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Estimation Genetic Action of Heritability Percentage and Inbreeding Depression of Four Hybrids Maize by Generation Mean Analysis (Field Traits)

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Abstract. With the aim of current study to estimate genetic action, heritability percentage in its broad and narrow sense and inbreeding depression resulting from inbreeding, using the generation mean analysis method to analyze the generation's means of hybrids maize that different in flowering dates and maturity. The genetic action, that controls inheritance of the field traits to the selected inbred lines and their resulting hybrids using the generation mean analysis. Five pure inbred lines of maize (ZA17WR, Zi17WZ, ZM74, ZM19 and ZM49W3E) were selected from fifteen different inbred lines with flowering dates and maturity in the spring season 2019 and were crosses according to the research target (late × late),(late ×early) ,(early ×late) and(early ×early). On 2019 fall season were entered into a backcross program to analyze the means generation analysis. On 2020 spring season to produce the (six generations) which are (P1, P2, F1, F2, BC1 and BC2) for the four crosses were evaluated in comparative experiments using a randomized complete block design (RCBD) and with three replicates. Genetic analysis was done for the components of genetic variance for the three criteria, according to [1] for the traits of the number of days to 75% tasselling, Number of days to 75% silking, plant height , ear, leaves area and yield of individual plant. Results showedThe dominance gene action is dominant in the inheritance of the silking and tassling traits in the four crosses. As for the trait of the number of leaves and the yield of the plant, the dominance gene action controlling its inheritance was in the first hybrid and the additive gene action in the second, third and fourth crosses, while the dominance action had the greatest contribution to the inheritance of the trait The area of leaves in hybrids 2, 3 and 4 and in the first hybrid was the largest additive gene action contribution, The percentages of heritability in the broad and narrow sense differed among the four hybrids for the traits studied. The highest percentage of heritability in the narrow sense for the trait of plant yield in the fourth hybrid was 91.50% due to the high additive variance, while the highest percentage of heritability in the broad sense was for the trait of leaf area in the third hybrid was 99.27%The highest percentage of genetic improvement for the trait of the number of leaves in the fourth cross was 27.64% , and the highest Inbreeding Depression for second generation F2 for yield in the same hybrid was 22.66%,

Keywords. Heritability, Generation mean analysis, Inbreeding depression and maize.

1. Introduction

The process of developing new hybrids and synthetic varieties of maize crop requires the availability of sufficient information regarding the effects of genetic actions and their Epistasis interactions on the structures of the parental inbred lines involved in the crossbreeding process. This is done through the use of different cross-breeding designs, including back-cross, which is mediated by reducing the time, cost and effort required to produce new individuals as a product of long work and for several generations [1,2]. It is used in the case of the target gene present in the quantitative traits of the crop, such as the ZMCCT9 gene responsible for flowering process, the ZMBAMID gene responsible for the physiological maturation process. Where one members of the true one generation F1 are crossed with one of the parents (the true one parent P1) to produce a parent called Back cross one (BC1), and other members of the true one generation F1 are crossed with the second parent (P2) to produce a parent called Back cross two (BC2). Carrying out the process of backcrossing for several generations until the target gene for the desired quantitative trait is stable in future generations [3]. Maize crop is an excellent model for studying genetic regulation because it has high genotypic and phenotypic variance that helps to choose the appropriate breeding method, and it has a wide genetic base available for testing [4]. The back cross method is one of the important techniques in finding hybrids that are tested to select the superior ones in their traits appropriate to the environmental conditions, through the information obtained about understanding the nature of genetic actions and identifying their interactions in the transmission and inheritance of the traits of maturity and flowering for different inbred lines with flowering and physiological maturity and their resulting hybrids F1. The traits of flowering and physiological maturity are among the factors affecting the increase in yield and its components, as flowering and physiological maturity are complex quantitative traits that are controlled by a group of pairs of genes and have a great influence on the environmental factors surrounding during the growing season, as well as genetic and environmental interaction lead to the result the Appearance of new genetic mutations or the reduction of gene action, which leads to the Appearance of populations with new traits [5]. Genetic variance is the difference between plants in the cultivated genotype (the ability in which the genotype is shared) under one environmental condition and the environmental variance is the difference between members with similar genotype (individuals carrying the same genotype) and cultivated under different environmental conditions. Environmental variance is one of the components of phenotypic variance [6] Genetic variance can be divided into its components: Additive variance, which results from the influence of genes in all isolated genetic loci of the organism's genome (origins between the two original individuals in the gene). Can division from the additive action of a gene arising from allelic ineraction between the alleles of a single genetic locus (the division of the mixture from of the two original population means).

[7] found that when they performed three crosses between three pure inbred lines of maize (EV-157 (SW-491 , EV-120) × SW-491 and EV-120) × EV-157 to obtain the four generations (F1, F2, BC1and BC2) ، To study the genetic variance by the mean generation mean analysis method. Significance of the biological product in all four crosses. The effect of the dominance gene action was significant in indicator of the dominance of the dominance genes over the action of other genes, and the effect of the additive genetic action was significant on the heritability of the trait, an indication of the possibility that selection would be effective in improving the studied trait.

[8] obtained when they cross-crossed five Pure inbred lines of maize, the effect of additive and non-additive genetic action is of great importance in the transmission and inheritance of the trait of plant height, the effect of the non-additive gene action had a significant effect on the trait under study. [9] found, through his study of four crosses of maize crop and the six generations (P1, P2, F1, F2, BC1and BC2) for the genetic action components that have the traits of plant height, ear height and silking, that the dominance genetic action is dominant and also found a role for the act Genetic Epistasis in the inheritance of studied traits. Diallel cross- was carried out from [10] for six internally inbred lines and 30 hybrids to study the heritability degree in the broad sense for the trait of plant height, their results showed that the values of the broad-spectrum heritability degree were high for the studied trait. The plant height and leaf area are under the influence of the additive genetic action, and the dominance degree is less than one value (1.00). It indicated that the studied traits fall under the influence of the partial dominance of the genes.

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[11] showed that the traits of tasselling and silking, plant height and leaf area are under the influence of additive genetic action and that the dominance degree is less than the one (1.00). It indicated that the studied traits fall under the influence of partial dominance of genes. [12] appear during their study of twenty genotypes of maize to study the genetic behavior of the trait of plant height in the segregation generation (F2, F3), the generation mean analysis method is used, the dominant genetic action, the Epistasis of the type (dominance ×dominance) is an important role in the transmission and inheritance of the studied trait.

[13] confirmed that, through their study of four crosses of maize and the six generations of silking trait, that the two genetic actions of the Duplicate type are responsible for the transmission and inheritance of the trait under study. While [14] indicated that the dominance degree average of is greater than the true one (1.00), it is indicating the dominance of the Epistasis dominance in the inheritance of the traits under study: tasselling , silking, plant height and leaf area. The action of the dominance gene is more important than the action of the additive gene in the transmission and inheritance of the studied traits. [15] appeared during their study of two hybrids of maize and the six generations (P1, P2, F1, F2, BC1and BC2) for the genetic action of the traits of ear length, plant height and silking, the dominant genetic action dominated the inheritance of the studied traits. The same researchers also showed in the same study that the heritability percentage in the broad and narrow sense for the traits of silking and plant height was an average of 0.38 for the character of plant height and 0.51 for the character of silking, and the of heritability percentage in the narrow sense was low for the two studied traits.

