The comparison of several methods for calculating the degree of heritability and calculating the number of genes in maize (*Zea mays* L.). I. Agronomic traits

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Abstract. The objective of present study was to compare of several methods for estimating the degree of heritability and calculating the number of genes using generation mean analysis of maize (*Zea mays* L.). The experiment was conducted at the field of Field Crop Dept. College of Agric / Univ. of Baghdad, for many seasons, spring and fall seasons 2009, 2010, spring 2011 and fall 2013. Six diverse inbred lines were crossed to produce F1, F2, BC1 and BC2 for four superior crosses. Broad-sense and narrow sense heritability estimates based on variance of different generations. The results showed that the four formulas used to estimate the heritability were different in estimating the values of heritability of different traits, as well as the different crosses used in the study. The broad sense heritability was differed according to the components of the formulas used to estimate. The number of genes that controlled the trait differed according to the different method of estimation and according to the studied trait, and to the all crosses. The highest number of genes (for all formulas) for plant yield, ranging from 15.85 (cross 4) to 155.7 (cross 2), because the yield is complex quantitative trait of several components, so the number of genes they control are the sum of genes that control the components. The inbreeding depression differed according to the parents involved in the crosses, and according to the studied trait, the inbreeding depression ranged from -7 for number of branches/tassel of cross 1 and leaf area of cross 3 to 68 for grain yield of cross 2. We can conclude that the best formula to estimate heritability depends on experimental design and methods of breeding.

1. Introduction

The heritability values of a given population may be very according to its composition and the environment in which it grows from the heritability values of the same population if its environmental conditions change depending on the amount of variance components affecting it. The primary goal of plant breeding is to develop cultivars that have consistently permanently good performance for the fundamental traits of interest. Primary traits will vary among crop species over time, but the ultimate goal remains the same [1]. Quantitative geneticists believed they could enhance breeding methods if the inheritance of quantitative traits was better understood [1]. Lush [2] defined heritability (\(h^2\)) either as the ratio of the additive genetic variance (\(\delta^2A\)) to the phenotypic variance (\(\delta^2p\)), or as the ratio of the total genetic variance (\(\delta^2G\)) to the \(\delta^2p\). The ratio \(\delta^2A/\delta^2p\) was designated as heritability in narrow sense, whereas \(\delta^2G/\delta^2p\) was designated as \(h^2\) in broad sense. These definitions provide information for specific situations (mass selection) but they have limited generality in plant breeding. Estimates of \(h^2\)
can be obtained from mating designs imposed on a population that provide estimates of variance, these estimates can be used to get estimates of $h^2$ for different combinations of progenies and testing conditions [3;4;5]. The success of any crop improvement programs not only depending on the amount of genetic variability present in the population but also on the extent to which it is heritable, which sets the limit of progress that can be achieved through selection [6;7]. Heritability is a measure of the phenotypic variance attributable to genetic causes and has predictive function in plant breeding. It provides information on the extent to which a particular morphogenetic traits can be transmitted to successive generations. Knowledge of heritability influences the choice of selection procedures used by the plant breeder to decide which selection methods would be most useful to improve the traits, to predict gain from selection and to determine the relative importance of genetic effects [8;9]. The most important function of heritability in genetics studies of quantitative traits is its predictive role to indicate the reliability of phenotypic value as a guide to breeding value [10]. Traits with high heritability can easily be fixed with simple selection resulting in quick progress [11]. The objective of present study was to compare of several methods for estimating the degree of heritability, calculating the number of genes in three formula and estimating inbreeding depression using generation mean analysis of maize (Zea mays L.).

