Estimation of Combining Ability, Heritability and Genes action of Yield Components of Inbred Corn Lines in Diallel Crosses

Achmad Amzeri
Faculty of Agriculture
University of Trunojoyo Madura, Indonesia
Po Box 2 Bangkalan, Indonesia
aamzeri@gmail.com

Kaswan Badami
Faculty of Agriculture
University of Trunojoyo Madura, Indonesia
Po Box 2 Bangkalan, Indonesia
aamzeri@gmail.com

Abstract—Crosses are among the breeding methods to obtain superior varieties. To obtain superior varieties requires information about the combining ability, heritability and genes action of lines for parental crosses. The purpose of the present study was to estimate the combining ability, heritability and the genes action of yield components of inbred corn lines in diallel crosses. The study was conducted at the Experimental Station of Agro-Technology Study Program of Agriculture Faculty, University of Trunojoyo Madura from February to July 2017. The parents used in the study were UTM 2, UTM 7, UTM 14, UTM 15, UTM 18, UTM 22 and UTM 31. The estimation of general combining ability (GCA), specific combining ability (SCA), heritability and the genes action was performed by using the Griffing's method I. The experiments used the randomized complete block design (RCBD) with three replications. Results showed that the characters of 50% flowering age, harvesting age and production per hectare were affected by the role of additive and dominant genes, while the cob length, cob diameter, and weight of 100 seeds were affected by the role of the dominant genes. The UTM 2 and UTM 31 parents were the best combiners for production per hectare, UTM 7 was the best combiner for cob size. Thus, the three parents could be used to assemble varieties with a high production per hectare. The heritability value in the broad and narrow sense was the highest for the harvesting age character.

Keywords—GCA, SCA, heritability, genes action, corn

I. INTRODUCTION

Corn (Zea mays L.) is the second major food commodity after rice in Indonesia. In addition to being used as food, corn is also used as livestock feed. For the last few years, the proportion of corn use by feed industry reached 50% of total national demand and after 2020 the figure is expected to increase more than 60% of the total national demand [1]. Based on the annual increase of corn, cultivation of this plant would be highly profitable and has a fairly good prospects for those cultivate it.

Hybridization is a potential technique to increase the yield of a plant commodity with the desired characters. Estimation of combining ability is an effective and efficient way to select a line/parent in hybridization in order to obtain hybrids with high grain yield and other good characters as desired [2]; [3]; [4].

The purpose of the present study was to estimate the general combining ability (GCA) and specific combining ability (SCA) of yield characters and yield components of several corn lines. This study is expected to identify prospective parents and cross combinations with high GCA and SCA values for yield characters and yield components.

II. METHODS

This study was conducted in February to July 2017. The experiments were conducted at the Experimental Station of Agro-Technology Study Program of Agriculture Faculty, University of Trunojoyo Madura using 7 genotypes of corn inbred lines were the UTM 2, UTM 7, UTM 14, UTM 15, UTM 18, UTM 22 and UTM 31 as parents (Table 1).

The experiments used the randomized complete block design (RCBD), consisting of 36 genotypes (yield of diallel crosses of 7 parents) with three replications, so there are 108 experimental units. Each experimental unit consisted of 50 plants which is planted in a sized bed 5 m x 1 m with a plant spacing of 20 cm x 70 cm.

TABLE I. DATA OF PARENTS USED IN THE STUDY

| Parents | From |
|---------|------|
| UTM 2   | University of Trunojoyo Madura, Indonesia |
| UTM 7   | University of Trunojoyo Madura, Indonesia |
| UTM 14  | University of Trunojoyo Madura, Indonesia |
| UTM 15  | University of Trunojoyo Madura, Indonesia |
| UTM 18  | University of Trunojoyo Madura, Indonesia |
| UTM 22  | University of Trunojoyo Madura, Indonesia |
| UTM 31  | Research Center of Serealia Maros, Indonesia |
Observations were made on 20 sample plants from each experimental unit. The observed characters were 50% flowering age (FA), harvesting age (HA), cob length (CL), cob diameter (CD), weight of 100 seeds (W100S) and production per hectare (PPH). Observations of weight per cob and cob size were performed on the same cob harvested in the second to fourth harvests. Estimates of general combining ability (GCA), specific combining ability (SCA) and heritability were obtained from diallel analysis using the random model of Griffing’s method I [5].