[16] noted in their study of three crosses with its six generations of maize crop, the heritability percentage in the broad and narrow sense for the traits of plant height and silking, the heritability percentage in the broad sense is high for all hybrids 43.00% and 41.3%, while the heritability percentage in the narrow sense is low for the two traits studied traits, it was 26.3% and 32.00% for the trait of silking and plant height sequentially. [17] indicated that the heritability percentage in the broad sense was high for the tasselling trait, reaching 73.42%, as a result of the high value of genetic variance, that the dominance degree mean of the was greater than one(1.00), reaching 4.85, the control of the over-dominance genes on the inheritance of the trait. While the heritability value of in the narrow sense of the tasselling trait was 5.73%. [18] indicated during their study of the six generations the effect of genetic action in the transmission and inheritance of tasselling and silking traits, the genetic action was significant in the second male P2 and the true one back cross BC1 and that the genetic action The additive factor is the most important factor without other genetic influences in the transmission and inheritance of the two studied traits.

[19] indicated during their research for four hybrids of maize and its six generations, the genetic effect of the traits of leaves number, plant height and leaf area, that the trait of the leaves number is under the additive influence, while the traits of plant height and leaf area are under the influence of the dominance action, and the dominance degree was for the trait. The leaves number was (0.638), while the two traits were plant height and leaf area (6.35 and 1.41), respectively. While, the heritability percentage in the broad sense was (86%, 93%, and 98%) sequentially, the heritability percentage in the narrow sense was (34%, 29% and 61%) sequentially.[20] showed that when they studied a number of parents and their individual hybrids of maize crop, the heritability percentage in the narrow sense for tasselling and silking traits was (12.5% and 17.4%), for the two traits, leaves number and leaf area were low (5.3% and 2.5%) respectively. The reason is due to the influence of the additive genetic action that is dominant on the inheritance of these traits, while the dominance degree average for tasselling and silking traits was (3.7 and 7.4) respectively, and for the two traits leaves number and leaf area (5.8 and 8.6) respectively. That evidence for the dominance of over-dominance genes in the transmission and inheritance of the studied traits. The current study aims to determine the type and nature of genetic action and to estimate the heritability percentage in the narrow and broad sense by the generation means analysis method for the field traits of four crosses maize, varying in flowering and physiological maturity, and then determining the appropriate breeding method.

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2. Materials and Methods

This study was carried out in the fields of the University of Baghdad, College of Agricultural Engineering Sciences / Al-Jadiriyah, and in four consecutive seasons of spring and fall for the years (2019 and 2020). when preparing the soil we add the NPK fertilizer at a rate of 240 kg hectares^{-1}, 46% urea fertilizer was added nitrogen 360 kg N hectares^{-1} and in two stages, the first one at the elongation stage and the second at the beginning of the flowering stage [21]. All agricultural operations were carried out, including irrigation, hoeing, weed control and the maize stem borer controlling (Sesamia critica) by feeding the growing tops of plants with the granulated diazinon (10% active substance) at a rate of 6 kg / hectare. It was added in two stages, the first one when the plants reached a height of 20 cm, and the second two weeks after the first control [22].

2.1. First Season (Spring 2019)

The experimental soil was prepared from plowing, smoothing, leveling and tamping, and the seeds of the fifteen pure inbred lines mentioned were planted on the furrows , the length of the furrows is 6 meters, and the distance between them is 0.8 m, by planting six lines for one inbred line, and in a hole at a distance of 0.25 m between one hole and another on 19-3-2019. For crossing program in next season we are calculating days to tasselling, silking, physiological maturity and flowering compatibility, developing the inbred lines by making self-pollinating between inbred lines. For cultivation in the next season the aim of increasing genetic purity, as well as selecting the inbred lines with good growth characteristics and yield.

2.2. Second Season (Fall 2019)

The seeds of the fifteen inbred lines were sown in the fall season on July 16, 2019 and the crossing experiment was conducted. The field designated for the experiment was divided into two parts. The first part was planted with half of the grains of the fifteen inbred lines on furrows, the distance from one to another (0.8) m, and in a hole, one from the other (0.25 m) at a rate of (6) furrows and at a rate of 2 seeds per hole, it was thinned out to One plant in the hole. A week after planting, the second part of the field was planted with the same grains, to ensure that flowering was compatible between the inbred lines and to obtain pollen with effective vitality throughout the crossing period. When the plants reached the flowering stage, the female inflorescence was wrapped before the emergence of the silk with paper bags to obtain the required pollination and to avoid open pollination between inbred lines. The male inflorescence was wrapped in paper bags one day before the start of the inoculation process between the pure inbred lines. On the next day, pollen grains were collected and what was ready from the female inflorescences to receive pollen were pollinated with it. This process was continued until all the required crosses were made between the pure inbred lines used in the study. Inbred lines were multiplied among themselves, and the number of male and female flowering days and physiological maturity for each inbred line were recorded. This is because, to select the resulting hybrids, according to the research objective (late × late), (late×early), (early × late) and (early × early). The process of self-pollination of the inbred lines was also carried out for the purpose of multiplying their seeds, and the process continued until the required crosses were completed and an average of (8-10) ears was obtained for each cross as a minimum to ensure that sufficient numbers of seeds were obtained for the experiment of the next season. At the end of the spring season and at full maturity, the hybrid ears and the self-pollinated parents were harvested individually. Four hybrids were selected, which were characterized by the success of the required cross-fertilization and obtaining the largest number of seeds sufficient for planting. The hybrids were as follows: the first hybrid (late × late) for the two inbred lines ((Zi17WZ x ZA17WR)), the second hybrid (early × late) for the two inbred lines ((ZM49W3E× ZM74)), and The third hybrid (late × early) for the two inbred lines (ZM19 x ZM74), and the fourth hybrid (early × early) for the two inbred lines (ZM19×ZM49W3E).

2.3. Third Season (Spring 2020)

The planting took place in this season on March 17, 2020, as the four hybrids and their parents were planted with 10 furrows for each parent and for each hybrid the length of the furrows was 4 m. The crossing of the first generation F1 was carried out with the first parent P1 and the second parent P2 to produce BC1 and BC2 seeds respectively, and plants were also pollinated The first generation F1 self to produce the seeds of the second generation F2. The process of self-pollination of the parents was carried out for the purpose of multiplying their seeds and using them in the comparison experiment and according to the recommendations, the process continued until the required crosses were completed and a rate of (10-15) ears was obtained for each cross and self-pollinated as a minimum to ensure that sufficient numbers of seeds were obtained from the six generations (P1, P2 , F1, F2, BC1 and BC2) for each of the four hybrids, and introduced into a comparative experiment in the next season.

2.4. Fourth Season (Fall 2020)

The comparison experiment was conducted during the autumn season (2020), where the seeds of the six generations were sown for each hybrid, on July 22, using a randomized complete block design (RCBD) with three replications. 50 thousand plants per hectare. Three seeds were sown in each hole and thinned to one plant after 15 days of emergence, and all agricultural operations were carried out as in the previous seasons. When the plants reached the stage of harvest maturity, 20 plants were selected from the guarded middle lines for each (P1, P2, F1) and 40 plants for the second generation (F2) and 30 plants for each of (BC1, BC2) and the following traits were calculated for them.

