in hybrid or cultivar development (Singh and Chaudhary, 1977; Yan and Kang, 2003; Bocanski *et al.*, 2011). Even though diallel analysis have been used in breeding programs, they are very labor-intensive, especially when the number of genotypes to be evaluated is increased (Fotokian and Agahi, 2014). Therefore, previously, Kempthorne (1957) suggested the use of line×tester for a faster and more reliable method in estimating combining ability and selecting lines for hybrid development by crossing it to broad genetic base tester.

Now a days, line×tester analysis is used extensively to analyze combining ability and selecting large number of lines for hybrid formation (Legesse *et al.*, 2009; Rahman *et al.*, 2013; Izhar and Chakraborty, 2013; Kamara *et al.*, 2014; Ruswandi *et al.*, 2015). Akaogu *et al.* (2012) classified 39 extra-early yellow-grained inbreds into 3 heterotic groups under drought stress, Striga infestation, optimal conditions and across research environments based on line×tester analysis using three testers. Ruswandi *et al.* (2015) reported significant GCA and SCA mean square for grain yield and more other trait on maize mutant lines base on line×tester using combination of 46 mutant lines and 3 testers.

Some methods are available to analyze diallel crosses, such as the most popular method of Griffing. Griffing (1956) partitions the total variance to GCA variance of parents and SCA variance of crosses. Yan and Hunt (2002) suggested a new approach of the principal component biplot technique for diallel analysis. This technique enhances the capability of interpreting the phenotypic variation to obtain combining ability and inter-relationships of parents based on graphical presentation using PC1 and PC2, which are derived through PC analysis of environment-centered yield data. Thus, combining ability analysis using GGE biplot is needed to visualize the GCA of each genotype, the SCA of each genotype, groups of parents with similar genetics and superior hybrids. Similar with multilocation trials, the first two components can be used to visualize GCA and SCA effects (Bertoia *et al.*, 2006). Even though GGE biplot analysis of diallel data is widely used to determine combining ability and heterotic responses in many crops for many traits, such as in wheat (Dehghani *et al.*, 2013; Malla *et al.*, 2010), melon (Dehghani *et al.*, 2012), linum (Rastogi *et al.*, 2011), opium (Rastogi *et al.*, 2013), cotton (Hamoud, 2014) and maize (Mostafavi *et al.*, 2012; Duarte and Pinto, 2002; Badu-Apraku *et al.*, 2010; Sibiya *et al.*, 2013; Badu-Apraku *et al.*, 2013; Njoroge and Gichuru, 2013). This method is rarely reported for line×tester data analysis. Fotokian and Agahi (2014) reported that identification of suitable parents, heterotic crosses and the best hybrids in line×tester data can be analyzed using GGE biplot.

The objectives of the present research were: (1) To analyze line×tester data for maturity and grain yield using GGE for identifying genetic interrelationships among parents and (2) To identify the best combinations for maturity and grain yield in maize hybrids.

## MATERIALS AND METHODS

**Genetic materials:** The genetic materials were evaluated in the study included forty six mutant lines; one hundred and thirty eight single cross hybrids derived from line×tester crosses of forty six mutant lines to three tester lines and three tester lines. The forty six mutant lines and three tester lines were developed previously by Ruswandi *et al.* (2014). Crosses were made during 2013 and the evaluation of genotypes in experimental trials were performed during the rainy season of 2014 at the experimental plots of Faculty of Agriculture, Padjadjaran University, in Arjasari, Bandung, West Java, Indonesia.

**Field evaluation:** The evaluation of genotypes was laid out on a completely random block design (Petersen, 1994), with two replicates and one hundred and seventy eight genotypes as treatment. The genetic materials were planted in experimental plot consist of single rows, 5 m long, with 0.75 m between rows and between plots and 0.20 m within rows. The variable gathered were grain yield and early maturity traits. The grain yield per plant was measured on fifteen randomly chosen competitive plants in each replication. The early maturity trait was measured on days to tasseling (dap) and days to harvest (dap). Analysis of variance for line×tester was done following Singh and Chaudhary (1977), where mutant lines, tester lines and hybrids were treated as fixed factor. Line×tester method was applied to estimate GCA and SCA. The significance of hybrids, GCA and SCA mean squares were estimated using F-test.

The concept of GGE originates from analysis of multi-environment trials of crop cultivars. The yield or any other measure of cultivar performance in an environment is the mixed effect of genotype main effect (G), environmental main effect (E) and genotype×environment interaction (GE). To extend the application of GGE biplot to the other types of two-way data with similar data structure, the cultivars were generalized as entries and environments as testers (Yan, 2001). When GGE biplot was used for line×tester cross analysis, the average yield and genotype stability corresponded to GCA and SCA of parents, respectively. Inconventional line×tester analysis SCA relates to a cross, not parental lines. GGE biplot analysis is expressed as:

$$Y_{ij}-b_j = a_1e_{i1}h_{j1}+a_2e_{i2}h_{j2}+e_{ij}$$

where,  $Y_{ij}$  is genotypic values of the combination (pure inbred lines or F1 hybrids) between inbred  $i$  and tester  $j$  for a given trait;  $b_j$  average value of all combinations with tester  $j$ ,  $a_1$  and  $a_2$  are singular values for PC1 and PC2.  $e_{i1}$  and  $e_{i2}$  are PC1 and PC2 eigenvectors for inbred  $i$  (entry), respectively;  $h_{j1}$  and  $h_{j2}$  are PC1 and PC2 eigenvectors for tester  $j$ , respectively;  $e_{ij}$  is the residual of model for inbred  $i$  and tester  $j$ . In line×tester crosses, a parent was an entry. This analysis was done using GGE biplot software (Yan, 2001).

## RESULTS AND DISCUSSION

### Genetic inter-relationships among parents based on GGE biplot model

**GCA of the mutant lines:** Figure 1 is the Average Tester Coordination (ATC) view of the biplot brought up by the Average Tester Coordination function of GGE biplot for days to tasseling, days to harvest and grain yield per plant, respectively. The arrow represents an average tester, which is defined by the average PC1 and PC2 values of all testers. According to Yan and Kang (2003), the line passing through the biplot origin and the average tester, with an arrow pointing to the average tester, is called the average tester axis or ATC abscissa and the line that passes through the origin and is perpendicular to the average tester axis is called average tester ordinate or ATC ordinate.



