Genotypic diversity, heritability and agronomic performance high-oil maize populations

R. Neni Iriany, Muhammad Azrai, A.Takdir Makkulawu
Indonesian Cereal Research Institute (ICERI)
Jl. Dr. Ratulangi No.274 Maros, 90514, Telp/Fax: (0411) 371 016/371 961, South Sulawesi, Indonesia
Email: rn_riany@yahoo.com

Abstract. High-oil corn is has greater energy than normal corn. High-oil maize is a high negative genetic correlation between kernel oil content and grain yield. To obtain high oil content and yields maize varieties, breeding procedure design are needed to improve that kind of maize with wide genetic diversity. This study aimed to determine the genotypic variability, heritability, and performance of agronomic traits high-oil maize populations. 129 maize oil populations and three maize population as check varieties were tested in Maros Experimental station (South Sulawesi), and Jambegede Experimental station (East Java). The experimental design was used Randomized Complete Block design with two replications. Each population was grown in single row of 4 m length plot, spaced 70 cm between rows and 20 cm within row. The result showed that the location effect, genotype x environment interaction effect was significant for all traits. The Genotypic variance was considered narrow for all traits, expected maize length, number of rows per ear, and 1000-kernel weight. Broad-sense heritability was low for all observed traits, excepted for 1000-kernel weight. The 20 best populations based on the highest grain yield in both locations were selected from the basic population, MHOC0-9 had highest grain yield and MHOC0-112 lowest grain yield.

1. Introduction
Maize (Zea mays L) is used as food, feed, industrial raw materials for oil, ethanol, drink, margarine, starch, sweeteners, protein, and salad dressing. Maize oil is a healthy edible oil which we use commonly in our cooking, because it is composed mainly of poly-unsaurated fatty acids and low on saturated fat. According to[1] Maize oil is composed mainly unsaturated fatty acids, which can reduce cholesterol and heart attack.

Maize is an important staple crop in Indonesia after rice, however utilization of maize for oil has not been optimally use, because maize varieties have developed high yield but showed low oil content, on the contrary have developed high-oil varieties however, these varieties tend to show lower yields, so they are not universally accepted by growers.

To obtain high oil content and yields maize varieties, breeding procedure design are needed to improve that kind of maize with wide genetic diversity. The parents selection has a broad genetic diversity in the population genetics is an important role for the progress breeding program. According to [2], occurred genetic diversity because of the influence of genes and different genes interactions in the population. When the genotypes grown at a homogen environment will showed different phenotype.
The influence of genetic factors on the level of trait diversity can be seen from the value of heritability. The estimated value of heritability is needed to estimate the progress of a selection, the selected characters are influenced by genetic or environmental factors. Genetic diversity and heritability is very useful in the selection process. The selection will be effective if the population has a high genetic diversity and high heritability. The research of genetic diversity and heritability in maize were reported by [3, 4, 5, 6, 7, 8, 9]. This study aims to determine the Genotypic variability, heritability, and performance of agronomic traits maize oil populations.

2. Materials and Methods

The study was carried out at the experimental station Jambegede (East Java) and experimental station Maros (South Sulawesi) from January to May 2017. The experimental material comprised 129 high-oil maize populations and three check varieties, namely Lembah Palu, MS6, and MS3. The experiment was organized in a randomized block design with two replications. Each plot consisted of a single row of 5-meter and a spacing of 0.7 m between rows and 0.2 m within a row, consisted of 25 plants per row. Crop management practices like fertilizer were applied following the standard recommendations at each location.

The data were recorded on days to 50% anthesis (DTA), days to 50% silking (DTS), plant and ear height (PHT and EHT), number of plant harvested (NPH), number of ear harvested (NEH), moisture content (MC), grain yield (YLD), ear length (ELH), Ear diameter (EDT), row number per ear (NRPE), kernel number per row (NKPR), 1000-kernel weight (1000KW).

Combined data of two location were subjected to analysis of variance using Crop Stat software version 7.2. The differences among the cycle means were tested for significance using the LSD test at 5% level of probability.