2. Materials and Methods

2.1 Field experiment
Six diverse inbred lines maize were tested in the Field Crop Dept., College of Agric. Univ. of Baghdad. Selfing was done at spring and fall seasons of 2009, and spring of 2010, to maintain and increase homozygosis. The homozygous inbred have been crossed to produced F1 generation. F1’s were planted on spring 2011 with their parents to produced BC1 and BC2, also selfing was done for F1 to produce F2 generation. Comparative field trial includes six population of each cross: P1, P2, F1, F2, BC1 and BC2 have been conducted on fall season 2013, in Randomized Complete Block Design with four replications. Dimensions of plots were 75cm ×25cm, population density was 53333 plants /ha., it added 200 kg /ha. of calcium super phosphate 46% P2O5 at soil preparation. 400 kg /ha. of urea, 46% N was added 3 times, at planting, elongation stage and before tassling. 8kg /ha. of diazenon was applied to protect the maize plant from attack of (Sesamia cretica). The observations were taken on 20 plant randomly selected from P1, P2, and F1 population, 30 plant of each BC1 and BC2, and 40 plant for F2 population . The data were recorded for plant height, number of leaves, leaf area, number of branches per tassel, number of ears per plant, ear weight and grain yield.

2.2 Statistical and genetic analysis:
Heritability broad sense and narrow sense were estimated using the following formula:

\[
H^2_{b.s} = \frac{VF2-(VP1×VP2)}{VF2} \times 100 \quad [12]
\]

\[
H^2_{n.s} = \frac{VF2-(VP1+VP2+VF1)}{VF2} \times 100 \quad [13]
\]

\[
H^2_{b.s} = \frac{VF2-(VP1+VP2)}{VF2} \times 100 \quad [13]
\]

\[
H^2_{n.s} = \frac{VF2-(VP1+VP2+2VF1)}{VF2} \times 100 \quad [14]
\]

\[
H^2_{n.s} = \frac{VF2-(VP1+VP2+2VF1)}{VF2} \times 100 \quad [14]
\]

Genes number was estimated by the following formula:

\[
N_e=(\mu_{F1}-\mu_{P1}) \times \frac{[4(\delta^2-BC1-0.5(\delta^2-F1+\delta^2-P1))]}{[6]}
\]

\[
N_e=(\mu_{P2}-\mu_{F1}) \times \frac{[4(\delta^2-BC2-0.5(\delta^2-F1+\delta^2-P2))]}{[7]}
\]

\[
N_e=(\mu_{P1}+\mu_{P2}) \times \frac{[4(\delta^2-BC2-\delta^2)]}{[8]}
\]

The inbreeding depression was also estimated as percentage according to the following formula:

\[
ID\%=(F1-F2)/F1 \times 100 \quad [18]
\]
3. Results and Discussions

Table 1. shows that heritability values in the broad and narrow sense and genes number were estimated on the basis of generations variance for several traits of maize.

3.1 Cross I (Rustico×FI01301):

Table 1. shows the four estimation methods gave relative values of broad sense heritability similar to the traits of the leaf area and the number of branches of tassel. Three methods of estimating Allard 2 Mather and Jinks and Mahmud and Kramer were given close values, 0.868, 0.864 and 0.872, while the heritability value of Allard I was less than that, it is 0.786, for the trait of plant height. The value of heritability for no. of ears plant⁻¹ is the same for the method of Allard 2 and Mahmud and Kramer (0.996 and 0.998), for Mather and Jinks it was lower than 0.932, and the lowest value for heritability 0.876 for method Allard I. In this cross all value of broad-sense heritability for four methods were high indicated that these traits controlled by dominance variance. But the values of narrow sense heritability for same traits illustrate that these traits governed by additive variance because all of these values were high, its range between 0.418 for plant height to 0.843 for leaf area. Broad sense heritability of traits were 29% - 87% and 42% - 87% for (KE7 2012 × K1263/1) and (B37×Mo17) crosses respectively [19]. The highest heritability estimates were observed for 100 grain weight (97.39%). All the other traits were observed to have heritability estimates ranging from 97.39% (100 grain weight) to 47.06% (number of leaves/plant) [20].

This corresponds to the results of Dorri et al [21] who reported that the broad sense heritability estimates based on variance of different generations for the grain yield of cross R59×OH43/1-42 was the highest 88% and the lowest was 23% for ear height. Similar results obtain by [22] who found the broad sense heritability of traits were 91.5% for no. of leaves to 99.7% for leaves area. While for tester its range from 91.5% for no. of leaves to 99.6% for leaves area. Low values of hᵢ².b.s in most traits found by [23]. Values of heritability were 37.5% 42.3% and 31.4% for no. of ears plant⁻¹ for Buhuth 106, Oh 40 and pop corn respectively [24].