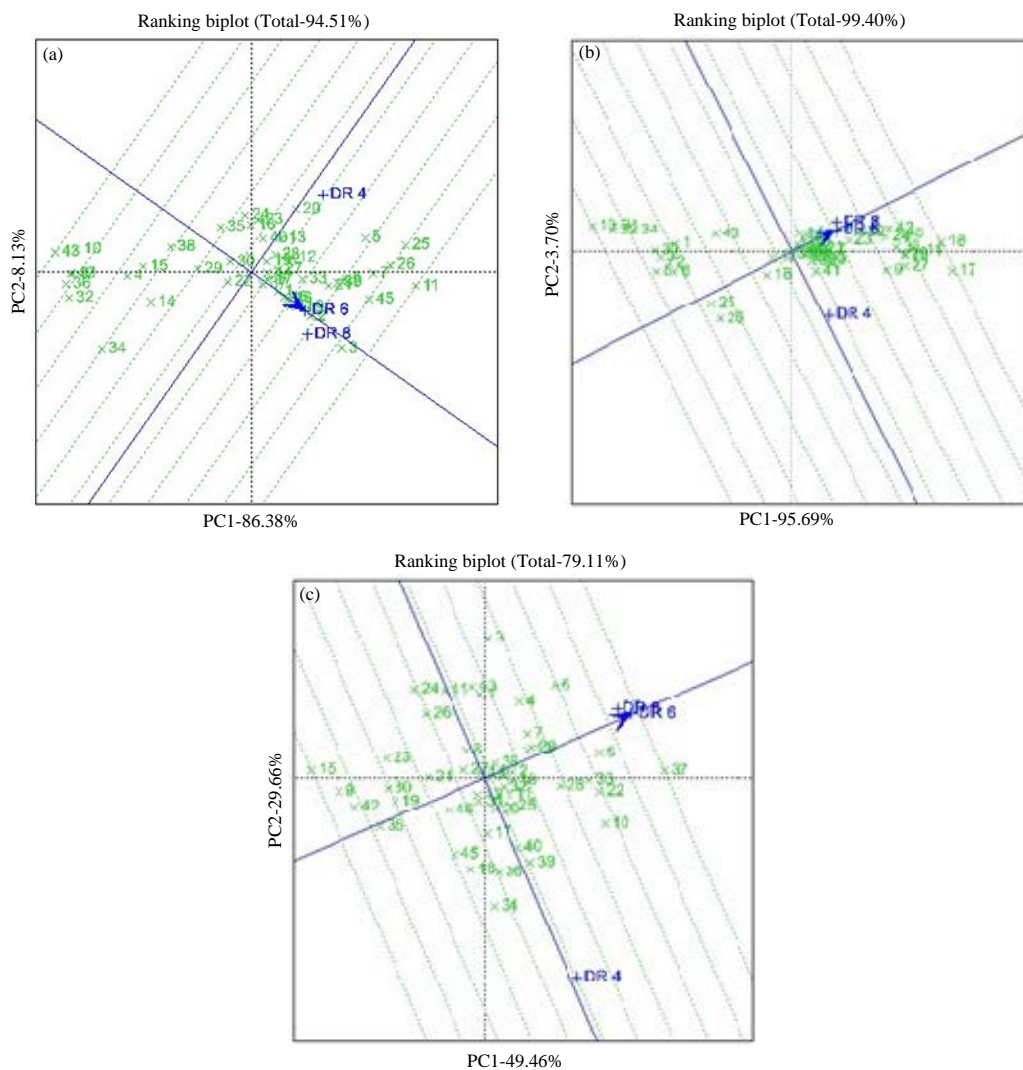


Fig. 1(a-c): Average Tester Coordination (ATC) view of the biplot based on line×tester. The arrow represents the average tester. Lines are in number code and three testers are in code DR 4, 6 and 8, (a) Days to tasseling, (b) Days to harvest and (c) Grain yield per plant

GCA and SCA are defined as properties of the entries. The GCA effects of the entries were approximated by their projections onto the ATC abscissa. Lines parallel to the ATC ordinate help rank entries relative to GCA effects. Inbred lines near the arrow will be able to combine well with all tester lines. Thus, mutant line No. 2 (M 5 DR1.2.3) and No. 9 (M 5 DR 4.1.3), mutant line derived from DR No. 1 and No. 4 parental line had the highest GCA effect for days to tasseling and good combiner if they are crossed to all tester lines, whereas mutant lines No. 10 and 43 had the lowest GCA effect. The GCA effects of the mutant lines are in the order of: 9~2~30~5>7>33~16>1~12~27~17~44~38>3~45~26~25>11>20~13~40~19~33~16~22~30>29~35~24>34~38>4~15>32~36~42> 10~43.

Mutant line No. 8 (M 5 DR 3.6.2) had the highest GCA effect for days to harvest and good combiner if they are crossed to all tester lines, whereas mutant lines No. 31, 32 and 10 had the

lowest GCA effect. The GCA effects of the mutant lines are in the order of: 8>23>7~29~19~37~12~14~21~15~33~44~38~41~40~20~46~35~13~18>43>26~25~1>2~6~30~34~3~5>31~32~10.

Mutant line No. 37 had the highest GCA effect for grain yield per plant and good combiner if they are crossed to all tester lines, whereas mutant lines No. 42, 9 and 15 had the lowest GCA effect. The GCA effects of the mutant lines are in the order of: 37>5>6~33~22~10>3~4~7~29~13~28>43~1~38~2~32~25~11~14~18~39~44>24~26~41~8~27~12~17~36~20~31~40>21~46~45~16~34>23~19>30~35>42~9~15.

**Best crosses between the lines and the testers:** The polygon of a biplot provides the best way to interpret the results based on interaction of genotype tester by Yan and Kang (2003). This polygon is drawn by connecting the entries furthest from the origin such that all other entries remain within the polygon. From the plot's origin, lines perpendicular to each side of the polygon are drawn; this divides the biplot into several sectors. Testers falling in the same sector share the same best-mating partner and this would be the entry at the vertex of the polygon in that sector. This entry has the highest distance from origin among other entry in this sector (Yan, 2001; Yan and Hunt, 2002). The value of the hybrid between an entry and a tester is visualized by measuring the perpendicular distance between the vector of the tester and the entry's marker position where, a vector of a tester is the line from the biplot origin towards the marker of the tester. The entries located on the vertex of polygon are the best-mating partners with the same sector's testers and the poorest-mating partners with other sector's testers. Entries located near the biplot origin are less responsive to the change of testers. The polygon view of the biplot for days to tasseling is presented in Fig. 2a. The biplot was divided into seven sectors, with entries 34, 32, 48, 20, 25, 11 and 3 as the vertex entries and are referred to as 34, 32, 48, 20, 25, 11 and sector 3, respectively. No tester fell in the 34, 32 and 48 sectors, respectively, suggesting that mutant 34, 32 and 48 were not the best mating partner with any of the three tester (4, 6 and DR 8) lines for medium to late days to tasseling. However, this suggests that mutant 34, 32 and 48 produced the earliest days to tasseling when they were mated with some or all of the testers. For example, mutant 34 (M 5 DR 16.2.1) were early days to tasseling when crossed to DR 4. Similar results were also shown by the following mutant when they were mated to tester DR 6 and DR 8. Those mutants were mutants 43 (M 5 BR 153.6.1), 10 (M 5 DR 4.8.8), 32 (M 5 DR 14.3.8) and 36 (M 5 DR 18.3.1). Furthermore, mutant 43 was line with the earliest days to tasseling line when it is mated with either 6 or 8 tester. The previous study by Ruswandi *et al.* (2015) did show that parent 34, 32 and 48 per se were early days to tasseling and it produced the earliest days to tasseling hybrids with DR 4, DR 6 and DR 8 (Table 1), which is consistent with the prediction from Fig. 2a.