Phenotypic, genotypic, and environmental variances were computed from the respective mean squares following the procedures suggested by [10] dan [11], thus: Genotype variance
\[ \sigma_g^2 = \frac{MS_g - MS_{gl}}{l}, \]
Genotype by environment interaction variance
\[ \sigma_{gl}^2 = \frac{MS_{gl} - MS_e}{r} \]
Phenotypic variance
\[ \sigma_p^2 = \sigma_g^2 + \left( \frac{\sigma_{gl}^2}{l} \right) \]

Where, \( M_{sg} \) = mean square of genotype; \( M_{sgl} \) = mean square due to genotype by environment interaction; \( M_{se} \) = error mean square (mean square of environment); \( l \) = number of location; \( r \) = number of replication.

The mean values were used for Genotypic analyses to determine phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), according to [12] as:
\[ GCV = \frac{\sqrt{\sigma_g^2}}{x} \times 100\% ; GCV = \frac{\sqrt{\sigma_p^2}}{x} \times 100\% \]

Varience Genotypic value and deviation standar of Genotypic variance determined a traits had categorized as low or high of Genotypic variance. Deviation standar of Genotypic variance was estimated according to the procedure suggested by [13] adalah
\[ \sigma_g^2 = \frac{2}{(r l)^2} \left[ \frac{M_z^2}{d_{b g} + 2} + \frac{M_z^2}{d_{b g} + 2} \right] \]

Broad-sense heritability was estimated according to the procedure suggested by Sing dan Chaudhary (1985)[12]:
\[ H = \frac{\sigma_g^2}{\sigma_p^2} \times 100 \]

Heritability percentage was categorized as low 0 < H ≤ 20% rendah; medium 20 ≤ H < 50%; 50 ≤ H < 100 high as indicated by [14].

3. Result and Discussion

The results of combined analysis of variance showing significant effect on location for grain yield, days to 50% anthesis, days to 50% silking, plant and ear height, number of plant harvested, number of ear harvested, ear length, Ear diameter and kernel number per row. Non-significant effect between
The genotype observed except ear length. Genotype by location interaction variance showing significant effect for all traits, except ear diameter and number of kernel per ear.

The result showing location, genotype, genotype by location interaction affect to observed traits. Location was the most important source of variation, then genotype and genotype by location interaction. [15]; [16] also found location, genotype, genotype by location interaction affect to traits of maize under drought tolerance.

**Table 1.** Combined analysis variance of high-oil maize populations at Maros and Jambegede Stations in dry Season 2017.

| Traits | Location | Genotype | G x L | Error | CV(%) |
|--------|----------|----------|-------|-------|-------|
| YLD    | 657.58*  | 2.24**   | 1.75* | 0.77  | 16.7  |
| DTA    | 5156.26* | 4.94**   | 4.14* | 1.56  | 2.1   |
| DTS    | 6054.82**| 5.77**   | 4.02* | 1.74  | 2.2   |
| PHT    | 1147560.00** | 1493.72** | 1388.47** | 958.42 | 21.4  |
| EHT    | 306990.00** | 367.72**  | 296.94**  | 119.59 | 16.1  |
| NPH    | 2118.31ns | 31.79**  | 26.37**  | 13.12  | 19.2  |
| NEH    | 8416.02*  | 31.09**  | 24.77**  | 9.98   | 18.8  |
| MC     | 4084.99ns | 13.18**  | 11.26**  | 4.48   | 6.8   |
| ELH    | 109.95*   | 7.26*    | 4.59*    | 2.09   | 9.9   |
| EDM    | 143.2700** | 0.39**   | 0.29ns   | 0.19   | 11.6  |
| NRPE   | 266.48ns  | 3.82**   | 2.55ns   | 1.89   | 10.9  |
| NKPR   | 17106.90** | 58.99**  | 47.76**  | 21.82  | 17.3  |
| 1000-KW| 776717.00ns | 77730.45ns | 5427.53** | 2387.14 | 16.2  |

* = significant at 1% level; **= significant at 5% level; ns = non significant

GCV, Genotypic variance, and deviation standard of variance Genotypic are presented in Table 2. Generally, genotypic diversity value was narrow for most of the traits, expect ear length, kernel row per ear, and 1000-kernel weight, suggesting that selection may be effective for these traits. [17] recorded the wide genotypic diversity for the same traits.