3.2 Number of genes

The three estimation methods for genes no. gave different values for various traits of maize. More than one gene was controlled most of traits indicating the polygenic inheritance of these traits (table,1). The third formula of estimate the genes number gave high number than two other formulas for plant height 26.67 and 12.35 for no. of leaves plant⁻¹. The formula 2 gave high number of genes than two other formulas for leaf area 3.28 , 29.31 for no. of branches tassel⁻¹ and 33.49 for ear weight. While the first formula gave the highest no. of genes for no. ears plant than other formula. The highest number of genes was 33.49 for ear height of formula 2 and the lowest no. was 0.24 for leaf area of maize. The lowest value of inbreeding depression was -7 for no. of branches tassel⁻¹, while the highest on was for 44.6 for ear weight followed by 37.5 for no. of ears plant⁻¹ and 29.2 for plant height of maize.

Table 1. Estimation of heritability, number of segregation genes and inbreeding depression for the various traits of the cross (FI01301×Rustico)

| Traits                  | H².b.s, % Allard(1960) | H².b.s, % Fom.1 Genes | H².b.s, % Fom.2 Genes | H².b.s, % Fom.3 Genes | Mean H².b.s, % Fom.1, Fom.2, Fom.3 Genes No. | ID % |
|-------------------------|------------------------|-----------------------|-----------------------|-----------------------|---------------------------------------------|------|
| Plant height(cm)        | 0.786                  | 0.868                 | 0.864                 | 0.872                 | 0.839, 0.418, 5.48, 0.71, 26.67             | 29.2 |
| No. of leaves           | 0.792                  | 0.952                 | 0.935                 | 0.964                 | 0.955, 0.764, 1.2, 5.75, 12.35              | 8.44 |
| Leaf area (m²)          | 0.998                  | 0.987                 | 0.992                 | 0.986                 | 0.990, 0.843, 0.241, 3.28, 2.84              | 7.32 |
| No. branches/tassel     | 0.953                  | 0.954                 | 0.972                 | 0.952                 | 0.958, 0.518, 21.41, 29.31, 3.19             | -7   |
| No. ears/plant          | 0.876                  | 0.996                 | 0.932                 | 0.998                 | 0.951, 0.665, 6.65, 4.72, 3.72              | 37.5 |
| Earweight (gm)          | 0.927                  | 0.960                 | 0.915                 | 0.975                 | 0.944, 0.655, 25.47, 33.49, 19.08            | 44.6 |
| Grain yield (gm)        | 0.884                  | 0.873                 | 0.855                 | 0.976                 | 0.897, 0.616, 45.74, 31.63, 12.86            | 32.9 |
3.3 Cross II (AntignaoHi39 x Nostred)

Heritability of grain yield/plant was ranged between 18% to 45% depending on season, and selection scheme used [25].

Narrow sense heritability were low in most cases due to the dominance of non-additive gene action in controlling the genetic variation of the most studied traits [26].

Heritability narrow sense range from 39% for grain yield to 96% for leaf area index [27].

High narrow sense heritability estimates were detected for all traits, emphasizing that the additive genetic variance was the major component of genetic variation in the inheritance of these traits and the effectiveness of selection for improving these traits, estimated were moderate for grain yield/plant and plant height.[28]. The number of genes which control the number of leaves/plant was 17.23 pairs for leaf area, 10 for plant height which indicate that these characters should be improved by crossing followed by selection, for they are quantitative traits. [29].

Three methods of estimation broad sense heritability gave similar values (0.80 , 0.82 and 0.82) except Alard high value 0.91 for plant height. For no. of leaves, method of Allard I and Mather x Jinks gave similar value 0.867 and0.894 , but the method of Allard 2 and Mahmud x Kramer gave less value 0.717 and 0.732 . All methods of estimation broad sense heritability gave close values 0.974 , 0.986 , 0.954 and 0.975 for leaf area and it is also close to the mean value. The same result is true of the no. of branches tassel[1]. Three methods of estimation gave approximated values (0.983, 0.973, 0.99) except for method Mather & Jinks, which gave less value 0.681. The broad sense heritability estimated for ear weight by three methods gave similar values (0.87, 0.89 and 0.87) and differed from Mather & Jinks method which gave value 0.933.