The polygon view of the biplot for days to harvesting is presented in Fig. 2b. The biplot was divided into five sectors, with mutant 26, 10, 42, 16 and 17 as the vertex entries and are referred to as 26, 10, 42, 16 and sector 17, respectively. No tester fell in the 26, 10 and 42 sectors, respectively, suggesting that mutants fell in the 26, 10 and 42 sectors were not the best mating partner with any of the three tester (DR 4, 6 and 8) for making hybrid with medium to late days to harvesting. Based on this sector division, the selected mutants to cross to three testers for making hybrid with early days to harvesting were mutants 10 (M 5 DR 4.8.8), 31 (M 5 DR 14.3.1), 32 (M 5 DR 14.3.8) and 34 (M 5 DR 16.2.1). Mutant 10 (M 5 DR 4.8.8) was the best mutant to form earliest maturity hybrid with the three testers.

The polygon view of the biplot for grain yield is presented in Fig. 2c. The biplot was divided into four sectors, with mutant 15, 3, 37 and 34 as the vertex entries and are referred to as sector 15,

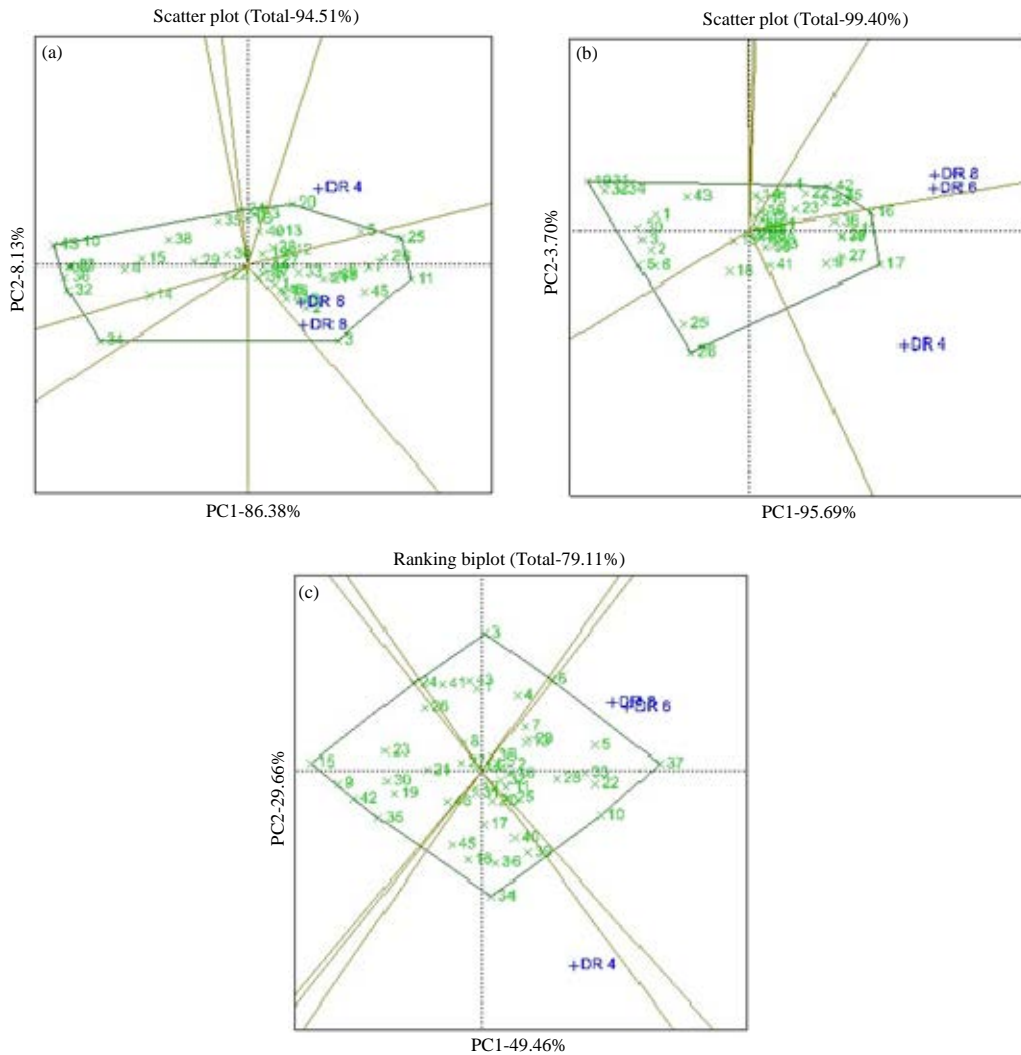


Fig. 2(a-c): Scatter plot. The arrow represents the average tester. Lines are in number code and three testers are in code DR 4, 6 and 8, (a) Days to tasseling, (b) Days to harvest and (c) Grain yield per plant

sector 3, sector 37 and sector 34, respectively. No tester fell in the 15 and 3 sectors, respectively, suggesting that mutants fell in the 15 and 3 sectors were not the best mating partner with any of the three tester (DR 4, 6 and 8) for making hybrid with high grain yield. Based on this sector division, the selected mutants to cross to three testers for making hybrid with high grain yield were mutants 34 (M 5 DR 16.2.1), 36 (M 5 DR 18.3.1), 16 (M 5 DR 7.4.1) and 39 (M 5 BR 153.1.2). Mutant 34 (M 5 DR 16.2.1) was the best mutant to form high grain yield hybrid with tester DR 4, whereas, mutants 37 (M 5 DR 18.4.1), 22 (M 5 DR 9.1.3), 5 (M 5 DR 3.1.2), 33 (M 5 DR 16.1.1), 32 (M 5 DR 14.3.8) and 10 (M 5 DR 4.8.8) were fit to form high yield hybrid with tester DR 6 and 8. Furthermore, mutant 37 (M 5 DR 18.4.1) was the best mutant to form highest yield hybrid when it was crossed to DR 6 and 8.

Table 1: Means, GCA effects of parents and SCA effects of 138 test crosses with three testers for days to tasseling