Heritability in the broad sense \( (h^2_{b}) = \frac{2\sigma^2_{DGU} + \sigma^2_{DGK}}{2\sigma^2_{DGU} + \sigma^2_{DGK} + 2\sigma^2_E} \times 100\% \) (1)

Heritability in the narrow sense \( (h^2_{n}) = \frac{2\sigma^2_{DGU}}{2\sigma^2_{DGU} + \sigma^2_{DGK} + 2\sigma^2_E} \times 100\% \) (2)

### III. RESULTS AND DISCUSSION

Results of variance analysis showed that genotypes had a very significant effect on all the characters observed (Table 2). Estimation of combining ability and heritability using the diallel analysis could be done when the mean square of the genotype had a significant effect [5]. Analysis of variance for general combining ability (GCA) and specific combining ability (SCA) shows that GCA and SCA had a very significant effect on all the characters observed (Table 3).

The actual value of GCA indicates that each line has a different ability to produce offspring and there is one or more lines that are good combiners for the characters. The actual SCA shows that a cross combination can produce better or worse offspring than the two parents. The mean square of GCA and SCA are significantly different shows that the action of additive and non-additive genes plays a role in controlling the characters [3]. The mean square comparison of GCA with SCA which is greater than one indicates that the action of additive genes is more important than the action of non-additive genes in controlling the characters [6]; [7]; [8].

#### TABLE II. ANALYSIS OF VARIANCE OF CORN YIELD COMPONENTS

| Sources of diversity | df | Mean of Squares |
|----------------------|----|----------------|
|                      |    | FA | HA | CL | CD | W100S | PPH |
| Replications         | 2  | 13,905** | 0,680* | 4,925** | 0,049** | 2,867 * | 679714,068** |
| Genotype             | 48 | 24,382** | 73,974** | 10,185** | 0,510** | 17,542** | 16447450,564** |
| Error                | 96 | 0,280 | 0,382 | 0,043 | 0,002 | 0,711 | 25447,742 |
| CV (%)               |    | 1,497 | 0,815 | 1,086 | 1,129 | 3,291 | 3,794 |

Notes: * = significant, ** = very significant, ns = not significant.

#### TABLE III. ANALYSIS OF VARIANCE OF DIALLEL CROSSES OF SEVEN CORN GENOTYPES

| Sources of diversity | df | Mean of Squares |
|----------------------|----|----------------|
|                      |    | FA | HA | CL | CD | W100S | PPH |
| GCA                  | 6  | 42,140** | 118,153** | 0,118** | 0,009** | 4,922** | 3768918,622** |
| SCA                  | 21 | 8,413** | 1,931** | 3003,641** | 142,227** | 5900,697** | 904327,687** |
| Reciprocal           | 21 | 846,006** | 3453,191** | 473,805** | 26,297** | 250,939** | 5329915,636** |
| Error                | 96 | 0,993 | 0,127 | 0,014 | 0,001 | 0,237 | 8482,381 |
| GCA : SCA            | 5,009 | 61,188 | 0,000 | 0,000 | 0,001 | 4,168 |

Notes: * = significant, ** = very significant, ns = not significant.

#### TABLE IV. GENERAL COMBINING ABILITY VALUES OF CORN YIELD COMPONENTS

| Genotypes | Yield Components |
|-----------|-----------------|
|           | Mean | FA | HA | CL |
| UTM 2     | 32,667 | -1,038 | 72,667 | -1,733 | 15,200 | 0,0248 |
| UTM 7     | 34,667 | -0,971 | 74,333 | -1,800 | 15,300 | 0,1048 |
| UTM 14    | 33,333 | -1,433 | 73,000 | -2,800 | 15,533 | -0,3019 |
| UTM 15    | 35,000 | -1,371 | 75,333 | -1,867 | 15,100 | -0,2419 |
| UTM 18    | 33,333 | -0,971 | 73,333 | -1,800 | 15,533 | -0,1419 |
| UTM 22    | 34,333 | -0,771 | 74,333 | -1,267 | 14,633 | -0,1019 |
| UTM 31    | 42,333 | -0,562 | 91,000 | -3,629 | 17,067 | -2,7943 |

#### TABLE V. GENERAL COMBINING ABILITY VALUES OF CORN YIELD COMPONENTS

| Genotypes | Yield Components |
|-----------|-----------------|
|           | Mean | CD | W100S | Mean | PPH |
| UTM 2     | 3,313 | -0,112 | 21,177 | 0,962 | 1924,667 | 1086,933 |
| UTM 7     | 3,230 | 0,004 | 21,327 | 0,596 | 2124,000 | -126,867 |
| UTM 14    | 3,250 | -0,027 | 21,557 | 1,112 | 1874,000 | -85,133 |
| UTM 15    | 3,297 | -0,026 | 21,517 | -1,833 | 1954,333 | -1147,267 |
The genotype of UTM 31 was the parent with larger cob size, larger 100-seed weight and higher production per hectare than the genotype of UTM 2, UTM 7, UTM 14, UTM 15, UTM 18 and UTM 22. A cross between genotypes is expected to produce offspring with a high production per hecetare and early maturity. A cross between a parents with a high per hecetare production (UTM 31) and UTM 7 is expected to produce offspring which has a high per hecetare production compared to its parents.