2.5. Studied Traits

- Number of days from planting until 75% of tasselling (day): It was calculated from the date of the true one watering until the appearance of male inflorescence in 75% of the plants for each experimental unit [23]
- The number of days from planting until 75% of silking (day): according to the appearance of the female inflorescence in 75% of the plants taken for each generation.
- Plant height (cm) calculated from the area of the stem exit from the surface of the soil to the base of the male inflorescence
- Ear upper height (cm) calculated from the surface of the soil to the phalanx of the upper ear (El-Sahookie ، 2009)
- Number of effective leaves per plant (leaf. plant^{-1}): The number of effective leaves of plants taken for each generation and for each hybrid under study was calculated.
- The total plant leave area (cm^2) was found according to the following equation:
- The leaf area of the plant (cm^2) = the square of the length of the leaf that lies under the upper ear × 0.75 (if the leaves number in the plant is 14 leaves or more) and the square of the length of the leaf that lies under the leaf of the upper ear × 0.65 (if the leaves number in the plant is 13 leaves or less [24].
- The individual grain yield of plant (g.): The grains were weighed with a sensitive electric balance, and then the weight was adjusted to a moisture content of 15.5% [25].

The expected genetic advance was estimated as a percentage of the mean GA% according to the following equations.

$$GA=K\times h^2_{.n.s}\times \sigma F2$$

$$GA\%=GA/(\overline{F2})$$

Where K = the intensity of selection and its value is 1.76 based on the selection of 10%
Where σP = phenotypic standard deviation
The ranges were adopted for the expected genetic advance limits as follows: - Less than 10% low, 10%-30% medium, more than 30% high suggested by [26].

Inbreeding Depression: It was calculated according to the equation developed by [27]

$$\text{Inbreeding Depression (ID)} = (\overline{F1}-\overline{F2}/\overline{F1}) \times 100$$

ID= Inbreeding dispersion.
$\overline{F}$ 1 = First generation hybrid average
$\overline{F}$ 2 = Second-generation hybrid average
The environmental variance E, the additive variance D, the dominance variance H, and the dominance degree (H/D) 1/2 and F was estimated according to 1 according to the following equations:

$$E=1/3(VP1+VP2+VF1)$$

$$D=2(VF2-VB1-VB2)$$

$$H=4(VF2-1/2VD-E)$$

$$\bar{a} = (H/D)1/2$$

$$F=BC1-BC2$$

The estimation of inheritance in the broad and narrow sense according to the following equations, according to [28].

$$h^2{}_{\cdot b.s} = (VG/VP) \times 100$$

$$h^2{}_{\cdot n.s} = (VA/VP) \times 100$$

Data were analyzed in Software Excel 2018, Genstate 2018, and Spar.2 out of the box.

3. Results and Dissection

3.1. First Hybrid (Late × Late) (Zi17WZ × ZA17WR)

3.1.1. Number of Days From Planting Until 75% of Tasselling

It appears from the data of Table (1) to analyze the variance components for the tasselling trait of the hybrid (Zi17WZ × ZA17WR) that the values of the environmental variance were less than the values of the additive and dominance variance, as they reached 15.52 and 50.66 respectively, and this confirms that the genetic variance contributes more than the environmental variance in the inheritance of this trait. The effect of dominance variance was greater than the additive and this was reflected on the dominance degree as it was greater than true one (1.81), and the heritability percentage in the narrow sense amounted to %22.15 and in its broad sense 94.46%, the high value of heritability in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the value of F, it indicates the extent of the correlation between D and H at all sites. The negative value (-2.2) indicates the participation of the additive effect in the inheritance of the trait. This confirms the results of the previous tables, which were similar to the results obtained by [29,17,30]. The results of Table (1) indicated the expected genetic advance value, which amounted to 6.37, while the genetic advance percentage was an average of %11.58. One of the results of the table is that the trait is under the control of the non-additive genetic action more than the influence of the additive genetic action, and through the hybrid vigor and the high genetic variance. Therefore, the trait can be improved by hybridization and the outstanding hybrids can be selected from them. There is a strong relationship between the hybrid vigor and the inbreeding dispersion that occurs as a result of the use of inbreeding in cross-pollinated crops such as maize. The reason is due to the participation of the same genetic sites in each of the two cases that show inbreeding dispersion depending on the dominance degree and its presence [31]. The results showed in Table (1) that the value of the inbreeding dispersion percentage associated with inbreeding was positive and significant for the tasselling trait, amounting to %2.36 , similar results obtained by [32].

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3.1.2. The Number of Days From Planting Until 75% of Silking

The results of Table (1) showed the variance components analysis for the silking trait of the same hybrid(Zi17WZ × ZA17WR). The data indicate that the values of the environmental variance were less than the values of the additive and dominance variance, as they reached 6.212 and 14.00 respectively, and this confirms that the genetic variance contributes more than the environmental variance to the inheritance of this trait. The effect of dominance variance was greater than the additive and this was reflected on the dominance degree as it was greater than true one (1.51), and the heritability percentage in the narrow sense amounted to %28.66 and in its broad sense %92.86, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the value of F, it indicates the extent of the correlation between D and H at all sites. The negative value (- 2.00) indicates the contribution of the additive influence to the inheritance of the trait. This confirms the results of the previous tables, which were similar to the results obtained by [16],[30] and [20]. The value of the genetic advance was positive, reaching 2.98, while the genetic advance percentage was 5.05% and it was low (Table, 13). From the results of the previous tables, we note that the trait is under the control of the over -dominance of genes and non-additive action. Therefore, the trait can be improved by hybridization and selecting outstanding hybrids to it. The results of the same table showed that the trait of silking showed a value of %2.20 lower than tassling for inbreeding depression, and this is close to what was found by [31].

3.1.3. Plant Height

The results of Table (1) show the variance components analysis for the plant height trait of the same hybrid. The data indicate that the values of the environmental variance were less than the values of the additive and dominance variance, as they reached 210.64 and 35.04 respectively, and this confirms that the genetic variance contributes more than the environmental variance in the inheritance of this trait. The effect of the additive variance was greater than the dominance and this was reflected in the dominance degree, as it was less than true one, and the heritability percentage in the narrow sense amounted to %79.09, that heritability in the high narrow sense indicates the greater contribution of the additive genetic action, while heritability in its broad sense amounted to% 92.24 and this confirms The greater contribution of genetic variance compared to environmental variance. As for the value of F, it indicates the extent of the correlation between D and H in all loci. The negative value (-4.1) indicates the role of additional alleles in the inheritance of the studied trait, and this confirms the results of the previous tables, as they were consistent with the results of [19] , [30]and [20]. Therefore, the plant breeder has to choose the selection method to obtain genetic structures characterized by an appropriate height resulting from crossing inbred lines two late in flowering and physiological maturity. The effect of the additive genes is over - dominance of the trait, as evident by the dominance degree is less than true one, the high heritability percentage in the narrow sense, and the positive and moral strength of the hybrid. Therefore, the advance of the trait under study is done by following the selection. As the results indicated in Table (1) that the amount of inbreeding depression was its value Positive and significant amounted to (%7.53) for the trait of plant height, and this is consistent with what was found by [33].