No.	Mutants	Parent		DR 4		DR 6		DR 8	
		mean	GCA	Days to tasseling	SCA	Days to tasseling	SCA	Days to tasseling	SCA
1	M 5 DR 1.1.3	63.34	0.22	61.00	-0.68	64.84	0.91	64.84	-0.23
2	M 5 DR 1.2.3	63.17	1.10*	61.17	-0.08	64.83	0.02	66.00	0.06
3	M 5 DR 1.2.12	62.00	1.55**	61.17	-0.53	65.17	-0.09	67.00	0.61
4	M 5 DR 1.6.3	60.00	-1.40**	59.00	-0.08	62.84	0.53	63.00	-0.44
5	M 5 DR 3.1.2	63.34	1.60**	63.34	1.42	64.34	-0.97	66.00	-0.44
6	M 5 DR 3.1.4	63.67	1.49**	62.33	0.69	64.84	-0.36	66.00	-0.33
7	M 5 DR 3.6.1	63.50	1.71**	62.83	0.64	65.00	-0.42	66.34	-0.22
8	M 5 DR 3.6.2	64.00	1.38**	62.34	0.47	64.50	-0.59	66.34	0.11
9	M 5 DR 4.1.3	63.34	0.99*	61.34	0.03	64.34	-0.36	66.17	0.33
10	M 5 DR 4.8.8	60.50	-1.90**	58.84	0.92	60.84	-0.97	63.00	0.06
11	M 5 DR 5.5.1	66.00	2.49**	63.34	1.03	65.17	-1.03	67.34	0.00
12	M 5 DR 7.1.2	62.34	0.88*	61.84	1.14	64.17	-0.42	65.00	-0.72
13	M 5 DR 7.1.9	62.67	0.33	62.00	0.69	63.84	-0.20	64.67	-0.50
14	M 5 DR 7.3.1	60.67	-0.95*	59.00	-0.19	62.84	0.08	64.00	0.11
15	M 5 DR 7.3.2	61.50	-1.12*	59.50	0.47	62.17	-0.42	63.67	-0.06
16	M 5 DR 7.4.1	63.00	0.77	61.17	0.25	64.00	-0.47	65.84	0.22
17	M 5 DR 7.4.2	63.00	0.55	61.17	0.64	63.67	-0.59	65.34	-0.05
18	M 5 DR 8.5.2	61.67	0.16	61.67	1.20	64.00	0.14	63.67	-1.33
19	M 5 DR 8.5.3	62.00	-0.01	61.50	0.03	63.17	-0.53	65.34	0.50
20	M 5 DR 8.6.3	62.84	0.27	62.84	1.09	62.67	-1.31	65.34	0.22
21	M 5 DR 8.8.1	61.17	0.83	62.00	-0.30	64.34	-0.19	66.17	0.50
22	M 5 DR 9.1.3	63.00	-0.45	60.50	-0.53	63.50	0.25	64.67	0.28
23	M 5 DR 9.1.5	62.17	-0.06	62.00	0.58	63.00	-0.64	64.50	0.06
24	M 5 DR 9.4.1	62.67	-0.41	61.83	0.76	63.17	-0.33	64.00	-0.43
25	M 5 DR 10.2.2	65.00	1.77**	63.67	0.42	66.00	0.53	65.67	-0.94
26	M 5 DR 10.2.9	65.00	1.60**	63.17	0.08	65.67	0.36	66.00	-0.44
27	M 5 DR 12.3.1	63.34	0.16	61.50	-0.14	63.67	-0.19	65.34	0.33
28	M 5 DR 12.3.2	63.17	0.10	61.67	0.09	63.67	-0.14	65.00	0.06
29	M 5 DR 14.1.1	62.00	-0.84	60.17	-0.47	63.67	0.80	63.67	-0.33
30	M 5 DR 14.2.2	63.17	-0.45	60.84	-0.19	63.50	0.25	64.34	-0.06
31	M 5 DR 14.3.1	59.00	-2.45**	58.33	-0.70	61.34	0.08	63.00	0.61
32	M 5 DR 14.3.8	60.17	-2.45**	57.84	-1.19	61.84	0.58	63.00	0.61
33	M 5 DR 16.1.1	63.00	0.49	61.67	-0.31	64.34	0.14	65.50	0.17
34	M 5 DR 16.2.1	61.00	-1.95**	57.50	-2.03**	62.67	0.91	64.00	1.11
35	M 5 DR 18.2.1	62.17	-0.62	61.17	0.31	63.67	0.58	63.34	-0.89
36	M 5 DR 18.3.1	60.67	-2.51**	58.00	-0.97	61.84	0.64	62.67	0.33
37	M 5 DR 18.4.1	61.50	-0.01	61.00	-0.47	63.84	0.14	65.17	0.33
38	M 5 DR 18.8.1	60.67	-1.23**	60.17	-0.08	62.83	0.36	63.34	-0.28
39	M 5 BR 153.1.2	64.00	0.94*	62.17	-0.25	64.50	-0.14	66.17	0.39
40	M 5 BR 153.2.2	64.00	-0.06	61.67	0.25	64.00	0.36	64.17	-0.61
41	M 5 BR 153.3.2	62.50	0.38	61.00	-0.86	64.67	0.58	65.50	0.28
42	M 5 BR 153.4.1	60.00	-2.45**	58.17	-0.86	62.34	1.08	62.17	-0.22
43	M 5 BR 153.6.1	60.34	-2.17**	58.50	-0.80	60.34	0.47	63.00	0.33
44	M 5 BR 153.7.1	63.17	0.05	61.17	-0.36	64.34	0.58	64.67	-0.22
45	M 5 BR 153.10.2	65.50	1.38**	62.34	-0.53	65.34	0.25	66.50	0.28
46	M 5 BR 153.13.1	61.67	0.27	61.17	-0.58	63.67	-0.31	66.00	0.89
47	DR 4	63.84	-1.86**						
48	DR 6	64.50	0.36**						
49	DR 8	62.84	1.50**						

\*, \*\*Significant at the 0.5, 0.01 probability level

**Best testers for assessing GCA of the lines:** Yang and Kang (2003) mentioned that an ideal tester for revealing the GCA effects of entries should fulfill two criteria, including representation of all testers and discrimination of the entries. Therefore, an ideal tester must be located on the ATC axis to be representative of all testers; its vector should be the longest of all testers to be most