The parents of UTM 2 and UTM 31 had a positive GCA value for per-hecetare production character, while UTM 7 had a positive GCA value for cob length and cob diameter characters (Tables 4 and 5). Thus, the parents of UTM 2 and UTM 31 were the best combiners for per hecetare production, whereas UTM 7 was the best combiner for cob size.

The parents with a large and positive GCA value are those with a good combining ability, while a negative GCA value indicates that the parents have a lower combining ability than that of other parents [9]. Good offspring are resulted from the parents with a high GCA value [10]. However, in certain characters with a negative GCA value is very desirable [11]. For the harvesting age character, the GCA value is expected negative [12], since it shows an early maturity and indicates that the parent has a good combining ability for the character.

The GCA value for harvesting age character indicates that all characters with a negative GCA value is very desirable [11].

| Genotypes | Yield Components |
|------------|------------------|
| UTM 2 X UTM 7 | UTM 2 X UTM 14 | UTM 2 X UTM 15 | UTM 2 X UTM 18 | UTM 2 X UTM 22 | UTM 2 X UTM 31 | UTM 7 X UTM 2 | UTM 7 X UTM 14 | UTM 7 X UTM 15 | UTM 7 X UTM 18 | UTM 7 X UTM 22 | UTM 7 X UTM 31 | UTM 14 X UTM 2 | UTM 14 X UTM 7 | UTM 14 X UTM 15 | UTM 14 X UTM 18 | UTM 14 X UTM 22 | UTM 14 X UTM 31 | UTM 15 X UTM 2 | UTM 15 X UTM 7 | UTM 15 X UTM 14 | UTM 15 X UTM 18 | UTM 15 X UTM 22 | UTM 15 X UTM 31 | UTM 18 X UTM 2 | UTM 18 X UTM 7 | UTM 18 X UTM 14 | UTM 18 X UTM 15 | UTM 18 X UTM 18 | UTM 18 X UTM 22 |
| Mean | FA | Mean | HI | Mean | CL |
| 33,333 | -0.745 | 74,000 | 0.033 | 19,200 | -0.520 |
| 33,667 | 0.055 | 73,667 | 0.700 | 19,133 | -0.180 |
| 33,667 | -0.011 | 73,667 | -0.233 | 19,267 | -0.107 |
| 34,000 | -0.078 | 73,667 | -0.300 | 19,467 | -0.007 |
| 35,333 | 1.055 | 73,333 | 0.833 | 20,367 | 0.853 |
| 41,333 | -0.278 | 86,000 | -1.033 | 20,233 | -0.040 |
| 33,667 | 15.222 | 73,333 | 30.755 | 19,633 | 9.237 |
| 33,667 | -0.011 | 73,667 | 0.767 | 19,567 | 0.173 |
| 33,667 | -0.078 | 73,333 | -0.500 | 19,233 | -0.220 |
| 34,667 | 0.322 | 74,333 | 0.433 | 19,567 | 0.013 |
| 34,333 | -0.011 | 74,333 | -0.100 | 20,200 | 0.607 |
| 42,000 | 0.322 | 86,333 | -0.633 | 20,300 | -0.053 |
| 34,000 | 15.489 | 73,667 | 31.022 | 18,333 | 8.197 |
| 33,667 | 13.622 | 72,667 | 28.755 | 19,300 | 8.937 |
| 34,333 | 1.055 | 73,667 | 0.833 | 19,267 | 0.220 |
| 33,667 | 41.855 | 73,000 | 90.300 | 19,333 | 23.393 |
| 34,000 | 0.122 | 72,333 | -1.100 | 18,333 | -0.853 |
| 40,333 | -0.878 | 84,333 | -1.633 | 20,333 | 0.387 |
| 32,667 | 14.355 | 72,333 | 29.555 | 19,200 | 0.097 |
| 34,000 | 14.155 | 74,667 | 30.622 | 18,267 | 7.937 |
| 33,333 | 13.422 | 72,667 | 28.555 | 19,200 | 9.131 |
| 34,333 | 0.589 | 73,667 | -0.167 | 19,367 | 0.160 |
| 34,333 | 0.389 | 73,333 | -1.033 | 19,367 | 0.120 |
| 34,000 | -0.611 | 88,333 | 1.433 | 19,633 | -0.373 |
| 33,000 | 14.622 | 72,333 | 29.822 | 19,067 | 8.884 |
| 33,667 | 13.755 | 73,333 | 29.555 | 19,633 | 8.224 |
| 33,667 | 13.689 | 72,667 | 28.822 | 19,367 | 9.217 |
| 35,667 | 15.889 | 75,333 | 31.355 | 18,633 | 8.517 |
| 34,000 | -0.345 | 74,333 | -0.100 | 19,367 | 0.020 |
| 42,000 | 0.322 | 87,000 | 0.033 | 20,067 | -0.040 |
| 32,333 | 14.089 | 72,667 | 29.889 | 19,167 | 8.691 |
| 34,000 | 14.222 | 73,667 | 29.622 | 19,333 | 8.631 |
| 34,000 | 14.155 | 73,333 | 29.222 | 19,400 | 8.957 |
| 35,000 | 15.355 | 75,333 | 31.089 | 19,267 | 8.857 |
| 34,333 | 14.622 | 74,333 | 30.355 | 19,433 | 8.944 |
| 43,000 | 1.122 | 89,333 | 1.833 | 20,267 | 0.120 |
| 34,333 | -73.778 | 73,667 | -151.045 | 22,100 | -44.109 |
| 37,000 | 58.555 | 75,667 | -120.689 | 22,333 | 35.437 |
| 37,333 | -72.378 | 75,667 | -150.378 | 21,633 | -44.543 |
| 37,333 | -72.178 | 76,333 | -149.845 | 22,367 | -43.776 |
| 37,333 | -72.911 | 74,333 | -151.578 | 21,700 | -44.523 |
| 37,000 | -72.445 | 76,000 | -150.178 | 22,433 | -44.083 |
The hybrids recommended for the best candidate hybrids resulted from crosses of parents with a high SCA value. Tables 6 and 7 present the SCA values of corn from diallel crosses. A high SCA value is generally obtained from parents with a high GCA value [13]. Research results showed that not all cross combinations of parents with a positive GCA and those with a positive GCA produced offspring with a high and positive SCA. However, there was a cross combination in which one of the parents had a positive GCA and a negative GCA generated a high and positive SCA, for example the crosses of UTM 2 X UTM 7, UTM 2 X UTM 14, UTM 2 X UTM 15, UTM 2 X UTM 18, and UTM 2 X UTM 22 for production per hectare character. This phenomenon may be due to the fact that the favorable genes of a genotype are due to the fact that the favorable genes of a genotype are.
capable of covering the adverse genes of the partner’s genotype and combining properly [10]. In addition, a high and positive SCA also results from crosses of parents with a negative GCA and a negative GCA, for example the crosses of UTM 7 X UTM 15, UTM 7 X UTM 18, and UTM 7 X UTM 22.