To increase genetic diversity, crossing between two populations that have a different genetic background is really important. Factors that influence population of genetic diversity include genetic background, which is segregated generation of crossing in a specific generation [18].

GCV (Genotypic Coefficient of Variance) was low than PCV (Phenotypic Coefficient of Variance) for most of the traits are presented in Table 2 and Table 3. Low GCV than PCV indicate high influence of environmental condition on observed traits. Our results is agreed with [19]. [20] reported coefficients of variation of phenotype and genotype were generally low for all the traits except for the yield parameters (number of ear per plant, ear and grain yield). According [21], low genotypic coefficient variance indicated individuals in the population is relatively homogen.
Table 2. Genotypic coefficient of variance, genotypic variance, and deviation standard of genotypic variance of maize oil populations at Maros and Jambegede Stations in dry Season 2017.

| Traits | GCV | $\sigma^2_g$ | $\sigma^2_{gxe}$ | $\sigma^2_e$ | $2\sigma^2_{ge}$ | Criteria |
|--------|-----|-------------|----------------|--------------|----------------|----------|
| YLD    | 0.17| 0.12        | 0.09           | 0.17         | Narrow        |
| DTA    | 0.01| 0.20        | 0.20           | 0.40         | Narrow        |
| DTS    | 0.01| 0.44        | 0.22           | 0.43         | Narrow        |
| PHT    | 0.04| 26.31       | 62.52          | 125.04       | Narrow        |
| EHT    | 0.06| 17.69       | 14.49          | 28.98        | Narrow        |
| NPH    | 0.12| 1.36        | 1.27           | 2.53         | Narrow        |
| NEH    | 0.14| 1.58        | 1.22           | 2.44         | Narrow        |
| MC     | 0.02| 0.48        | 0.53           | 1.06         | Narrow        |
| ELH    | 0.06| 0.67        | 0.26           | 0.53         | Wide          |
| EDM    | 0.04| 0.02        | 0.05           | 0.03         | Narrow        |
| NRPE   | 0.04| 0.32        | 0.14           | 0.28         | Wide          |
| NKPR   | 0.06| 2.81        | 2.33           | 4.65         | Narrow        |
| 1000-KW| 0.45| 18075.73    | 2388.78        | 4777.56      | Wide          |

Low heritability estimate was observed for grain yield, days to 50% anthesis, days to 50% silking, plant and ear height, number of plant harvested, number of ear harvested, ear length (cm), ear diameter (mm), and kernel number per row (kernel). High heritability estimation was observed for 1000-kernel weight (Table 3). [4] reported low heritability for ear length [22] reported low heritability for plant height, ear height, days 50% anthesis, ear length, and ear diameter. The low heritability observed in the present study indicated high effect of environment and low Genotypic potential in determining these traits.

Table 3. Genotypic variance, genotypic by environment interaction variance, error variance, phenotype variance, phenotypic coefficient variance, and heritability of high-oil maize populations in dry Seasons 2017.

| Traits | $\sigma^2_g$ | $\sigma^2_{gxe}$ | $\sigma^2_e$ | $\sigma^2_f$ | PCV | H | Criteria |
|--------|-------------|----------------|--------------|--------------|-----|---|----------|
| YLD    | 0.12        | 0.49           | 0.77         | 1.38         | 0.58 | 0.09 | Low      |
| DTA    | 0.20        | 1.29           | 1.56         | 3.05         | 0.03 | 0.07 | Low      |
| DTS    | 0.44        | 1.14           | 1.74         | 3.32         | 0.03 | 0.13 | Low      |
| PHT    | 26.31       | 215.03         | 958.42       | 1199.76      | 0.24 | 0.02 | Low      |
| EHT    | 17.69       | 88.68          | 119.59       | 225.96       | 0.22 | 0.08 | Low      |
| NPH    | 1.36        | 6.62           | 13.12        | 21.10        | 0.46 | 0.06 | Low      |
| NEH    | 1.58        | 3.39           | 9.98         | 18.95        | 0.48 | 0.08 | Low      |
| MC     | 0.48        | 3.39           | 4.48         | 8.35         | 0.09 | 0.06 | Low      |
| ELH    | 0.67        | 1.25           | 2.09         | 4.01         | 0.14 | 0.17 | Low      |
| EDM    | 0.02        | 0.05           | 0.19         | 0.26         | 0.14 | 0.09 | Low      |
| NRPE   | 0.32        | 0.33           | 1.89         | 2.54         | 0.13 | 0.12 | Low      |
| NKPR   | 2.81        | 12.97          | 21.82        | 37.59        | 0.23 | 0.07 | Low      |
| 1000-KW| 18075.73    | 2387.14        | 21983.07     | 4777.56      | 0.49 | 0.82 | High     |