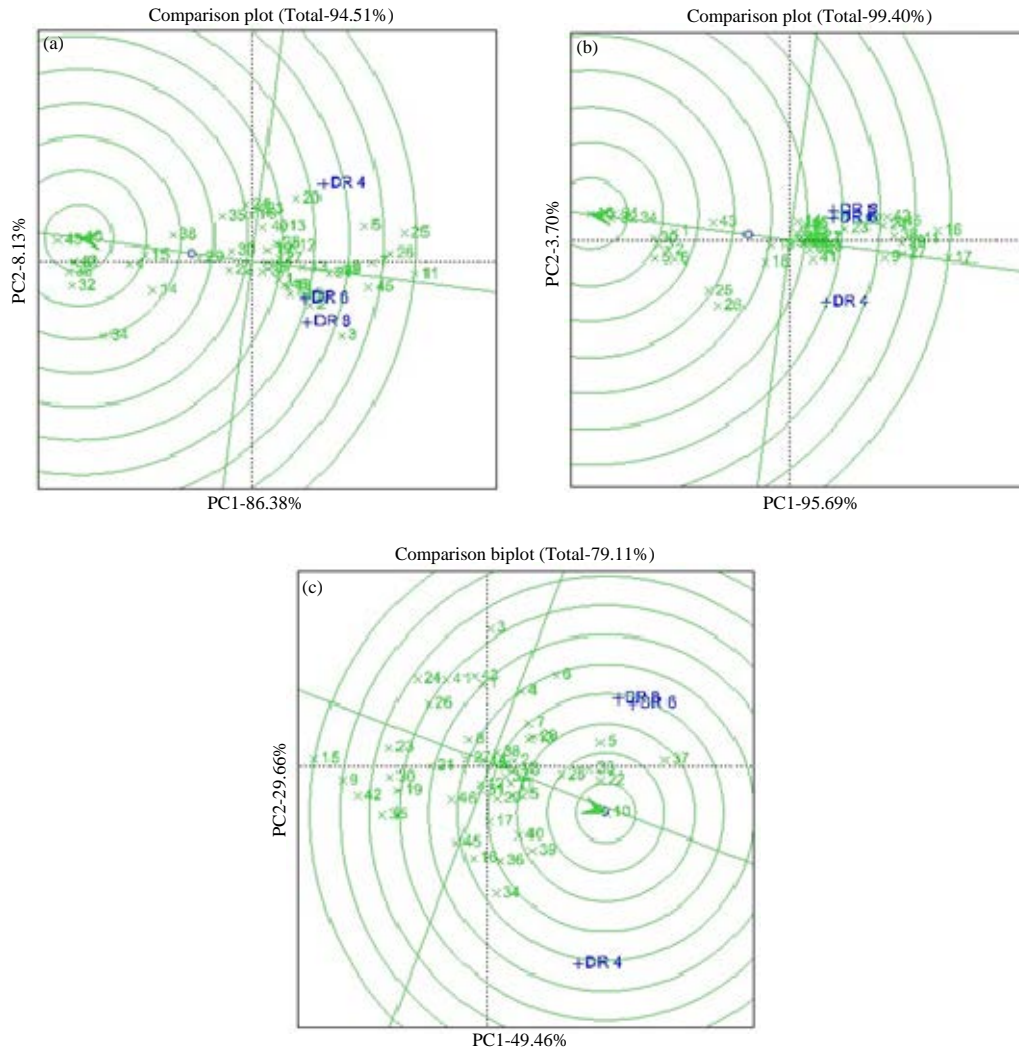


Fig. 3(a-c): Comparison plot for genotype. The arrow represents the average tester. Lines are in number code and three testers are in code DR 4, 6 and 8, (a) Days to tasseling, (b) Days to harvest and (c) Grain yield per plant

discriminating. Such tester is indicated by the center of the concentric circles. The concentric circles are drawn for this purpose with the hypothesized ideal tester at the center (Fig. 3a-c and 4a-c). The closer a line/tester is to this ideal center, the more desirable it is. This condition is fit for grain yield and other yield components, whereas for early maturity components such as early days to tasseling and early days to harvesting the contrast condition will be fit to identify the ideal tester. For early days to tasseling, based on the comparison plot as presented on Fig. 3a, mutant 11 (M 5 DR 5.5.1) is the best line to form early maturing hybrids by crossing to tester DR 4, 6 and 8; whereas DR 4 is the best tester form early maturing hybrids (Fig. 3b). For early days to harvesting, mutant 17 (M 5 DR 7.4.2) is the best line to form early maturing hybrids by crossing to tester DR 4, 6 and 8 (Fig. 3c); whereas DR 4 is the best tester to form early maturing hybrids (Fig. 4a). For grain yield, mutant 10 (M 5 DR 4.8.8) is the best line to form highest grain yield hybrids by crossing to tester DR 4, 6 and 8 (Fig. 4b); whereas DR 6 is the best tester to form high yield hybrids (Fig. 4c).

Table 2: Means, GCA effects of parents and SCA effects of 138 test crosses with three testers for days to harvest

No.	Mutants	Parent mean	GCA	DR 4		DR 6		DR 8	
				Days to harvest	SCA	Days to harvest	SCA	Days to harvest	SCA
1	M 5 DR 1.1.3	93.17	0.39	92.50	-0.38	96.00	0.77	97.00	-0.39
2	M 5 DR 1.2.3	93.83	0.83*	93.34	-0.66	95.67	0.33	96.00	0.33
3	M 5 DR 1.2.12	97.00	1.28**	92.67	-1.10	95.67	0.22	95.50	0.88
4	M 5 DR 1.6.3	100.67	-1.55**	97.00	-0.44	102.34	0.72	104.34	-0.28
5	M 5 DR 3.1.2	91.17	1.39**	93.33	0.95	95.00	-0.72	95.17	-0.23
6	M 5 DR 3.1.4	92.00	1.28**	94.00	0.06	95.67	-0.11	96.00	0.05
7	M 5 DR 3.6.1	99.00	1.56**	98.00	0.28	101.67	-0.22	103.17	-0.06
8	M 5 DR 3.6.2	98.84	1.23**	98.34	0.12	101.50	-0.39	103.00	0.27
9	M 5 DR 4.1.3	103.67	0.78*	101.00	-0.43	103.32	-0.11	105.17	0.55
10	M 5 DR 4.8.8	89.84	-2.27**	88.67	0.12	93.00	-0.56	94.17	0.44
11	M 5 DR 5.5.1	103.34	2.11**	101.00	0.23	105.34	-0.62	106.67	0.38
12	M 5 DR 7.1.2	99.00	0.23	97.00	0.12	101.00	-0.06	102.34	-0.06
13	M 5 DR 7.1.9	100.34	0.34	96.50	0.67	99.17	-0.17	100.83	-0.50
14	M 5 DR 7.3.1	100.17	-1.22**	96.00	-0.77	101.00	0.39	102.34	0.38
15	M 5 DR 7.3.2	100.00	-1.39**	96.34	-0.10	101.67	-0.11	102.17	0.21
16	M 5 DR 7.4.1	103.67	0.50	101.17	-0.33	107.00	-0.17	107.17	0.50
17	M 5 DR 7.4.2	105.00	0.22	103.17	-0.05	106.17	-0.23	107.50	0.27
18	M 5 DR 8.5.2	99.67	-0.05	97.17	0.73	99.67	0.39	99.17	-1.12
19	M 5 DR 8.5.3	99.50	0.17	96.67	0.34	101.00	-0.67	102.34	0.33
20	M 5 DR 8.6.3	100.00	0.45	97.50	1.40*	101.00	-1.45*	101.83	0.05
21	M 5 DR 8.8.1	100.83	1.00**	97.50	0.01	102.00	-0.33	102.17	0.33
22	M 5 DR 9.1.3	101.17	-0.28	98.00	-0.21	103.00	0.11	105.17	0.10
23	M 5 DR 9.1.5	101.67	0.00	98.00	1.01	103.00	-0.67	103.83	-0.34
24	M 5 DR 9.4.1	102.00	-0.16	99.00	1.01	105.00	-0.33	105.00	-0.67
25	M 5 DR 10.2.2	94.00	1.95**	97.00	0.73	96.00	0.39	97.00	-1.12
26	M 5 DR 10.2.9	94.00	1.78**	98.17	0.40	96.00	0.22	97.00	-0.62
27	M 5 DR 12.3.1	102.50	0.34	101.34	0.17	104.83	-0.33	105.34	0.16
28	M 5 DR 12.3.2	102.67	0.28	100.67	0.40	105.00	-0.28	105.67	-0.12
29	M 5 DR 14.1.1	99.17	-0.67	97.34	-0.16	100.50	0.66	102.50	-0.51
30	M 5 DR 14.2.2	93.50	-0.27	92.17	0.12	95.00	0.11	96.00	-0.23
31	M 5 DR 14.3.1	91.00	-2.28**	89.48	-0.38	93.50	-0.06	95.50	0.44
32	M 5 DR 14.3.8	91.33	-2.27**	89.67	-0.88	93.67	0.44	95.00	0.44
33	M 5 DR 16.1.1	100.00	0.67	98.17	0.01	101.84	0.00	102.00	-0.01
34	M 5 DR 16.2.1	93.33	-1.72**	90.34	-1.77**	94.67	0.89	95.67	0.88
35	M 5 DR 18.2.1	100.00	-0.44	96.84	0.62	101.00	0.44	100.67	-1.06
36	M 5 DR 18.3.1	102.34	-2.33**	100.00	-0.66	104.50	0.50	105.84	0.16
37	M 5 DR 18.4.1	99.17	0.17	96.67	-0.16	100.34	0.00	102.34	0.16
38	M 5 DR 18.8.1	100.67	-1.05**	98.00	0.23	101.00	0.22	102.00	-0.45
39	M 5 BR 153.1.2	105.00	0.95**	100.67	-0.27	105.50	-0.11	105.17	0.38
40	M 5 BR 153.2.2	99.17	0.11	97.00	0.56	100.84	0.22	101.84	-0.78
41	M 5 BR 153.3.2	98.84	0.56	98.67	-0.55	101.00	0.44	101.84	0.11
42	M 5 BR 153.4.1	103.84	-2.28**	98.67	-0.55	104.84	0.94	105.84	-0.40
43	M 5 BR 153.6.1	95.33	-2.55**	93.17	0.06	98.67	-0.78	98.00	0.72
44	M 5 BR 153.7.1	100.00	0.22	97.50	-0.05	100.84	0.44	102.00	-0.40
45	M 5 BR 153.10.2	103.84	1.56**	99.34	-0.21	105.34	0.11	106.00	0.10
46	M 5 BR 153.13.1	100.17	0.45	97.00	-0.27	100.83	-0.45	101.67	0.71
47	DR 4	103.34	-2.18**						
48	DR 6	105.67	0.50**						
49	DR 8	104.50	1.67**						