The method of Allard 2 and Mahmud x Kramer gave the same value of broad sense heritability (0.99) but the two other methods gave less value 0.844 and 0.768. Broad sense heritability ranged from 42% and 45% for grain weight (300) in drought and normal irrigation [30] Low broad sense heritability 65% was recorded for grain weight (100), and 13% for grain yield (31). This confirms the results Hadi and Wuhaib[32] that reported that the broad sense heritability for several traits ranged from 25% for leaves area/plant in spring season under high level of nitrogen and low population density to 95% for leaf area and high level of nitrogen and density. In fall season, the heritability was 97% for leave area under high level of nitrogen and low density. The Narrow sense heritability values were high for most traits, ranging from 0.553 for no. of ears plant1 to 0.695 for plant height, except for the no. of branches tassel[1] was low 0.282. These results show that these traits are controlled by additive gene effect but the no. of branches tassel-1 is determined by Dominance variance .The results are consistent with [33]who illustrate that the h^2n.s under insufficient water were higher than sufficient for three combinations. It ranged between 31.16% - 55.62% in insufficient water and between 28.42% - 48.57%[22] who found that h^2n.s for tester ranged from 27.54% for plant height to 74.5% for no. of leaves. While Dorri et al[21] reported that the narrow sense heritability of grain yield was 82%.

The number of grains governing the trait differed according to the formula used in its estimation as well as the different traits. Also the number of genes controlling the traits in this cross differed from the number of genes of same traits in cross I.

3.4 Number of genes

The highest number of genes in formula I and 3 were for the trait grain yield 56.33% and 24.46 genes respectively, while the highest one for formula 2 was 240.32 for ear weight. Ear weight in formula I governed by 27.20 genes followed by 19.06 genes by plant height. The lowest numbers of genes were for number of branches/tassel 0.518 and 0.59 for number of leaves. In formula 2 the trait grain yield come after ear weight, the number of genes controlled it 155.7 genes, followed by 14.96 genes for plant height, the lowest number of genes 1.06 and 1.09 for trait number of leaves and leaf area. The number of genes controlling number of branches/tassel were 22.08 genes followed 21.68 genes for plant height and 18.93 genes for ear weight (Formula 3), and 17.32, 14.35 and 10.82 genes for number of ears/plant, number of leaves and leaf area respectively. This means that these traits governed by
more than one gene indicated the polygenic inheritance of these traits in maize. As the result of crossing the vigor of crosses is decrease. The highest depression was 68.23 and 60.68 for grain yield and ear weight, followed by 40.10, 36.79 for number of branches/tassel and number of ears/plant; 15.9 for plant height, the lowest inbreeding depression was 5.64 and 1.3 for number of leaves and leaf area. The estimated number of genes for grain yield in the late maturity hybrid was around 10, while in the early maturity hybrid it ranged from 3 to 5. [19].

Table 2. Estimation of heritability, number of segregation genes and inbreeding depression for the various traits of the cross (AntignaoHi39× Nostred)

| Traits                  | $H^2_{b.s}$ | $H^2_{b.s}$% | $H^2_{b.s}$% | $H^2_{b.s}$% | Mean $H^2_{b.s}$% | Fom1. No. | Fom2. No. | Fom3. No. | ID%  |
|-------------------------|--------------|--------------|--------------|--------------|------------------|-----------|-----------|-----------|------|
| Plant height (cm)       | 0.911        | 0.80         | 0.82         | 0.82         | 0.695            | 19.06     | 14.96     | 21.68     | 15.9 |
| No. of leaves           | 0.867        | 0.717        | 0.894        | 0.732        | 0.80             | 0.619     | 0.59      | 1.06      | 17.32 |
| Leaf area (m$^2$)       | 0.974        | 0.986        | 0.954        | 0.987        | 0.975            | 0.644     | 2.96      | 1.09      | 10.82 |
| No. branches/tassel     | 0.973        | 0.938        | 0.927        | 0.942        | 0.945            | 0.282     | 0.518     | 5.23      | 22.08 |
| No. ears/plant          | 0.983        | 0.973        | 0.681        | 0.99         | 0.917            | 0.553     | 1.93      | 6.42      | 14.35 |
| Ear weight (gm)         | 0.87         | 0.89         | 0.933        | 0.87         | 0.891            | 0.609     | 27.20     | 240.32    | 18.93 |
| Grain yield (gm)        | 0.844        | 0.99         | 0.768        | 0.99         | 0.898            | 0.635     | 56.33     | 155.7     | 24.46 |