3.1.4. Ear Height

It is noted from the data of Table (1) that the variance components analyzed for the ear height trait of the same hybrid. The data indicate that the environmental variance values were less than the additive and dominance variance values, as they reached 52.8 and 24.52 respectively. Confirms that genetic variance contributes more than environmental variance to the inheritance of the trait of the ear height.
The effect of the additive variance was greater than the dominance and this was reflected on the dominance degree as it was less than true one true (0.40), and the heritability percentage in the narrow sense amounted to% 66.19 and in its broad sense %96.92, the high value of heritability in the broad sense indicates the greater contribution of genetic variance compared to variance environmental. As for the F value, it indicates the linkage of the association between D and H in all loci. The positive

value indicates the contribution of the dominance alleles (4.16) to the inheritance of the trait. This confirms the results of the previous tables, which were close to what was obtained by [29],[30] and [34]. The value of the expected genetic advance was low, amounting to 6.87, while the genetic advance percentage was% 9.42 were low. , that the effect of the additive genes is over- dominance the trait, as evidenced by the dominance degree is less than one , and the heritability percentage in the narrow sense is high, so the advance of the trait under study is done by following the selection method. The hybrid vigor recorded in the first generation decreases by %50 in each generation of self-breeding from the previous generation, the inbreeding depression associated with self-breeding reached %90.91 (Table, 1), that the hybrid vigor obtained in the true one generation for the trait of the ear height a clear inbreeding depression in the second generation [35].

3.1.5. Number of Leaves plant^{-1}

Table (1) shows the analysis of the variance components for the leaves number for the same hybrid. The data indicate that the values of environmental variance were less than the values of additive and dominance variance, as they reached 2.186 and 2.188 respectively, and this confirms that genetic variance contributes more than environmental variance in the inheritance of these traits. The effect of dominance variance was greater than the additive and this was reflected on the dominance degree as it was greater than the true one, and the heritability percentage in the narrow sense amounted to %47.89. The high heritability value in the broad sense indicates the greater contribution of genetic variance (4.374) compared to environmental variance (0.19).As for the F value, it indicates the association linkage between D and H in all loci. The positive value indicates the dominance of the dominance alleles (0.56) in the inheritance of the trait, and this confirms the results of the previous tables that matched the results of many studies, including [30] and [20].

It appears from the Table (1) that the expected genetic advance value was 1.11 a low value, while the genetic advance percentage reached a medium value of %10.45 .The effect of the non-additive genes is over dominance the trait, as evident by the dominance degree greater than one, the heritability high percentage in the broad sense, its low in the narrow sense, and the positive hybrid vigor. Therefore, the advance of the trait under study is through hybridization. The results of Table (1) show the estimation of inbreeding depression in the trait of the leaves number Table (13) that the value was significant, amounting to (%15.17) found similar results [36].

3.1.6. Leaves Area

Table (1) analyzes the variance components for the trait of the total plant leave area for the same hybrid, the data indicate that the values of environmental variance were less than the values of additive and dominance variance, as they reached 0.042 and 0.001 sequentially. This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The effect of additive variance was greater than the dominance and this was reflected on the dominance degree as it was less than true one , and the heritability percentage in the narrow sense amounted to %96.67 and in its broad sense %97.67 , the heritability value in the broad sense indicates the greater contribution of the additive action. As for the F value, it indicates the extent of the relationship between D and H, as it reached (0.06), which is a value close to zero and indicates the contribution of both the dominance and the additive effects to the inheritance of this trait. As for the of F value, it indicates the linkage of the correlation between D and H, as it reached (0.06), which is a value close to zero and indicates the contribution of both the dominance and the additive effects to the inheritance of this trait [19]. It was found from the previous tables and the results of Table (1) that the value of the expected genetic advance was 0.07, while the genetic advance percentage was medium, amounting to %14.26 . The effect of both additive and non-additive genes is dominance on the trait, as evident by the high genetic advance percentage inheritance in the broad sense and in the narrow sense and the positive and moral the hybrid vigor. Therefore, the advance of the studied trait is by following the selection method followed by hybridization. The inbreeding depression degree resulting from in -breeding reflects the loss in the members vitality of the second generation F2, and a low positive value for the trait of effective leave area reached (%8.42) similar results obtained by [9].

3.1.7. Grain Yield

It is clear from the results analysis shown in Table (1) that the variance components of the grain yield trait in grams of the individual plant of the same hybrid were analyzed. The data indicates that environmental variance effects to in the inheritance of this trait. The effect of dominance variance was greater than the additive and this was reflected on the dominance degree as it was greater than the true one (1.01), and the inheritance percentage in the narrow sense amounted to 48.12% and in its broad sense 98.20%, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the F value, it indicates the linkage of the association between D and H in all loci. The positive value (42.6) indicates the influence of the dominance alleles on the inheritance of the trait. This confirms the results of the previous tables for this trait, which matched the results of many studies, including [37],[38], [20], and [39]. The results of Table (13) showed that the value of the expected genetic advance was low because It reached 4.24, while the genetic advance percentage of was %2.86 . From the results of the previous tables, we conclude that the trait is under the influence of both the additive and non-additive genetic action, and the trait falls under the over-dominance genes. The trait under study can be improved through hybridization and then selection method. The results of Table (1) confirmed the occurrence of inbreeding depression in the second generation, positive and significant, achieving a value of 19.14 for the trait of individual plant yield [31].

Table 1. Estimation of the variances, the degree of dominance, heritability in its broad and narrow sense, and the inbreeding Depression and genetic improvement of the first cross (late×late) (Zi17WZ×ZA17WR .

Traits	E	D	H	$(H/D)^{1/2}$	F	h^2.n.s	h^2.b.s	▲G	%▲G	$\bar{a}$%ID
No.Days to tassling	3.88	15.52	50.66	1.81	-2.2	22.15	94.46	6.37	11.58	2.36
No.Days to silking	1.553	6.212	14.00	1.62	-2.00	28.66	92.86	2.98	5.05	2.20
Plant height	20.64	210.64	35.04	0.40	-4.1	79.09	92.24	14.62	9.16	7.53
Ear height	2.45	52.8	24.52	0.68	4.16	66.19	96.92	6.87	9.42	90.91
No.leaves plant^{-1}	0.19	2.186	2.188	1.00	0.56	47.89	95.83	1.11	10.45	15.17
Leaves area	0.001	0.042	0.003	1.19	0.06	5.75	96.67	0.07	14.26	8.42
Grain yield plant^{-1}	34.75	933.84	971.68	1.01	42.6	48.12	98.20	4.24	2.86	19.14

3.2. Second Hybrid (Early ×Late) (ZM49W3E ×ZM74)

3.2.1. Number of Days From Planting Until 75% of Tasselling

It appears from Table (2) the variance components analysis for the tasselling trait of the same hybrid; the data indicate that the values of the environmental variance were less than the values of the additive and dominance variance, as they reached 6.64, 32.66 sequentially. This confirms that the genetic variance contributes more than the environmental variance to the inheritance of the tasselling trait. The effect of the dominance variance was greater than the additive and this was reflected on the dominance degree, it was greater than true one (2.21), the heritability percentage in the narrow sense decreased to% 16.21 due to the decrease in the additive variance, and in its broad sense % 95.91, the high heritability value of the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the value of F, it indicates the linkage of the correlation between D and H in all sites. The positive value (1.00) indicates the role of the dominance influence in the inheritance of the trait. This confirms the results of the previous tables, which were close to the results of [29] ,[17] and [30]. The results of Table (2) indicated that the value of genetic advance was low, amounting to 2.18, and the genetic advance percentage was low by%4.30 . One of the results of the previous tables [40] is that the effect of non-additive genes is dominance on the inheritance of the trait through the heritability percentage in the broad sense is high and the hybrid vigor is positive, so it is possible to improve the trait under study by hybridization and then conducting selection. The result in the vitality of the second generation, and a negative and insignificant value for the tasselling trait reached -3.38 [9].