3.1 Agronomic Performance and Yield Components of Best Yielding Genotypes
A total of 129 populations including 3 check varieties were evaluated at Maros and Jambegede Stations. The 20 highest yields genotypes were selected and were compared to 3 checks varieties for fat content analysis in the laboratory.

The result showed of yield average ranges 0.3 - 7.3 t.ha-1 at Jambegede station, MHOC0-9 population showed a non-significant difference with check varieties MS3. MHOC0-9 population has
the highest grain yield but fat content only 4.35% and no population has a higher fat content than MS3 in the 20 highest yield genotype were selected.

The result showed of yield average ranges 0.5 - 3.6 t.ha\(^{-1}\) at Maros station. MHOC0-93 have the highest grain yield with fat content 4.74%. MHOC0-9 population has the highest grain yield at Jambegede Station, but it ranks 4th in Maros Station. The average of grain yield at Maros was relatively lower than Jambegede due to water stress at early generative phase. The statement similarity with genetic variance analysis included in the narrow category, it means the performance of yield traits is influenced by environment.

Table 4. Grain yield of 20 best high-oil maize population selected at Jambegede and Maros station, dry Season 2017.

| No  | Populations     | Yield (t.ha\(^{-1}\)) | Fat(%) |
|-----|----------------|------------------------|--------|
|     |                | Jambegede   | Maros   | Average  |
| 1   | MHOC0-9        | 7.3\(^{ab}\)   | 2.8\(^{ab}\)   | 5.0\(^{ab}\) | 4.35 |
| 2   | MHOC0-110      | 4.8\(^{ab}\)   | 2.9\(^{a}\)   | 3.9\(^{a}\) | 4.57 |
| 3   | MHOC0-122      | 4.0\(^{a}\)   | 2.9\(^{a}\)   | 3.5\(^{a}\) | 4.78 |
| 4   | MHOC0-57       | 5.5\(^{ab}\)   | 1.1\(^{a}\)   | 3.3\(^{a}\) | 4.01 |
| 5   | MHOC0-27       | 4.4\(^{a}\)   | 2.1\(^{a}\)   | 3.2\(^{a}\) | 4.26 |
| 6   | MHOC0-78       | 5.6\(^{ab}\)   | 0.8\(^{a}\)   | 3.2\(^{a}\) | 3.96 |
| 7   | MHOC0-81       | 5.6\(^{ab}\)   | 0.6\(^{a}\)   | 3.1\(^{a}\) | 4.03 |
| 8   | MHOC0-93       | 2.9\(^{a}\)   | 3.2\(^{a}\)   | 3.1\(^{a}\) | 4.74 |
| 9   | MHOC0-51       | 4.0\(^{a}\)   | 2.0\(^{a}\)   | 3.0\(^{a}\) | 3.94 |
| 10  | MHOC0-34       | 3.7\(^{a}\)   | 2.2\(^{a}\)   | 3.0\(^{a}\) | 3.49 |
| 11  | MHOC0-58       | 4.2\(^{a}\)   | 1.6\(^{a}\)   | 2.9\(^{a}\) | 4.85 |
| 12  | MHOC0-67       | 4.4\(^{a}\)   | 1.5\(^{a}\)   | 2.9\(^{a}\) | 5.28 |
| 13  | MHOC0-77       | 5.4\(^{ab}\)   | 0.3\(^{a}\)   | 2.8\(^{a}\) | 5.92 |
| 14  | MHOC0-101      | 3.8\(^{a}\)   | 1.8\(^{a}\)   | 2.8\(^{a}\) | 5.16 |
| 15  | MHOC0-56       | 4.7\(^{a}\)   | 0.9\(^{a}\)   | 2.8\(^{a}\) | 7.33 |
| 16  | MHOC0-23       | 4.3\(^{a}\)   | 1.2\(^{a}\)   | 2.7\(^{a}\) | 7.16 |
| 17  | MHOC0-120      | 4.8\(^{ab}\)   | 0.6\(^{ab}\)   | 2.7\(^{ab}\) | 4.54 |
| 18  | MHOC0-96       | 4.8\(^{ab}\)   | 0.6\(^{ab}\)   | 2.7\(^{ab}\) | 3.99 |
| 19  | MHOC0-33       | 4.8\(^{ab}\)   | 0.6\(^{ab}\)   | 2.7\(^{ab}\) | 7.34 |
| 20  | MHOC0-26       | 4.7\(^{ab}\)   | 0.1\(^{ab}\)   | 2.6\(^{ab}\) | 5.90 |
| 129 | MHOC0-112      | 0.3\(^{a}\)   | 0.5\(^{a}\)   | 0.3\(^{a}\) |        |
| Checks: |            |            |            |        |
| Lembah Palu | 2.8 | 0.1 | 1.5 | 8.02 |
| MS6 | 3.4 | 2.3 | 2.9 | 5.60 |
| MS3 | 7.8 | 2.8 | 5.3 | 9.63 |
| Average | 3.1 | 0.9 | 2.0 |        |
| KK | 13.9 | 19.4 | 16.7 |        |
| SE | 0.7 | 0.5 | 0.7 |        |
| 5%LSD | 2.0 | 1.4 | 1.9 |        |