\*, \*\*Significant at the 0.5, 0.01 probability level

The result of line×tester analysis using GGE biplot for grain yield and maturity of mutants were similar with the results derived from the Kempthorne's line×tester analysis method, which has been published previously by Ruswandi *et al.* (2015) (Table 2 and 3). The GGE biplot predictions for estimating GCA of line and tester and for identifying the best hybrids are consistent with the Kempthorne's method. For example the GCA values and the best hybrids for grain yield and maturity from biplot analysis and Kempthorne's method are similar (Ruswandi *et al.*, 2015; Supriatna and Ruswandi, 2014). Fotokian and Agahi (2014) reported similar result, when he compared his biplot analysis of line×tester data and Kempthorne's analysis of line×tester data from

Table 3: Means, GCA effects of parents and SCA effects of 138 test crosses with three testers for grain yield per plant

No.	Mutants	Parent mean	GCA	DR 4		DR 6		DR 8	
				Grain yield per plant	SCA	Grain yield per plant	SCA	Grain yield per plant	SCA
1	M 5 DR 1.1.3	205.00	-3.40	107.33	-19.93	177.67	12.43	182.00	7.50
2	M 5 DR 1.2.3	121.67	4.10	156.67	-2.76	198.33	15.26	157.00	-12.50
3	M 5 DR 1.2.12	170.00	-3.73	79.34	-33.60*	193.00	20.43	192.67	13.16
4	M 5 DR 1.6.3	195.00	4.27	123.34	-19.60	162.00	-3.07	227.67	22.66
5	M 5 DR 3.1.2	181.00	18.71*	169.66	-10.88	209.67	6.32	220.33	4.55
6	M 5 DR 3.1.4	233.33	8.99	121.67	-25.15	208.67	15.54	211.00	9.61
7	M 5 DR 3.6.1	166.67	6.27	141.67	-12.43	172.00	-0.07	211.33	12.50
8	M 5 DR 3.6.2	196.67	-3.79	134.66	-5.88	151.67	-0.18	178.33	6.05
9	M 5 DR 4.1.3	60.00	-23.62*	125.67	9.46	71.33	-20.51	148.66	11.05
10	M 5 DR 4.8.8	157.34	21.93*	209.67	5.90	193.33	-5.07	216.00	-0.84
11	M 5 DR 5.5.1	108.34	4.82	169.33	2.85	163.00	-3.12	184.00	0.28
12	M 5 DR 7.1.2	133.34	-0.56	161.67	4.40	151.00	-3.74	171.34	-0.67
13	M 5 DR 7.1.9	185.00	6.71	150.33	-8.54	173.34	0.16	204.00	8.39
14	M 5 DR 7.3.1	122.33	-0.90	150.00	-1.10	165.00	3.60	167.00	-2.50
15	M 5 DR 7.3.2	118.00	-29.51**	106.00	5.51	89.33	-5.62	115.00	0.11
16	M 5 DR 7.4.1	201.67	1.10	201.34	22.57	108.67	-26.57	184.00	4.00
17	M 5 DR 7.4.2	208.33	1.93	184.00	13.07	161.34	-1.06	153.66	-12.01
18	M 5 DR 8.5.2	171.67	4.71	162.34	-0.54	179.00	4.99	174.33	-4.45
19	M 5 DR 8.5.3	112.00	-13.96	145.00	9.46	97.00	-17.34	161.66	7.88
20	M 5 DR 8.6.3	125.33	2.93	174.00	7.07	152.34	-6.56	178.66	-0.51
21	M 5 DR 8.8.1	163.00	-10.01	138.34	2.18	160.33	10.37	128.67	-12.56
22	M 5 DR 9.1.3	215.00	20.38*	191.33	-1.71	180.67	-9.84	237.67	11.55
23	M 5 DR 9.1.5	180.00	-16.90	119.33	-0.43	111.00	-7.40	155.66	7.83
24	M 5 DR 9.4.1	147.33	-14.68	88.00	-18.32	156.33	13.04	155.00	5.28
25	M 5 DR 10.2.2	130.67	5.83	176.67	5.51	151.34	-9.96	194.34	4.44
26	M 5 DR 10.2.9	161.00	-11.29	106.00	-12.71	124.66	-6.18	189.00	18.89
27	M 5 DR 12.3.1	91.66	-3.90	144.00	-1.10	162.34	5.27	157.67	-4.17
28	M 5 DR 12.3.2	81.33	13.32	178.00	-1.32	177.66	-4.29	211.67	5.61
29	M 5 DR 14.1.1	114.67	6.77	148.67	-9.43	195.66	11.26	183.67	-1.83
30	M 5 DR 14.2.2	180.67	-15.90	135.34	6.57	109.67	-9.07	147.00	2.50
31	M 5 DR 14.3.1	202.66	-0.51	164.34	5.68	164.00	2.71	156.00	-8.39
32	M 5 DR 14.3.8	138.00	4.38	165.66	1.46	129.67	-19.34	218.33	17.89
33	M 5 DR 16.1.1	161.00	17.93	182.00	-3.93	193.00	-1.23	220.00	5.16
34	M 5 DR 16.2.1	173.33	4.38	222.67	29.96	191.00	11.32	100.00	-41.28*
35	M 5 DR 18.2.1	141.67	-16.79	152.33	15.96	132.66	3.32	101.67	-19.28
36	M 5 DR 18.3.1	167.34	5.77	209.67	22.07	124.00	-23.57	188.33	1.50
37	M 5 DR 18.4.1	176.66	30.43**	196.33	-9.27	223.67	1.60	250.00	7.66
38	M 5 DR 18.8.1	199.33	1.27	148.67	-3.93	168.00	2.93	178.33	1.00
39	M 5 BR 153.1.2	63.00	9.49	209.00	18.01	198.67	10.04	136.67	-28.06
40	M 5 BR 153.2.2	152.00	7.60	199.33	15.07	163.67	-5.57	170.00	-9.50
41	M 5 BR 153.3.2	214.33	-9.90	95.34	-19.43	181.00	20.60	151.67	-1.17
42	M 5 BR 153.4.1	90.00	-20.73*	137.33	12.40	85.66	-16.24	140.00	3.83
43	M 5 BR 153.6.1	183.34	-5.57	100.00	-21.43	204.00	27.77	150.00	-6.34
44	M 5 BR 153.7.1	172.33	-0.34	152.66	-0.32	191.00	16.04	141.67	-15.72
45	M 5 BR 153.10.2	73.34	-3.07	186.66	19.40	144.00	-4.73	138.33	-14.67
46	M 5 BR 153.13.1	55.67	-4.96	162.33	9.12	140.33	-4.68	155.00	-4.45
47	DR 4	251.66	-4.24						
48	DR 6	130.00	-1.43						
49	DR 8	158.33	5.67*						