The significant effect of SCA on the production per hectare and harvesting age showed that there was at least one best cross combination which could be recommended as a hybrid variety with a high production per hectare and early maturity. The result of diallel crosses indicated that there were two cross combinations which produced the best hybrids, i.e., the crosses of UTM 31 X UTM 2 (with a production per hectare character of 1,0476.00 kg/hectare and a harvesting age of 73.677 days) and UTM 31 X UTM 22 (with a production per hectare character of 1,0365.667 kg/hectare and harvesting age of 76 days).

Table 8 shows that heritability of 50% flowering age, harvesting age and production per hectare character are affected by the role of the additive and dominant genes, whereas the cob length, cob diameter, and 100-seeds weight are affected by the role of dominant genes. Character inheritance that are affected by the role of additive and dominant genes showed that the breeding efforts are directed to assemble pure line varieties and hybrid varieties.

The heritability value can be classified into three criteria: high (>50%), moderate (20–50%) and low (<20%) [14]. Heritability in the broad sense observed ranges from 99.400 to 93.000%, meaning that the observed character ratio is high (>90%). The heritability value in the broad and narrow sense was the highest for the harvesting age character.

IV. CONCLUSION

The 50% flowering age, harvesting age and production per hectare were affected by the role of additive and dominant genes, while the cob length, cob diameter, and weight of 100 seeds were affected by the role of the dominant genes. The UTM 2 and UTM 31 parents were the best combiners for production per hectare, UTM 7 was the best combiner for cob size. Thus, the three parents could be used to assemble varieties with a high production per hectare. The cross combinations of UTM 31 X UTM 2 and UTM 31 X UTM 22 could be directed to hybrid varieties with a high production properties and early maturity. The heritability value in the broad and narrow sense was the highest for the harvesting age character.

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