\(^a\) = significant different with Lembah Palu, \(^b\) = significant different with MS6, \(^c\) = significant different with MS3.
Agronomic traits and yield component of 20 high-oil maize populations represented in Table 2 dan 3. Generally, days to anthesis, days to silking, plant height, ear height, number of plant harvested, number of ear harvested, moisture content, ear length, ear diameter, number of row per ear, number of kernel per row similar with checks varieties.

Table 5. Agronomic traits high-oil maize population selected at Jambegede and Maros Station in dry season 2017.

| No | Populations  | DTA | DTS | PHT | EHT | NPH | NEH | MC  |
|----|--------------|-----|-----|-----|-----|-----|-----|-----|
| 1  | MHOC0-9      | 59.8| 61.0| 135.8| 62.5| 15.8| 14.5| 30.6|
| 2  | MHOC0-110    | 57.5| 59.8| 148.7| 68.3| 13.0| 18.0| 31.5|
| 3  | MHOC0-122    | 57.8| 59.0| 155.6| 71.9| 10.8| 11.0| 30.1|
| 4  | MHOC0-57     | 59.3| 60.8| 141.2| 66.3| 15.5| 12.0| 30.0|
| 5  | MHOC0-27     | 57.0| 58.8| 152.9| 69.3| 15.5| 13.3| 30.3|
| 6  | MHOC0-78     | 58.3| 59.0| 151.5| 68.8| 10.8| 12.0| 30.3|
| 7  | MHOC0-81     | 59.3| 60.5| 133.2| 64.9| 8.5  | 9.0  | 32.7|
| 8  | MHOC0-93     | 57.8| 58.5| 144.9| 66.6| 14.5| 18.0| 31.2|
| 9  | MHOC0-51     | 58.0| 59.0| 144.1| 67.5| 18.5 | 16.3 | 27.8|
| 10 | MHOC0-34     | 57.3| 59.0| 141.8| 58.8| 13.3| 12.8| 32.6|
| 11 | MHOC0-58     | 58.8| 60.3| 123.5| 64.0| 8.0  | 8.5  | 33.4|
| 12 | MHOC0-67     | 57.8| 59.5| 160.3| 90.1| 8.0  | 9.5  | 32.0|
| 13 | MHOC0-77     | 58.5| 59.8| 124.2| 58.6| 6.0  | 4.5  | 31.9|
| 14 | MHOC0-101    | 59.8| 61.3| 138.7| 69.2| 13.0| 13.8| 31.8|
| 15 | MHOC0-56     | 59.8| 60.8| 156.0| 79.2| 11.5| 12.3| 32.1|
| 16 | MHOC0-23     | 57.8| 59.0| 148.9| 80.8| 14.5| 10.3| 28.2|
| 17 | MHOC0-120    | 58.5| 59.3| 161.3| 80.9| 10.0| 11.5| 33.8|
| 18 | MHOC0-96     | 58.3| 59.8| 142.8| 74.3| 10.8| 11.5| 30.6|
| 19 | MHOC0-33     | 59.0| 60.3| 140.7| 68.2| 12.0| 10.0| 32.0|
| 20 | MHOC0-26     | 57.8| 58.8| 227.0abc| 73.5| 11.0| 10.3| 28.7|
| 29 | MHOC0-112    | 59.0| 59.5| 142.6| 73.6| 2.3  | 2.3  | 33.4|
|    | Checks:      |     |     |     |     |     |     |     |