\*, \*\*Significant at the 0.5, 0.01 probability level

Maleki *et al.* (2014). Furthermore, Yan and Hunt (2002) explained that the advantage of the GGE biplot is its graphical presentation of the data, which improve the ability to understand patterns of the data. Fotokian and Agahi (2014), also revealed that the heterotic crosses as well as the best hybrids are easily to distinguish in a polygon view of the biplot. In contrary, in Kempthorne's line×tester data, the parents are evaluated only on their GCA effects and the SCA is associated with crosses and has little impact on the understanding of the parents.

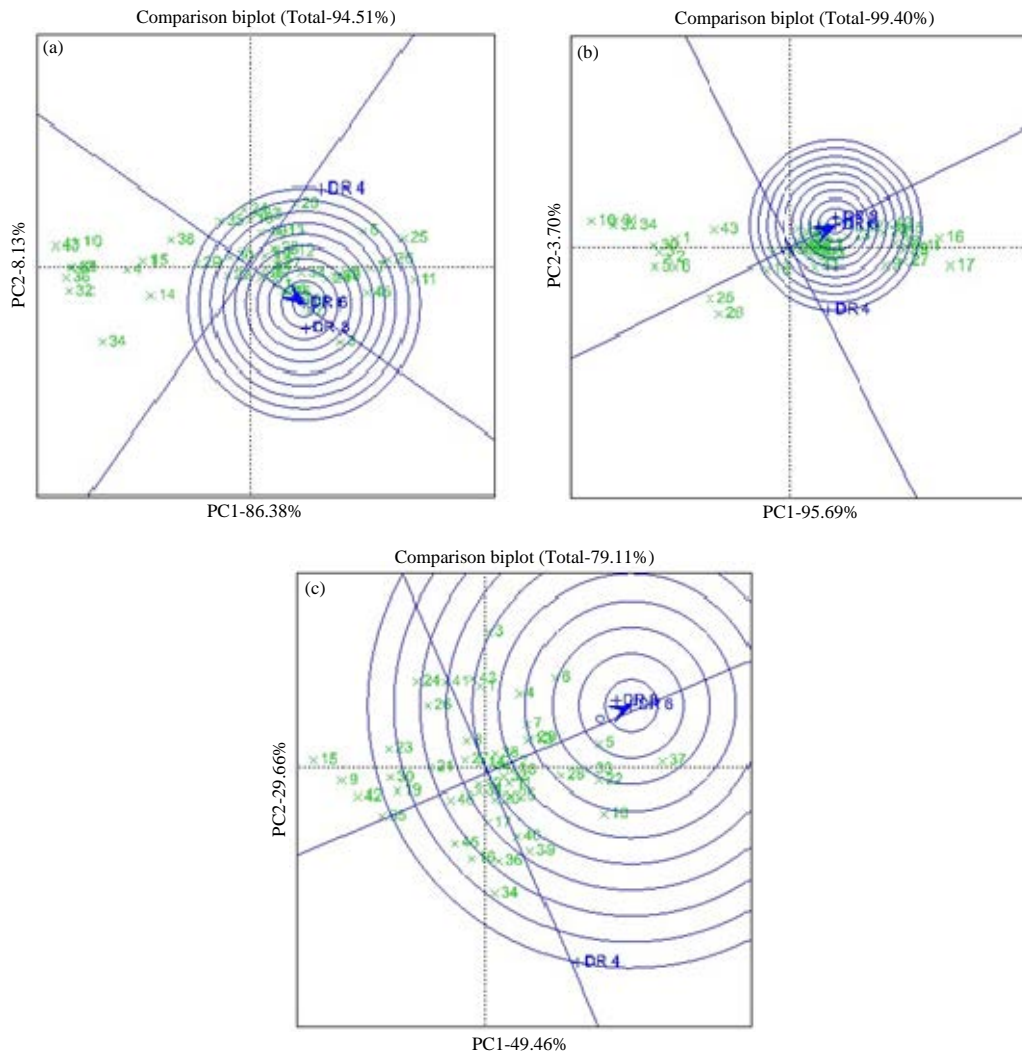


Fig. 4(a-c): Comparison plot for tester. The arrow represents the average tester. Lines are in number code and three testers are in code DR 4, 6 and 8, (a) Days to tasseling, (b) Days to harvest and (c) Grain yield per plant

In this study, since line×tester data was analyzed by GGE biplot, therefore the GGE biplot method is more compatible with line×tester data. Fotokian and Agahi (2014) and Mohring *et al.* (2011) explained that in diallel data, genotypes are both entries and testers in the entry×testers classification; whereas in line×tester data, entries and testers are different. Furthermore, in diallel data, GCA effects was estimated twice: The first time when substracting tester and entry main effects from the data and the second time by suitable projections in the biplot. Thus, in a diallel data, the row and column main effects are identical, representing GCA effects, so it is wasteful to estimate row and column main effects separately.

## CONCLUSION

The GGE biplot graphic allowed a rapid and effective overview of General Combining Ability (GCA) and Specific Combining Ability (SCA) effects of the inbred lines; best lines and tester, as well

as their performance in crosses. The GCA and SCA effects were significant for days to tasseling, days to harvesting and grain yield. Based on Average Tester Coordination function of GGE biplot, the following mutant line were selected for high GCA effect including: Mutant 2 and 9; mutant 8 and mutant 7 for days to tasseling, days to harvest, and grain yield, respectively. It was revealed that the following parental lines are the best testers including DR 4 for early maturity and DR 6 for grain yield. The maximum best-parent heterosis values and the highest SCA effects resulted from mutants (10, 34, 32, 36, 48); mutants (10, 31, 32 and 34) and mutants (5, 7, 10, 32, 34, 36, 37 and 48) crosses to testers (4, 6 and 8) for early days to tasseling, early days to harvesting and grain yield, respectively, which would be potentially useful in maize breeding programs to obtain high-yielding hybrids in the same climate of Indonesia.

#### **ACKNOWLEDGMENTS**

The authors would like to put into words their appreciation to the Directorate General Higher Education, Ministry of Culture and Education, Republic Indonesia and Universitas Padjadjaran for the research funding through Hibah Penelitian Pasca Sarjana 2010-2012 and PUPTN 2013-2015 granted to the 1st author.