3.2.2. Number of Days from Planting Until 75% of Silking

The results of Table (2) of the variance components analysis the silking trait of the same hybrid, the data indicate that the values of the environmental variance were less than the values of the additive and dominance variances, as they reached 2.212 and 8.66 respectively. This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The dominance variance effect was greater than the additive, and this was reflected on the dominance degree as it was greater than the correct one (2.02), and the percentage of heritability in the narrow sense amounted to 18.73% and in its broad sense %95.15 , the high heritability value in broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the value of F, it indicates the extent of the linkage between D and H in all locations. The negative value (-2.00) indicates the contribution of the additive effect to the inheritance of the trait, and this is clear from the Epistasis effects (Table 15). This confirms the results of the previous tables, which were implicitly in agreement with what was mentioned by each [16], [30], [20] and [34]. The results of Table (2) indicated that the expected genetic advance value was low, amounting to 2.77, while the genetic advance percentage of was low by 5%. From the results of the previous tables that the effect of non-additive genes is dominance on the inheritance of the trait through the heritability percentage in the broad sense is high and the hybrid vigor is positive. Therefore, the studied trait can be improved through hybridization and then selection method. The hybrid vigor was linkage with a negative and insignificant inbreeding depression degree in Table (17), which indicates the small genetic stock of the members studied for the silking trait, which amounted to(%-4.39) to the presence of recessive genes sequence unwanted in these members [41].

3.2.3. Plant Height

It is clear from the data in Table (2) for the plant height trait of the same hybrid, that the environmental variance values (5.56) were less than the values of the additive and dominance variance, as they reached 6.66 and 24.72 respectively. This confirms that the genetic variance contributes more than the environmental variance in the inheritance of this trait. The dominance variance effect was greater than the additive and this was reflected on the dominance degree as it was greater than true one (6.11), and the heritability percentage of in the narrow sense amounted to 18.00% and in its broad sense %84.81, the high of heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the F value, it indicates the linkage of the association between D and H in all loci. The positive value (13.65) indicates the dominance of the dominance alleles in the inheritance of the studied trait.This confirms the results of the previous tables, which were in line with what was reached by [19, 30 and 34]. The results of Table (2) indicated that the expected genetic advance value was low; reaching 1.22 and the genetic advance percentage was also low. It reached %0.87. One of the results of the previous tables is that the effect of non-additive genes is more responsible for the trait than the additive effect, and indicates the positive or negative hybrid vigor and the heritability percentage of in the narrow sense is low, so the trait can be improved by following the hybridization followed by selection method .The plant height trait showed a level of inbreeding depression resulting from self-breeding By% 5.03 [42]

3.2.4. Ear Height

It is noted from Table (2) to the variance components analyze of Ear height trait of the same hybrid, that the environmental variance values (2.436) were less than the additive and dominance variance values, as they reached 89.06 and 7.242 respectively. It emphasized that genetic variance effect contributes more than environmental variance to the inheritance of this trait. The additive variance was greater than the dominance and this was reflected on the dominance degree as it was less than the true one (0.28), and the heritability percentage in the narrow sense amounted to 90.03% and in its broad sense %97.55, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the value of F, it indicates the linkage association between D and H at all sites. The positive value is indicating the contribution of the dominance alleles (0.84). This confirms the results of the other tables [40], which consistent with results of the study of [20] and [30]. The results of Table (2) indicated that the value of the expected genetic advance was low, amounting to 1.22, while the f genetic advance percentage was low by %0.87. One of the results of the previous tables is that the additive genes effect of is more responsible for the trait than the non-additive effect, and indicates the positive or negative hybrid vigor and the heritability percentage high in narrow sense, so the trait can be improved by following the hybridization followed by selection method. The plant height trait showed a level of the inbreeding depression degree in Table (17) resulting from in-breeding by %5.03 according to [42]

3.2.5. Number of Leaves plant $^{-1}$

The results of the analysis in Table (2) for the number of effective leaves for the same hybrid showed that the environmental variance values (0.22) were less than the additive and dominance variance values , as they reached 8.58 and 0.8, respectively. This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The additive variance effect of was greater than the dominance and this was reflected on the dominance degree as it was less than the true one (0.30), and the heritability percentage in the narrow sense amounted to% 89.37 and in its broad sense %97.70, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the F value, it indicates the linkage of the association between D and H in all loci. The positive value (0.83) indicates the contribution of the dominance alleles to the inheritance of the trait. This confirms the results of the previous tables 40 which are in agreement with what was mentioned by [19 ,30 and 20]. The results of Table (2) confirmed that the expected genetic advance value amounted to 3.41 and the genetic advance ratio was 25.37%, and from the results of the previous tables we find the influence of the additive genes that are responsible for the trait, and the hybrid vigor positive and the heritability percentage in the narrow sense is high. Therefore, the trait can be improved through selection method. The results showed in the same Table that the inbreeding depression value associated with in- breeding was positive and significant for the number of leaves trait amounted to %14.95 [33].

3.2.6. Leaves Area

It is evident from the results of components of variance analysis for the trait of leaves area (Table 2) for the same hybrid, that the environmental variance values (0.00013) were less than the additive and dominance variance values , as they reached 0.0026 and 0.0029 respectively. This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The dominance variance effect was greater than the additive and this was reflected on the dominance degree as it was greater than true one (1.06), and the heritability percentage in the narrow sense amounted to %45.82and in its broad sense% 97.72, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the F value, it indicates the linkage of the association between D and H in all loci. A positive value indicates the participation of the dominance alleles (0.06) in the inheritance of the trait. This confirms the results of the previous tables that agree with what was reached by [43 and 19].The results of Table (2) indicated that the expected genetic advance value was low and less than the true one, as it amounted to 0.03, and the genetic advance percentage was low, reaching% 6.74. From the results of the previous tables, the non-additive genes effect is responsible for the inheritance of the trait and indicates the hybrid vigor positive or negative, and the heritability percentage in the narrow sense is low. it can improve the trait by following the hybridization method. The hybrid vigor recorded in the first generation decreases by %50 in each generation of in-breeding from the previous generation, due to the inbreeding depression associated with in-breeding. It was 8.33 that the hybrid vigor obtained in the first generation for the trait of leaf area with clear inbreeding depression in the second generation [35].