|    | LembahPalu   | 57.8| 58.5| 146.0| 69.8| 9.8  | 9.3  | 31.8|
|    | MS6          | 57.5| 59.0| 160.8| 68.0| 11.5| 14.5| 31.3|
|    | MS3          | 58.8| 60.3| 159.7| 78.6| 14.8| 14.5| 33.2|
|    | Average      | 58.6| 59.9| 144.7| 68.0| 9.9  | 9.0  | 31.0|
|    | KK           | 2.1 | 2.2 | 21.4 | 16.1| 19.2| 18.8| 6.8 |
|    | SE           | 1.1 | 1.2 | 18.6 | 8.6 | 2.6 | 2.5 | 1.7 |
|    | 5%LSD        | 3.1 | 3.4 | 52.1 | 24.1| 7.2 | 7.0 | 4.7 |

Annotation: DTA= days to anthesis, DTS= days to silking, PHT= Plant Height, EHT= Ear Height, NPH= Number of plant harvested, NEH= Number of ear harvested, MC= Moisture Content, a = significant different with Lembah Palu, b = significant different with MS6, c = significant different with MS3.
Days to 50% silking is an important trait, usually, determine earliness to maturity of the maize crop. Plant height ranged from 123.5 – 227.0 cm. Plant height plays an important role in plant lodging. Consequently, maize breeders give special attention to this trait in maize breeding (Khan, et al. 2018)[23].

MHOC0-26 significant highest than the all check varieties for plant height traits. Number of plant harvested and ear harvested traits, MHOC0-51 was significantly more than Lembah Palu. MHOC0-93 has a significantly higher then Lembah Palu for ear harvested.

The average ear length of the oil maize population evaluated was not significantly different with check MS6 and MS3 varieties, but there were some populations significantly different with Lembah Palu. For ear diameter traits, all populations were significantly different from Lembah Palu, except for MHOC0-33 and MHOC0-37 populations. All populations were not significantly different from the three check varieties for number of row per ear.

MHOC0-112 Population has an average ear diameter and 1000-kernel weights which is large but has lowest yield, causing by imperfect pollination so that the cob was not filled with seeds and made the yield not optimal.

MHOC0-58 population has a significantly higher number of seeds per row than the MS6 check, and the number of seeds per row of the MHOC0-57 population was significantly higher than the three check varieties.