3.5. Cross 3(Lo1391 × Rustico).
The values of four estimation methods of broad sense heritability for all studied traits were close, and all of these were high. The mean values range from 0.855 for number of leaves to 0.988 for number of branches/tassel. The values of narrow sense heritability range from 0.497 for plant height to 0.728 for number of leaves. High broad sense heritability estimates were found for all traits of maize, it range from 89.72% for number of ears/plant to 99.94% for grain yield of plant of reciprocal crosses, and from 70.54% to 99.8% for reverses crosses, where's the narrow sense heritability range from 3.23% for number of ears/plant to 39.18% of number of rows/ear, for reciprocal crosses, while it range from 4.5% for number of ears/plant to 64.18% for grain yield for reverses crosses [29]. Broad sense heritability ranged from 0.25 for number of leaves to 0.49 for grain yield [35].

3.6. Number of genes
The number genes that controlled the studied traits differs according to the formula used to estimated. The number of genes for formula 3 was higher than other two formula. The higher number of genes was 22.06, 20.37 and 51.49 for three methods of calculation for grain yield.

The lowest number of genes in formula I was 0.138 and 0.243 for leaf area and number of branches/tassel. Its 0.277, 0.447 and 0.33 for leaf area, number of ears/plant and ear weight. All number of genes for all studied traits in formula 3 were more than one, indicating the polygenic Inheritance of these traits. As the genes that control the quantitative traits are segregate in groups so that these formulas would have under estimated the number of genes, and the number of genes is greater than these estimations. Table 3 showed that the inbreeding depression for most traits was low 2.74 for trait ear weight and also negative -2.77 and -7.0 for number of leaves and leaf area respectively. The highest one was 37.12 for grain yield followed by 16.66, 14.78 and 14.5 for number of ears/plant height and number of branches/tassel.
Table 3. Estimation of heritability, number of segregation genes and inbreeding depression for the various traits of the cross (Lo1391 × Rustico)

| Traits                  | $H^2_{b.s.}$ | $H^2_{b.s.}$ | $H^2_{b.s.}$ | Mean $H^2_{b.s.}$ | Fom1. Genes No. | Fom2. Genes No. | Fom3. Genes No. | ID% |
|-------------------------|--------------|--------------|--------------|-------------------|-----------------|-----------------|-----------------|-----|
| Plant height(cm)        | 0.943        | 0.947        | 0.962        | 0.973             | 0.956           | 0.497           | 2.83            |     |
| No. of leaves           | 0.824        | 0.859        | 0.850        | 0.885             | 0.855           | 0.728           | 4.43            | 5.31 |
| Leaf area (m2)          | 0.991        | 0.977        | 0.987        | 0.981             | 0.984           | 0.559           | 0.138           | 0.277 |
| No. branches/tassel     | 0.992        | 0.990        | 0.983        | 0.990             | 0.988           | 0.653           | 0.243           | 1.889 |
| No. ears/plant          | 0.990        | 0.817        | 0.921        | 0.820             | 0.887           | 0.606           | 1.21            | 0.447 |
| Ear weight (gm)         | 0.961        | 0.981        | 0.889        | 0.980             | 0.953           | 0.599           | 1.06            | 0.33  |
| Grain yield (gm)        | 0.943        | 0.976        | 0.919        | 0.987             | 0.956           | 0.568           | 22.06           | 20.37 |

