Implementation of partial diallel analysis to determine general combining ability and agronomic character genetic parameters of shade-tolerant maize lines

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Abstract. Information about combining ability and genetic parameters guide maize breeders in selecting parents and gene action of the desired trait. This study aims to determine the general combining ability of the yield characters of shading tolerant maize lines and the genetic parameters of their agronomic characters. This research was conducted at IP2TP Bajeng in December 2020-March 2021. The study was arranged in a randomized block design with three replications. The genotypes used were nine hybrids obtain from a partial diallelic (2x6). The results showed that line SHD3 showed good general ability for yield. High heritability values were shown by variables days to anthesis, days to silk, plant height, ear height, leaf length, leaf width, 100 grains weight and ear diameter.

1. Introduction
Plantation land has the potential to be used as extensification maize. Indonesia's oil palm area in 2016 is estimated to reach 11.67 million ha. Meanwhile, the rubber reached 3.6 million ha. Plantation land that can be used for maize cultivation was land under the staple crops with shade intensity below 40%.

Light is one of the limiting factors for plant production which is very important in the photosynthesis process. maize that is included in the C4 plant group that requires high lighting, so the reduced light intensity due to shade causes photosynthetic enzymes decrease that function as catalysts in CO2 fixation[1]. This will affect the growth and development of maize. Maize that is subjected to shade stress will decrease in photosynthetic capacity, and fertility and has barren ears. Furthermore, according to [2] shade stress cause maize become tall and thin, the number of leaves is reduced and the ears are smaller.

Breeding for shade stress-tolerant hybrids is the right strategy to increase maize yield in a shaded environment. The breeding of hybrid maize requires the general combining ability (GCA) and the specific combining ability (SCA) information of the lines [3]–[5]. Information about GCA and SCA is a prerequisite for hybrid maize breeding to be effectively and efficiently [6]–[8] Diallel analysis is one of the methods used in estimating the line’s combining ability ([9]. Besides being reliable to predict the combining ability, diallelic analysis also able to estimate the effect of additive and non-additive genes in the character phenotypic [10][11]. The diallelic method allows crosses between all genotypes of the parents including themselves. and their reciprocals [12], these genotypes can be defined as individuals, clones, homozygous lines, and so on.
Diallel analysis in its often faces various restrictions. The restrictions are, the number of crosses will increase exponentially according to the number of parents used. This means that when testing facilities are limited, diallelic testing can only be carried out on a small number of parental lines. The partial dialle introduced by [13] a plant breeder is not only able to estimate the gca of a large number of parental lines but can also make selection among crosses from a wide range of parents. GCA of each line may be estimated with relatively low precision but larger genetic gains may result from the more intense selection that can be applied to them. This study aims to determine the general combining ability of the yield characters of shading tolerant maize lines and the genetic parameters of their agronomic characters.

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2. Materials and Methods
This research was conducted at IP2TP Bajeng in December 2020-March 2021. The study was arranged in a randomized block design with three replications. The study was arranged in a randomized block design with three replications. The genotypes used was nine hybrids obtain from a partial diallelic (2x6). Crossing sce ne is shown in Table 1.

Table 1. Crossing scheme

| Line | SHD9 | SHD3 | SHD2 | SHD7 | SHD8 | SHD10 |
|------|------|------|------|------|------|-------|
| SHD9 |      |      |      |      |      | SHD9 x SHD2 |
| SHD3 |      |      |      |      |      | SHD3 x SHD7 |
| SHD2 |      |      |      |      |      | SHD2 x SHD8 |
| SHD7 |      |      |      |      |      | SHD7 x SHD10 |
| SHD8 |      |      |      |      |      | SHD8 |
| SHD10|      |      |      |      |      | SHD10 |

Variables observed were days to anthesis, days to silk, plant height, ear height, stalk diameter, leaf angle, leaf length, Leaf width, ear harvested weight, shelling percentage, grain moisture, yield which were corrected to 15% moisture, 100 grains weight, ear length, ear diameter rows per ear and kernels per row.

The estimates of general combining ability were calculated by the expressions: $\bar{g}_i = Y_i - m$; $\bar{g}_j = Y_j - m$; $s_{ij} = Y_{ij} - (m + \bar{g}_i + \bar{g}_j)$, respectively, where $Y_i$ is the general mean of the hybrid combinations with the i-th parent, and $Y_j$ the general mean of the hybrid combinations with the j-th parent.

Genetic ratio that the progeny performances could be predicted by the use of the ratio of combining ability variance components [14]:

$$\text{Genetic ratio} = \frac{2\text{MS}_{GCA}}{\text{MS}_{GCA} + \text{MS}_{SCA}}$$

Broad sense heritability was calculated by formula: $h_b^2 = \frac{\sigma_A^2 + \sigma_D^2}{\sigma_P^2}$
3. Result and Discussion

Analysis of variance for crosses GCA and SCA is shown in Table 1. Significant differences in both GCA and SCA was shown by ear harvested weight, shelling percentage, yield, 100 grains weight, and ear length showed differences. While the variables days to anthesis, days to silk, plant height, ear height, stalk diameter, leaf length, leaf width and ear diameter show significant differences only for GCA and other variables did not show differences in either GCA and SCA (Table 2).