For 1000-kernel weight, almost all populations were significant than MS6 and MS3 check varieties. Population MHOC0-58 has number of kernel per row significant than MS6, and number of kernel per row of the MHOC0-57 population was significantly more than the three check varieties.
Table 6. Yield component of high-oil maize population selected at Jambegede and Maros Station in dry season 2017.

| No | Populations | ELH (cm) | EDM (mm) | NRPE (row) | NKPR (kernel) | 1000-KW (g) |
|----|-------------|----------|----------|------------|---------------|-------------|
| 1  | MHOC0-9     | 15.7a    | 4.0a     | 12.0       | 27.9          | 319.3bc     |
| 2  | MHOC0-110   | 15.5     | 3.7a     | 12.1       | 29.0          | 281.1bc     |
| 3  | MHOC0-122   | 15.3     | 4.1a     | 13.5       | 29.9          | 309.4bc     |
| 4  | MHOC0-57    | 16.5a    | 4.0a     | 12.1       | 48.4abc       | 357.3abc    |
| 5  | MHOC0-27    | 16.4a    | 4.1a     | 12.8       | 32.3          | 314.3bc     |
| 6  | MHOC0-78    | 16.5a    | 4.1a     | 13.8       | 26.3          | 339.4bc     |
| 7  | MHOC0-81    | 14.7     | 4.0a     | 12.1       | 21.6          | 380.4abc    |
| 8  | MHOC0-93    | 15.9a    | 3.6a     | 12.5       | 28.9          | 289.4bc     |
| 9  | MHOC0-51    | 15.1     | 3.8a     | 12.4       | 25.9          | 280.8bc     |
| 10 | MHOC0-34    | 15.6a    | 3.9a     | 13.7       | 31.2          | 271.6bc     |
| 11 | MHOC0-58    | 17.2a    | 3.7a     | 13.8       | 33.4b         | 316.1bc     |
| 12 | MHOC0-67    | 16.6a    | 3.9a     | 11.9       | 29.1          | 385.1abc    |
| 13 | MHOC0-77    | 13.5     | 3.4      | 12.2       | 23.0          | 298.3bc     |
| 14 | MHOC0-101   | 16.1a    | 4.0a     | 12.7       | 29.8          | 358.4abc    |
| 15 | MHOC0-56    | 16.1a    | 3.8a     | 12.1       | 29.7          | 351.6abc    |
| 16 | MHOC0-23    | 15.0     | 4.0a     | 13.6       | 29.4          | 299.9bc     |
| 17 | MHOC0-120   | 13.2     | 3.9a     | 12.4       | 23.6          | 328.3bc     |
| 18 | MHOC0-96    | 16.1a    | 4.0a     | 12.6       | 28.2          | 283.4bc     |
| 19 | MHOC0-33    | 13.7     | 3.6      | 13.0       | 23.2          | 303.7bc     |
| 20 | MHOC0-26    | 17.2a    | 3.8a     | 12.0       | 26.8          | 297.5bc     |
| 21 | MHOC0-112   | 14.4     | 4.1a     | 12.0       | 28.3          | 382.1abc    |

Checks:

|          | ELH (cm) | EDM (mm) | NRPE (row) | NKPR (kernel) | 1000-KW (g) |
|----------|----------|----------|------------|---------------|-------------|
| Lembah Palu | 12.5     | 3.0      | 12.1       | 28.2          | 239.1       |
| MS6      | 17.2     | 4.4      | 13.4       | 33.3          | 330.3       |
| MS3      | 16.6     | 4.7      | 13.5       | 28.9          | 362.1       |

Average | 14.6  | 3.7  | 12.7  | 26.9  | 301.9 |

KK | 9.9 | 11.6 | 10.9 | 17.3 | 16.2 |
SE | 1.1 | 0.2  | 0.8  | 3.5  | 36.8 |

5% LSD | 3.0 | 0.6 | 2.2 | 9.7 | 103.0 |

Annotation: ELH = Ear Lenght, EDM = Ear Diameter, NRPE = Number of Row per Ear, NKPR = Number of Kernel per Row, 1000-KW = 1000 Kernel weight, a = significant different with Lembah Palu, b = significant different with MS6, c = significantly different with MS3.
4. Conclusion
1. Length ear, number of row per ear, and 1000-kernel weight have narrow variance genetic value.
2. Low heritability values in broad-sense were yield, days to anthesis, days to silking, plant height, ear height, number plant harvest, number ear harvest, moisture content, ear length, ear diameter, number of row per ear, and number of kernel per row.
3. Population of MHOC0-9 had the highest yield, and MHOC0-112 had the lowest yield in both locations.

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