3.7. Cross 4 (Rusticocangini × Rustico).

The value of broad sense heritability for methods Mather & Jinks and Mahmud & Kramer is close 0.987 and 0.998, and the heritability value calculated by Allard methods is convergent but is less valuable than the previous two methods (0.957 and 0.967), for plant height (table 4). Three methods of estimating broad sense heritability gave similar values, while Allard's method I gave the higher value 0.972 for number of leaves and leaf area, thought the values of heritability leaf area less than the values of heritability for number of leaves, for all methods of estimation. For trait number of branches/tassel, Mather & Jinks method gave less value to broad sense heritability than heritability value calculated by other heritability methods. The highest value of broad sense heritability for number of ears/plant is for method I of Allard, while the methods 2 gave less value, but the two other methods gave close value. Method I of Allard and Mahmud & Kramer method gave same value of broad sense heritability and higher than two other methods were gives 0.874 (Mather & Jinks) and 0.843 (Allard I) for ear weight. All values of broad sense heritability by all estimation methods were high for grain yield. The average value of the all traits is high and ranged between 0.875 for leaf area and 0.977 for plant height. The value of the narrow sense heritability ranged for medium (0.431 for ear weight, 0.455 for number of ears/plant and 0.457 for leaf area) to high for the other traits. High heritability estimate for trait indicates its worth in selection due to larger heritable variance which may offer the possibility of improvement for this trait through selection [36].

3.8. Number of genes

The number of genes that control the trait varies according to the method of estimating. The number of genes calculated by formula 3 was higher than the number of genes calculated by others formulas, except for the number of branches/tassel, the number of genes calculated by formula 3 was less than number of genes in calculated of formulas 1 and 2. The higher number of genes were 37.27 and 34.7 for number of branches/tassel in formula 1 and 2, followed by 28.42 and 34.43 for grain yield, while the highest one in formula 3 was 48.04 for plant height followed by 29.04 and 27.89 for number of leaves and ear weight, the lowest number was 4.93 for number of branches/tassel. The highest value of inbreeding depression was 37.26 for number of branches/tassel followed by 33.08 and 29.60 for ear weight and number of ears/plant, while the lowest was 4.96 and 7.9 for plant height and number of leaves of maize.
Table 4. Estimation of heritability, number of segregation genes and inbreeding depression for the various traits of the cross (Rustiocangini × Rustico)

| Traits                  | $H^2_{a,s}$ | $H^2_{a,s}$ | $H^2_{a,s}$ | Mean          | Fom.1 | Fom.2 | Fom.3 | ID% |
|-------------------------|-------------|-------------|-------------|---------------|-------|-------|-------|-----|
|                         | %Allard(60) | %Allard(960)| %Allard(96) | %Mather &Jinks(1982) |   |             |             |     |
| Plant height(cm)        | 0.957       | 0.967       | 0.987       | 0.998         | 0.977 | 0.654 | 1.036 | 2.06 |
| No. of leaves           | 0.972       | 0.920       | 0.925       | 0.949         | 0.942 | 0.621 | 3.06  | 1.06 |
| Leaf area (m²)          | 0.932       | 0.8638      | 0.830       | 0.8723        | 0.8745 | 0.457 | 2.13  | 1.648|
| No. branches/tassel     | 0.951       | 0.957       | 0.909       | 0.976         | 0.9483 | 0.648 | 37.27 | 34.7 |
| No. ears/plant          | 0.984       | 0.940       | 0.966       | 0.964         | 0.964 | 0.455 | 0.169 | 1.24 |
| Ear weight (gm)         | 0.843       | 0.951       | 0.874       | 0.954         | 0.906 | 0.431 | 8.33  | 10.45|
| Grain yield (gm)        | 0.9437      | 0.9535      | 0.9322      | 0.962         | 0.942 | 0.618 | 28.42 | 34.43|

4. Conclusion

It is obvious that broad sense heritability is the highest value of narrow sense heritability, because the first includes all additive and dominance variation, while the second includes additive variation only. In accordance with the method of estimation, broad sense heritability was different depending on the component of the calculate. Also, the number of genes controlling the studied traits differed according to the formula used to calculate. In general, the number of genes that govern most of the studied traits is greater than one, so they are genetically controlled, and the effect of environment is small because the number of genes governing the traits are very numerous. As we know, the genes responsible for the trait are linked and segregated in groups, so the number of genes is expected to be higher than those calculated.