#### **REFERENCES**

- Abdel-Moneam, M.A., M.S. Sultan, S.E. Sadek and M.S. Shalof, 2014. Estimation of heterosis and genetic parameters for yield and yield components in maize using the diallel cross method. *Asian J. Crop Sci.*, 6: 101-111.
- Akaogu, I.C., B. Badu-Apraku, V.O. Adetimirin, I. Vroh, M. Oyekunle and R.O. Akinwale, 2012. Genetic diversity assessment of extra-early maturing yellow maize inbreds and hybrid performance in Striga-infested and Striga-free environments. *J. Agric. Sci.*, 151: 519-537.
- Badu-Apraku, B., R.O. Akinwale and M.A.B. Fakorede, 2010. Selection of early maturing maize inbred lines for hybrid production using multiple traits under Striga-infested and Striga-free environment. *Maydica*, 55: 261-274.
- Badu-Apraku, B., M. Oyekunle, M.A.B. Fakorede, I. Vroh, R.O. Akinwale and M. Aderounmu, 2013. Combining ability, heterotic patterns and genetic diversity of extra-early yellow inbreds under contrasting environments. *Euphytica*, 192: 413-433.
- Bertoia, L., C. Lopez, R. Burak, 2006. Biplot analysis of forage combining ability in maize landraces. *Crop Sci.*, 46: 1346-1353.
- Bocanski, J., A. Nastasic, D. Stanisavljevic, Z. Sreckov, B. Mitrovic, S. Treskic and M. Vukosavljev, 2011. Biplot analysis of diallel crosses of NS maize inbred lines. *Genetika*, 43: 277-284.
- Dehghani, H., E. Feyzian, M. Jalali, A. Rezai and F. Dane, 2012. Use of GGE biplot methodology for genetic analysis of yield and related traits in melon (*Cucumis melo* L.). *Can. J. Plant Sci.*, 92: 77-85.
- Dehghani, H., M. Moghaddam, M.R. Bihamta, N. Sabaghnia and R. Mohammadi, 2013. Biplot analysis of diallel data in strip rust of wheat. *Aust. Plant Pathol.*, 42: 601-608.
- Duarte, J.B. and R.M.C. Pinto, 2002. Biplot AMMI graphic representation of specific combining ability. *Crop Breed. Applied Biotechnol.*, 2: 161-170.
- Falconer, D.C., 1981. *An Introduction to Quantitative Genetics*. 2nd Edn., Longman, New York, USA., pp: 67-68.
- Fotokian, M.H. and K. Agahi, 2014. Biplot analysis of genotype by environment for cooking quality in hybrid rice: A tool for line x tester data. *Rice Sci.*, 21: 282-287.

- Griffing, B., 1956. Concept of general and specific combining ability in relation to diallel crossing systems. *Aust. J. Biol. Sci.*, 9: 463-493.
- Hallauer, A.R., 1990. Improvements in yield of maize hybrids. *UDC*, 63: 193-198.
- Hamoud, H.M.E., 2014. Use of biplot approach for genetic analysis of yield and related traits in cotton (*Gossypium barbadense*). *J. Plant Breed. Crop Sci.*, 6: 41-47.
- Izhar, T. and M. Chakraborty, 2013. Combining ability and heterosis for grain yield and its components in maize inbreds over environments (*Zea mays* L.). *Afr. J. Agric. Res.*, 8: 3276-3280.
- Kamara, M.M., I.S. El-Degwy and H. Koyama, 2014. Estimation combining ability of some maize inbred lines using line x tester mating design under two nitrogen levels. *Aust. J. Crop Sci.*, 8: 1336-1342.
- Kempthorne, O., 1957. *An Introduction to Genetic Statistics*. John Wiley and Sons Inc., London, UK.
- Legesse, B.W., K.V. Pixley and A.M. Botha, 2009. Combining ability and heterotic grouping of highland transition maize inbred lines. *Maydica*, 54: 9-14.
- Maleki, M., M.H. Fotokian, F.D. Kajouri, M.Z. Nouri and K. Agahi, 2014. Study of combining ability and gene action of cooking quality traits in rice (*Oryza sativa* L.) using line x tester analysis. *J. Biodiver. Environ. Sci.*, 4: 220-226.
- Malla, S., A.M.H. Ibrahim, K.D. Glover and W.A. Berzonsky, 2010. Combining ability for *Fusarium* head blight resistance in wheat (*Triticum aestivum* L.). *Commun. Biometry Crop Sci.*, 5: 116-126.
- Mohring, J., A.E. Melchinger and H.P. Piepho, 2011. REML-based diallel analysis. *Crop Sci.*, 51: 470-478.
- Mostafavi, K., R. Choukan, M. Taeb, E.M. Heravan and M.R. Bihamta, 2012. Heterotic grouping of Iranian maize inbred lines based on yield-specific combining ability in diallel crosses and GGE biplot. *J. Res. Agric. Sci.*, 8: 113-125.
- Njoroge, K. and L. Gichuru, 2013. Diallel analysis of turicum leaf blight resistance in Kenyan maize lines. *Afr. J. Agric. Res.*, 8: 2877-2883.
- Petersen, R.G., 1994. *Agricultural Field Experiments: Design and Analysis*. Marcel Dekker Inc., New York, USA.
- Rahman, H., A. Ali, Z. Shah, M. Iqbal, M. Noor and Amanullah, 2013. Line x tester analysis for grain yield and yield related traits in maize variety Sarhad-White. *Pak. J. Bot.*, 45: 383-387.
- Rastogi, A., B.K. Mishra, M. Srivastava, A. Siddiqui and S. Shukla, 2011. Biplot approach for identification of heterotic crosses in linseed (*Linum usitatissimum* L.). *J. Bot.* 10.1155/2011/353102
- Rastogi, A., B.K. Mishra, A. Siddiqui, M. Srivastava and S. Shukla, 2013. GGE biplot analysis based on diallel for exploitation of hybrid vigour in opium poppy (*Papaver somniferum* L.). *J. Agric. Sci. Technol.*, 15: 151-162.
- Ruswandi, D., Agustian, E.P. Anggia, A.O. Canama, H. Marta, S. Ruswandi and E. Suryadi, 2014. Mutation breeding of maize for anticipating global climate change in Indonesia. *Asian J. Agric. Res.*, 8: 234-247.
- Ruswandi, D., J. Supriatna, A.T. Makkulawu, B. Waluyo, H. Marta, E. Suryadi and S. Ruswandi, 2015. Determination of combining ability and heterosis of grain yield components for maize mutants based on line x tester analysis. *Asian J. Crop Sci.*, 7: 19-33.
- Sibiya, J., P. Tongoona and J. Derera, 2013. Combining ability and GGE biplot analyses for resistance to northern leaf blight in tropical and subtropical elite maize inbred lines. *Euphytica*, 191: 245-257.



- Singh, R.K. and B.D. Chaudhary, 1977. *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, Ludhiana, New Delhi, pp: 191-200.
- Supriatna, J. and D. Ruswandi, 2014. Selection of mutant lines of maize for yield and early maturity based line x tester analysis. *Proceedings of the 3rd International Conference on Applied Life Sciences*, October 22-24, 2014, Malaysia.
- Yan, W., 2001. GGEbiplot-A windows application for graphical analysis of multi environment trial data and other types of two-way data. *Agron. J.*, 93: 1111-1118.
- Yan, W. and L.A. Hunt, 2002. Biplot analysis of diallel data. *Crop Sci.*, 42: 21-30.
- Yan, W. and M.S. Kang, 2003. *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticist and Agronomists*. CRS Press, Boca Raton, FL., pp: 207-228.