3.2.7. Grain Yield

The results shown in Table (2) for analyzing the components variance for the trait of grain yield for the same hybrid indicate that the environmental variance value (75.31) was lower than the genetic variance value (86.9). This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The dominance variance effect was greater than the additive and this was reflected on the dominance degree as it was greater than one true (5.11), and the heritability percentage in the narrow sense amounted to% 3.18 and in its broad sense% 87.15, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance The total variance percentage was %86.6. As for the F value, it indicates the linkage of the association between D and H in all loci, and that the negative value (-1.27) indicates the participation of additive alleles in the inheritance of the trait.This confirms the results of the previous tables, which agreed with what was obtained by [27,20 and 39] . the results of the previous tables and from Table (2) confirmed that the expected genetic advance value was high as it reached 10.12, while the genetic advance percentage value was average amounted to %10.5, that the studied trait control of the non-additive genes and the additive genes. Therefore, the studied trait can be improved by hybridization followed by selection method. The results showed in Table (2) that the trait of the individual plant yield showed a positive value of the yield for inbreeding depression by% 17.54. [32] obtained similar results.

Table 2. Estimation of the variances, the degree of dominance, heritability in its broad and narrow sense, and the inbreeding Depression and genetic improvement of the second cross (early×late) (ZM49W3E×ZM74).

Traits	E	D	H	$(H/D)^{1/2}$	F	h^2.n.s	h^2.b.s	G▲	G%▲	ID%
No.Days to tassling	1.66	6.64	32.66	2.21	1.00	16.21	95.91	2.18	4.30	-3.38
No.Days to silking	0.533	2.212	8.66	2.021	-2.00	18.73	95.15	2.77	5.00	-4.39
Plant height	5.62	6.66	24.72	6.11	13.65	18.00	84.81	1.22	0.67	5.03
Ear height	2.436	89.06	7.424	0.28	0.84	90.03	97.55	10.62	10.86	9.74
No.leaves $plant^{-1}$	0.22	8.58	0.8	0.30	0.83	89.37	97.70	3.41	25.37	14.95
Leaves area	0.000131	0.002642	0.002992	1.06	0.06	45.82	97.72	0.03	6.74	8.33
Grain yield $plant^{-1}$	11.599	2.772	72.542	5.11	-1.27	3.18	87.15	10.12	10.05	17.54

3.3. Third Hybrid (Late × Early) (ZM19 ×ZM 74)

3.3.1. Number of Days From Planting Until 75% of Tasselling

We find in the results of Table (3) to the components of variance analyze for the tasselling trait of the hybrid (ZM74×ZM19) resulting from crossing late female and early male with flowering and physiological maturity, that the environmental variance value was 1.443 less than the genetic variance value of 3.79, and this confirms that genetic variance contributes more than environmental variance in the inheritance of this trait. The effect of the dominance variance was greater than the additive and this was reflected on the dominance degree as it was greater than one true (2.72), and the inheritance percentage in the narrow sense amounted to% 8.64 and in its broad sense %72.43, heritability value in the low narrow sense indicates the lesser contribution of the additive variance compared to the dominance variance. As for the F value, it indicates the linkage of the association between D and H at all loci.

The negative value (-2.66) indicates the role of additive alleles in the inheritance of the trait. This confirms the results of the previous tables that are in agreement with the findings of [29, 17 and 30]. The results of the previous tables and from Tables. indicated that the expected genetic advance value was low, reaching 1.94, while the genetic advance percentage is 3.73%, which is also considered low, and that the studied trait is control of the non-additive genes more than the additive genes, so the studied trait can be improved by following of hybridization method and then selection. The results in Table (3) indicated that the inbreeding depression value of associated with in- breeding was (4.00-%) and not significant for male flowering trait [36].

3.3.2. Number of Days From Planting Until 75% of Silking

It appears from Table (3) to the components variance analyze for the silking trait of the hybrid (ZM74 × ZM19) resulting from crossing (late females and early males) inbreed lines with flowering and physiological maturity, that the values of the environmental variance were less than the additive and dominance variance values , as they reached 3.108 and 3.34 respectively. This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The dominance variance was greater than the additive effect, and this was reflected on the dominance degree as it was greater than one true (1.07), and the heritability percentage in the narrow sense amounted to 45.04% and in its broad sense %92.10 , the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the F value, it indicates the linkage of the correlation between D and H at all sites. The negative value (-1.34) indicates the contribution of the additive effect to the inheritance of the trait.This confirms the results of the previous tables, which were similar to what was obtained by [16,30,20]. The genetic advance was low at %2.59 . The first generation members are outstanding over their parents, and the hybrid vigor positive studied trait. It is under the influence of both additive and non-additive genetic action. Therefore, hybridization can be carried out followed by selection to improve the trait. The hybrid vigor recorded in the first generation of the silking trait coincided with inbreeding depression. Negative and insignificant in the second generation amounted to %-1.81 [31]

3.3.3. Plant Height

Table (3) for components variance analyzing of plant height trait of the hybrid (ZM74×ZM19) resulting from crossing (late female and early male) inbred lines with flowering and physiological maturity, shows that the values of the environmental variance were less than the additive and dominance variance values , as they reached 79.76 and 26.17, respectively. This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The the additive variance effect was greater than the dominance and this was reflected on the dominance degree as it was less than the true one (0.67), and the heritability percentage in the narrow sense amounted to% 72.82 and in its broad sense% 96.71, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the value of F, it indicates the linkage of the association between D and H in all loci, and that the positive value (6.05) indicates the dominance of the dominance alleles secondary to the inheritance of the studied trait, and this confirms the results of the previous tables that were similar to what was reached by [19,30 and 34]

It appears from the results of the previous tables and from Table (3) that the expected genetic advance value was significant, reaching 7.77, and the genetic advance percentage was low, which amounted to %4.60 . The trait is under the control of genetic over -dominance, Heterosis positive and high heritability in the broad sense. The trait can be improved by following hybridization followed by

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selection method later. The results in Table (3) confirmed the occurrence of a positive and significant inbreeding depression in the second generation, achieving a value of% 6.83 for the plant height trait. These results are consistent with what was reached by [31].

3.3.4. Ear Height

Table (3) shows the components of variance analysis for the trait of the ear upper height of the hybrid (ZM74 × ZM19), which resulted from cross-inbred lines late female and early males with flowering and physiological maturity. This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The additive variance effect was greater than the dominance and this was reflected on the dominance degree as it was less than one true, and the heritability percentage in the narrow sense amounted to %62.43 and in its broad sense %97.36 , the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the F value, it indicates the linkage of the correlation between D and H in all loci. The negative value (-22.05) indicates the contribution of additive alleles to the inheritance of the trait, and this confirms the results of the previous tables that agree with the results of other studies mentioned by [29 and 30].

The above tables and the results of table (3) show that the expected genetic advance value was 9.96, while the average of genetic advance percentage was% 12.23. The additive genes effect is dominance on the trait, as evident by the high heritability percentage in the broad sense and in the narrow sense and the positive, negative and moral the hybrid vigor. Therefore, the improvement of the trait under study is done by selection method. The results of Table (3) showed that the value of the inbreeding depression percentage associated with in-breeding was positive and significant for the trait of the ear upper, amounting to %13.22 [32] .