Table 2. Anova for crosses GCA and SCA

|        | Replication | Cross | GCA       | SCA       | Error     |
|--------|-------------|-------|-----------|-----------|-----------|
| DA     | 0.0556      | 5.9306** | 8.1944** | 2.1574   | 0.9306    |
| DS     | 0.8889      | 6.1389** | 9.3778** | 0.7407   | 0.6389    |
| PH     | 80.2222     | 298.7654 | 447.8276* | 50.3284  | 91.1250   |
| EH     | 2.8854      | 125.6553 | 176.7695* | 40.4649  | 46.3244   |
| SD     | 33.7047     | 10.7338 | 15.8396* | 2.2241   | 3.7294    |
| LA     | 0.7403      | 11.9485 | 15.5065  | 6.0185   | 7.2542    |
| LL     | 11.1843     | 49.6375** | 75.8964** | 5.8726   | 5.4799    |
| LW     | 0.0147      | 0.6833** | 0.9765** | 0.1945   | 0.1040    |
| EHW    | 0.0091      | 2.8501*  | 3.0072*  | 2.5883*  | 0.4924    |
| SP     | 0.0000      | 0.0012** | 0.0014** | 0.0008*  | 0.0002    |
| GM     | 0.0939      | 2.6488  | 3.3313   | 1.5111   | 2.9976    |
| Y      | 0.0712      | 2.6789* | 2.883*   | 2.3387*  | 0.4628    |
| GW     | 0.7361      | 23.0775 | 34.7286* | 3.6589** | 5.1219    |
| EL     | 4.6614      | 5.6267* | 4.5222*  | 7.4676*  | 1.1885    |
| ED     | 1.6684      | 27.1401** | 40.5152** | 4.8483  | 3.0006    |
| RE     | 1.5606      | 0.5125  | 0.6873   | 0.2211   | 0.4081    |
| KR     | 1.0756      | 5.3439  | 7.0179   | 2.5538   | 4.7481    |

Table 3. GCA values for each variable

| Line   | DA    | DS    | PH    | EH    | SD    | LA    | LL    | LW    | EHW  | SP    | GM    | Y     | GW    | EL    | DL    | RE    | KR    |
|--------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| SHD9   | 0.93  | 1.36* | -12.82* | -3.52* | -2.28* | -0.42 | -1.47* | -0.18 | -0.96 | 0.00  | -0.74* | -0.80 | -3.62 | -1.21 | -3.99* | -0.42 | 0.25  |
| SHD3   | -0.99 | -1.47* | 9.83*  | 6.46* | 3.08* | 3.24  | 8.25* | 0.45* | 1.16  | 0.02* | 0.29* | 1.2*  | 1.38  | 1.13  | 3.68* | -0.56 | 0.76  |
| SHD2   | 0.43  | -0.14 | 11.09* | 13.25* | 2.35* | -0.92 | 5.45* | 0.97* | 1.10  | 0.00  | 0.73* | 0.89  | -1.03 | 0.83  | 4.12* | -0.29 | -0.02 |
| SHD7   | -0.32 | -0.64* | -0.20  | 2.76  | 0.86* | -2.29 | -2.32* | -0.26 | -0.16 | 0.00  | 1.66* | -0.31 | 0.32  | -0.27 | 0.06  | 0.13  | -0.73 |
| SHD8   | 1.26* | 1.53* | -10.13* | -9.57* | -0.98* | -0.31 | -3.93* | -0.36* | -0.90 | -0.03* | -0.76* | -0.92  | -0.09 | -0.78 | -3.11* | 0.89  | -1.92 |
| SHD10  | -1.32* | -0.64* | 2.22*  | -9.38* | -3.02* | 0.70  | -5.98* | -0.61* | -0.25 | 0.01  | -1.18* | -0.06 | 3.03  | 0.39  | -0.78 | 0.26  | 1.66  |

| variance | 0.99  | 0.50  | 1.67  | 3.18  | 0.46  | 1.18  | 1.35  | 0.29  | 1.17  | 0.02  | 0.08  | 1.11  | 0.80  | 2.00  | 1.40  | 0.10  | 0.32  |

Noted: DA=Days to anthesis, DS= Days to Silk, PH= Plant Height, EH= ear height, SD= stalk diameter, LA= Leaf angle, LL= leaf length, LW=Leaf width, EHW= Ear Harvested weight, SP= shelling percentage, GM= Grain Moisture, Y= yield which were corrected to 15% moisture, GW= 100 grains weight, EL= ear length, ED= ear diameter RE=rows per ear, KR= kemels per row, *=Significant at 5%, **=significant at 1%

General combining ability shows the average performance of a line when crossed with all parents in a cross set. GCA value can be positive or negative depending on the deviation of line mean to total
mean. selection of lines and the crosses with good combining ability is not always a positive value but is based on the preference of these traits [15]. The GCA values for each variable are shown in Table 3.