3.3.5. Number of Effective Leaves Per Plant

The results of Table (3) the components variance analysis for the number of effective leaves of the hybrid (ZM74 × ZM19), which resulted from crosses inbred lines of late female and early males with flowering and physiological maturity, showed that the environmental variance values were less than the additive and dominance variance the values , as they reached 6.3 and 1.32, respectively. This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The additive variance effect was greater than the dominance and this was reflected on the dominance degree as it was less than one true (0.45), and the heritability percentage in the narrow sense amounted to %76.92 and in its broad sense % 93.04 , the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the F value, it indicates the linkage of the correlation between D and H at all sites, and the positive value indicates the role of the dominant alleles (0.9) in the inheritance of the trait.

This confirms the results of the previous tables [40] that support the results of the studies, [19 , 30 ,20 and 34]. The results of Table (21) showed the genetic advance value was high, reaching 2.72, while they reached the genetic advance percentage with an average of %20.59, and from the results of the previous tables, the hybrids outstanding their parents and through the trait falling under the influence of the over-dominance genes and low heritability in the narrow sense. It makes the possibility of improving the trait by conducting selection and then conducting hybridization. The results indicated in Table (21) that the inbreeding depression value associated with in-breeding was (%10.62%) significant for the trait of number of leaves (41).

3.3.6. The Total Plant Leaves Area

It appears from the results of the data table (3) the components variance analysis for the leave area trait of the hybrid (ZM74×ZM19), which resulted from crossing inbred lines late female and early males with flowering and physiological maturity, that the environmental variance values were less than the additive and dominance variance values, as they reached 0.0002 and 0.0116 respectively. This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The dominance variance effect was greater than the additive, and this was reflected on the dominance degree as it was greater than one true (2.4), and the heritability percentage in the narrow sense amounted to% 14.59 and in its broad sense% 99.27, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance.

As for the F value, it indicates the extent of the linkage between D and H at all sites. The positive value indicates the contribution of the dominance alleles (0.07) to the inheritance of the trait, and this confirms the results of the previous tables that agreed with the results of [44, 45 and 19]. The results of Table (3) showed the expected genetic advance value amounted to 0.01 and the genetic advance percentage was low, which amounted to %1.66, and from the results of the previous tables, the positive hybrid vigor value for this hybrid and the high heritability percentage of in the broad sense. The trait falls under the influence of the over-dominance genes. Therefore, the trait can be improved by following the hybridization method. The results in Table (3) showed that the inbreeding depression value associated with in- breeding was positive for the leaf area trait, which amounted %10.44 [32].

3.3.7. Grain Yield

The results of the analysis table are indicated in Table (3) the components variance to analyze for the trait of the individual grain yield of the hybrid (ZM74 × ZM19) resulting from the crossing of inbreeding lines late female and early males by flowering and physiological maturity, that the environmental variance values 2.5 were less than the additive and dominance variance values , which amounted to 19.12 and 2.08, respectively. This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The additive variance effect was greater than the dominance and this was reflected on the dominance degree as it was less than the true one (0.32), and the heritability percentage in the narrow sense amounted to %80.67 and in its broad sense% 89.45, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance As for the F value, it indicates the linkage of the association between D and H in all loci. The positive value (3.82) indicates the contribution of the dominance alleles to the inheritance of the trait. This confirms the results of the previous tables that are consistent with the results mentioned by [46,47 and 20]. The results of Table (3) showed the expected genetic advance value 4.77, while the high percentage as it reached 38%. From the results of the previous tables, we conclude that the trait is under the influence of both the additive and non-additive genetic action, and the trait falls under the over-dominance genes, so the trait under study can be improved through hybridization and then selection method. The results from Table (3) indicated that the inbreeding depression amount had a significant value of %7.75 for the trait of individual grain yield of plant [33].

Table 3. Estimation of the variances, the degree of dominance, heritability in its broad and narrow sense, and the inbreeding Depression and genetic improvement of the third cross (late × early) (ZM19 ×ZM 74).

Traits	E	D	H	$(H/D)^{1/2}$	F	h^2.n.s	h^2.b.s	▲G	%▲G	%ID
No.Days to tassling	0.996	1.336	30.00	4.7	-1.33	4.13	96.91	6.54	14.01	1.41
No.Days to silking	0.886	0.864	6.66	2.7	-1.66	10.24	89.6	2.78	5.34	-2.64
Plant height	21.49	56.1	14.16	0.50	-5.53	61.14	76.57	7.82	5.27	8.44
Ear height	144.51	85.28	9.84	0.33	- 0.8	77.78	86.76	10.46	12.20	-0.97
No.leaves $plant^{-1}$	0.573	8.56	3.628	0.65	0.5	67.07	95.50	2.83	27.74	19.43
Leaves area	0.00033	0.002	0.01068	2.31	0.07	15.37	97.46	0.01	2.77	10.44
Grain yield	10.380	163.54	4.804	0.17	-1.14	91.50	94.19	15.26	16.79	22.66

plant^{-1}

3.4. Fourth Hybrid (Early × Early) (ZM19× ZM49W3E)

3.4.1. Number of Days From Planting to 75% of Tasselling

The results of the components variance analysis for the tasselling trait of the hybrid (ZM19× ZM49W3E) resulting from crossing of inbreed lines early female and male by flowering and physiological maturity are table (4). The environmental variance value decreased, as it was 0.996, which is less than the additive and dominance variance values , as it reached 1.33 and 30.00 respectively. This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The dominance variance effect was greater than the additive, and this was reflected in the dominance degree as it was greater than the true one (4.7), and the inheritance percentage in the narrow sense was %4.13 and in its broad sense was% 96.91. A high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. A low of heritability value in the narrow sense indicates a lower contribution of additive variance. . As for the F value, it indicates the linkage of the correlation between D and H in all loci. The negative value (-1.33) indicates the role of additive alleles in the inheritance of the trait, and this confirms the results of the previous tables [44], similar results obtained by [29, 17 and 30]. Their results showed the dominance genes of the dominance action on the trait of tasselling. The results of table (4) showed the expected genetic advance value of 6.54, while the genetic advance percentage averaged %14.01.

From the previous table's results, which indicated the high heritability percentage in the broad sense, the positive hybrid vigor, the control of the over-dominance genes, the additive and non-additive genetic action in the inheritance of the trait. Therefore, the trait can be improved through hybridization and then selection method. The hybrid vigor recorded in the first generation decreases by %50 in each generation of in-breeding from the previous generation, due to the inbreeding depression associated with in-breeding, which amounted to %1.41 (Table 4). The hybrid vigor obtained in the first generation of tasselling trait has a clear inbreeding depression in the second generation [35].

3.4.2. Number of Days From Planting to 75% Silking

The results of Table (4) the components variance analyze for the silking trait of the hybrid (ZM19 × ZM49W3E), which resulted from crossing inbreed lines early female and male with flowering and physiological maturity. Confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The dominance variance effect was greater than the additive and this was reflected on the dominance degree as it was greater than the true one (2.7), and the heritability percentage in the narrow sense amounted to 10.28% and in its broad sense 89.16%, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the F value, it indicates the linkage of the correlation between D and H at all sites. The negative value (-1.66) indicates the contribution of the additive effect to the inheritance of the trait, and this confirms the findings of [16, 30 and 20]. From Table (4) the expected genetic advance value of was 2.78, while the genetic advance percentage was low, which amounted to% 5.34, and from the previous results tables, which indicated that the non-additive genetic action is dominance in the inheritance of the trait. Thus, the trait can be improved by hybridization followed by selection method .The results of estimating inbreeding depression in silking trait from table (4) showed that the value was negative, amounting to% -2.64 [36].

3.4.3. Plant Height

It is noticed through table (4) to the components variance analyze the plant height trait of the hybrid resulting from inbreed lines female and male with early flowering and physiological maturity, that the environmental variance values were less than the additive and dominance variance values, as they reached 56.1 and 14.16, respectively. This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The additive variance effect was greater than the dominance and this was reflected on the dominance degree as it was less than one true (0.50), and the heritability percentage in the narrow sense amounted to %61.14 and in its broad sense %76.67, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the F value, it indicates the linkage of the association between D and H at all loci. A negative value (-5.53) indicates the predominance of additional alleles in the inheritance of the studied trait. This confirms the results of the previous tables that are consistent with the results of previous studies conducted by [19 and 20]. It appears from the r previous results tables and from Table (4) that the expected genetic advance value amounted to 7.82, while the genetic advance percentage was %5.27 that the trait is under the control of the additive genes more than the non-additive genes. Therefore, the studied trait can be improved by selection method. The results indicated in Table (4) that the value of the inbreeding depression associated with in-breeding was %8.44 and for the trait of plant height and this confirms what was found [35].

3.4.4. Ear Height

Noticed through the table (4) data of components variance analysis for the trait of the height of the upper ear of the hybrid (ZM19 × ZM49W3E), which resulted from cross-inbreed lines early female and male with flowering and physiological maturity sequentially. The data indicate that the environmental variance values were less than the additive and dominance variance values , as they reached 85.28 and 9.84, respectively. This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The additive variance effect was greater than the dominance and this was reflected on the dominance degree as it was less than the true one (0.33), and the heritability percentage in the narrow sense amounted to% 77.78 and in its broad sense %86.76, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. The additive variance effect was greater than the dominance and this was reflected on the dominance degree as it was less than the true one (0.33), and the heritability percentage in the narrow sense amounted to 77.78% and in its broad sense %86.76, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the F value, it indicates the linkage of the correlation between D and H at all sites. The negative value (-10.8) indicates the role of additive alleles in the inheritance of the studied trait. This confirms the results of the aforementioned tables (22, 23 and 24), which were in agreement with the results of both [29 and 20] .The results of Table (4) confirmed the expected genetic advance value amounted to 10.46, while the genetic advance averaged percentage %12.20, and from the results of the previous tables that the hybrid vigor is positive and that the trait is under the over dominance control genes, as well as the additive and non-additive effect of the genes action. Accordingly, the trait can be improved by hybridization followed by the selection method for outstanding member. The results indicated in Table (4) that the inbreeding depression value associated with in-breeding was negative for the trait of ear upper height, amounting to -0.97 [36].

3.4.5. Number Leaves plant^{-1}

The results of Table (4) the components variance analyze for the number of effective leaves of the hybrid (ZM19 × ZM49W3E), which resulted from cross-inbreed lines early female and male with flowering and physiological maturity, that the environmental variance values were less than the additive and dominance variance, values which reached 8.56 and 3.62 respectively. This confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The additive variance effect was greater than the dominance, and this was reflected in the dominance degree, as it was less than the true one (0.65). The Heritability percentage in the narrow sense amounted to %67.07 and in its broad sense %95.50, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the F value, it indicates the linkage of the association between D and H at all sites, and the positive value

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indicates the contribution of the dominance alleles (0.5) to the inheritance of the trait, and this confirms the results of the previous tables that agree with the results of studies [19, 20 and 30].

3.4.6. Leaves Area

it is clear from Table (4) the components variance analysis for the leaf area trait of the hybrid (ZM19×ZM49W3E), which resulted from crossing inbreeding lines early female and male by flowering and physiological maturity, that the genetic variance values were greater than the environmental variance values , as they reached 0.00033 and 0.012 respectively. This confirms that genetic variance contributes more than environmental variance to the inheritance of leaf area. The dominance variance effect was greater than the additive and this was reflected on the dominance degree as it was greater than the true one (2.51), and the heritability percentage in the narrow sense amounted to %15.37 and in its broad sense %97.46, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the F value, it indicates the linkage of the association between D and H in all loci. Positive values indicate the participation of the dominance alleles (0.07) in the inheritance of the trait. This confirms the results of the previous tables, which were similar to the results obtained by [43, 44 ,19 and 20]. The previous results tables and from Table (4) indicated that the expected genetic advance value was 0.01 low, while The genetic advance percentage of was low, amounting to 2.77%, that the trait is under the control of the non-additive genes more than the additive genes. Therefore, the studied trait can be improved by following the hybridization method. The results showed in Table (4) that the trait of leaf area showed a positive value of the resultant inbreeding depression was %10.44, and this is consistent with the results of [31].

3.4.7. Grain Yield

The results of Table (4) the components variance analysis for the trait of the individual grain yield of plant of the hybrid (ZM19×ZM49W3E) resulting from crossing inbreed lines female and male with early flowering and physiological maturity. Confirms that genetic variance contributes more than environmental variance to the inheritance of this trait. The additive variance effect was greater than the dominance and this was reflected on the dominance degree as it was less than the true one, and the heritability percentage in the narrow sense amounted to %91.50 and in its broad sense %94.19, the high heritability value in the broad sense indicates the greater contribution of genetic variance compared to environmental variance. As for the value of F, it indicates the linkage of the association between D and H in all loci. The negative value (-31.14) indicates the predominance of additive alleles in the inheritance of the trait. This confirms the previous results tables that agreed with the results of [37,47, 20 and 30]. The results of table (4) showed the expected genetic advance value amounted to 15.26, while the genetic advance percentage was amounted to %16.79, and from the results of the previous tables, we find the additive genes effect that are responsible for the trait, and the high heritability percentage in the narrow sense confirms the possibility of improving the trait through selection. Method %22.66 [31].

Table 4. Estimation of the variances, the degree of dominance, heritability in its broad and narrow sense, and the inbreeding Depression and genetic improvement of the fourth cross (early × early) (ZM19× ZM49W3E).

Traits	E	D	H	$(H/D)^{1/2}$	F	h^2.n.s	h^2.b.s	▲G	%I▲G	%ID
No.Days to tassling	1.443	0.452	3.34	2.72	-2.66	63.80	72.43	1.94	3.73	-4.00
No.Days to silking	0.553	3.108	3.34	1.077	-1.34	45.04	92.10	1.45	2.59	-1.81
Plant height	3.593	79.76	26.172	0.67	6.05	72.82	96.71	7.77	4.60	6.83
Ear height	5.09	120.54	67.44	0.74	2.74	62.43	97.36	9.96	12.23	13.22
No.leaves plant^{-1}	0.58	6.3	1.32	0.45	0.9	76.92	93.04	2.72	20.59	10.62

Leaves area	0.0001	0.002	0.0116	2.40	0.07	14.59	99.27	0.01	1.66	10.44
Grain yield plant^{-1}	2.5	19.12	2.08	0.32	3.82	80.67	89.45	4.77	3.38	7.75

Conclusion

We conclude from the current study that the mean generation analysis method is an important tool for plant breeders to detect the genetic actions of the yellow corn hybrids, and that the sovereign genetic act had the greatest role in the inheritance of the traits under study, so we recommend using the cross-breeding method to improve the traits under study.

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