Line SHD9 showed significant GCA values for variable plant height, ear height, grain moisture. Significant GCA value for line SHD3 was indicated by days to silk, stalk diameter, leaf length, leaf width, shelling percentage, yield and ear diameter. line SHD2 strain showed significant GCA values on variables stalk diameter, leaf length, leaf width, ear diameter. SHD7 showed significant GCA on days to silk and stalk diameter variables. SHD 8 shows significant GCA only on grain moisture. SHD10 showed significant GCA on variables days to anthesis, days to silk, ear height and grain moisture (Table 3).

Line SHD3 potential to be used as a tester in the line x tester test because it has a significant GCA in yield variable. [16] Stated that genotypes with high GCA value on grain yield trait can be used as random mating parents to develop a synthetic variety. Population created serves as genetic material in population improvement through recurrent selection method and can be used as a tester for further line x tester evaluation. Meanwhile, SHD10 which shows significant GCA in variables days to anthesis and days to silk can be used as genetic material to improve early maturing hybrids.

Variation of the significant difference of GCA and SCA shows different gene actions in those variables. Variables that shown significance in both GCA and SCA indicate that these variables are influenced by additive and non-additive genes [17], [18]. Variables show significant differences only for GCA only indicate that the additive genes are more influenced [19][20]

Table 4. Genetic ratio and heritability of variable

| Variable                        | Genetic Ratio | Heritability |
|---------------------------------|---------------|--------------|
| Days to anthesis                | 1.58          | 0.80         |
| Days to silk                    | 1.85          | 0.85         |
| Plant height                    | 1.80          | 0.58         |
| Ear height                      | 1.63          | 0.52         |
| Stalk diameter                  | 1.75          | 0.53         |
| Leaf angle                      | 1.44          | 0.27         |
| Leaf length                     | 1.86          | 0.84         |
| Leaf width                      | 1.67          | 0.80         |
| Ear harvested weight            | 1.07          | 0.82         |
| Shelling percentage             | 1.25          | 0.84         |
| Grain moisture                  | 1.38          | -0.32        |
| Yield which were corrected to 15% moisture | 1.10 | 0.82 |
| 100 grains weight               | 1.81          | 0.69         |
| Ear length                      | 0.75          | 0.81         |
| Ear diameter                    | 1.79          | 0.85         |
| Rows per ear                    | 1.51          | 0.02         |
| Kernels per row                 | 1.47          | -0.08        |

Noted: DA=Days to anthesis, DS= Days to Silk, PH= Plant Height, EH=ear height, SD= stalk diameter, LA= Leaf angle, LL= leaf length, LW=Leaf width, EHW= Ear Harvested weight, SP= shelling percentage, GM= Grain Moisture, Y= Yield, GW= 100 grains weight, EL= ear length, ED= ear diameter RE=rows per ear, KR=kernels per row

Table 4 shows that almost all variables are more influenced by additive genes except ear length. The non-additive gene action played an important role in ear length. This can be seen from the ear length genetic ratio which is less than one while the other variables are more than one. The genetic ratio is used to determine the additive or non-additive gene action that influenced the traits. [14] used a
mean squared ratio to determine the proportion of additive or non-additive genes that control a variable. A variable is more controlled by genes if the genetic ratio is more than 1. genetic ratio with a value greater than one indicates additive gene effect, whereas the genetic ratio with a value lower than one indicates non-additive gene effect [21].

Heritability describes the proportion of genetic variance to phenotypic variance. broad sense Heritability values ranged from 0-1. Heritability value 0 means that phenotypic diversity is caused mainly by environmental factors, while 1 means that genotype diversity is caused by genetic factors [22]. Broad sense heritability describes the total genetic effect without dividing it into additive and non-additive effects, while narrow heritability describes the effect of additive genes on phenotype appearance [23].

High heritability values were shown by variables days to anthesis, days to silk, plant height, ear height, leaf length, leaf width, 100 grains weight and ear diameter. Leaf angle shows moderate heritability and rows per ear variable was low. There are two variables with negative heritability values, i.e grain moisture and kernels per row. Biologically, the heritability value may not be more than one or negative. According to [24] the negative heritability value due to uniformity caused by different environments, the statistical method used cannot effectively separate genetic and environmental variations. and sampling errors.

4. Conclusions
1. SHD3 showed good general ability for yield.
2. High heritability values were shown by variables days to anthesis, days to silk, plant height, ear height, leaf length, leaf width, 100 grains weight and ear diameter.

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