References

[1] Hallauer, A. R. (2007). History, contribution, and future of quantitative genetics in plant breeding ; Lessons from maize. Crop Sci. 47(53):54-519
[2] Lush, J.L. 1945. Animal Breeding plans. 3rd ed. Iowa state Univ. press, Ames, IA.
[3] Hanson, W.D., and H.F. Robinson (ed) 1963. Genetic statistics and plant breeding. NAS-NRC publ. 982.
[4] Nyquist, W. E. 1991. Estimation of heritability and prediction response in plant population. Crit. Rev. Plant Sci. 10: 235-322.
[5] Holland, T.M., W. Nyguist, and C. Carvantes. 2003. Estimating and interpreting heritability for plant breeding. Plant Breeding reviews, 22, John wiley &sons, Inc.
[6] Wang, X.J. Chang, G. Qin, S. Zhang, X. Cheng and C.Li. 2011. Analysis on yield components of elite maize variety X undan 20 with super high yield potential. Afr. J. Agric. Sci., b(24): 5490-5495.
[7] Sumathi, P., A. Nirmalakumari, and K.Mohanraj . 2005. Genetic variability and traits inter relationship studies in industrially utilized oil rich CIMMYT Lines of maize (Zea mays L.). Madras Agric. J. 92(10-12): 612-617.
[8] Haq, W.U., M., F.Malik, M.Rashid, M.Munir, and Z. Akram. 2008. Evaluation and estimation of heritability and genetic advancement for yield related attributes in wheat lines. Pak. J. Bot., 40(4): 1699-1702.
[9] Laghari, K.A., M.A.Siad, M. A.Afzal Arain, A.A.Mirbahar, A.J.Pirzada, M.U.Dahot and S.M.Mangrio. 2010. Heritability studies of yield and yield associated traits in bread wheat. Pak. J. Bot. 42(1): 111-115.
[10] Falconer, D.S. and T.F.C.Mackay .1996. Introduction to Quantitative Genetic. 4th ed. Benjamin Cummings, England P. 464.
[11] Najeeb, S., A.G.Rather, G.A.Parray, F.A.Sheikh and S.M.Razvi 2009. Studies on genetic variability, genotypic correlation and path coefficient analysis in maize under high altitude temperate ecology of Kashmir, Maize Genetics Cooperation Newsletter. 83: 1-8.
[12] Muhmud ,I.,and H. H. Kramer.1951. Segregation for yield ,high, and maturity following a soybean cross.Agron,J.43:605-609.
[13] Allard,R.W.1960.Priniples of Plant Breeding. 2nd edition John Wiley and Sons Inc, New York.
[14] Mather, K. and J.L. Jinks.1982. Biometrical Genetics 3rd Edition Chapman and Hall London P 396.
[15] Chen,X.M.,and Line,R.F.1995. Gene number and heritability of wheat cultivars with durable , high –temperature , adult –plant(HTAP)resistance to puccinia striiforms. Phytopathology 85:573 578.
[16] Dehgani, H., M. Moghaddam, M.R. Ghannadha, M. Valizasdeh and M.Torabi 2002 Inheritan ce of the latent period of strip rust in wheat. Journal of Genetic and Breeding 56:155-163.
[17] Baktash,F.Y and A.Y.AL-Younis.1994.Advance generations of maize .Iraqi J.of Agric.Sci.25(2):49-52.
[18] Singh, R.K., and B.D. Chaudhary.1985.Biometrical Methods in Quantitative genetic Analysis.Kalyani Publishers, New Delhi- Ludhiana.pp.318.
[19] Shahrokhi, N., S.Kh. Khorasani and A. Ebrahimi. 2011. Generation mean analysis for yield and yield components in maize (Zea mays L.). J. of Plant Physiology and Breeding. 1(2) : 59-72.
[20] Abed, N.Y. 2012. Estimation of gene action and number of genes for several growth characters in maize. The Iraq J. of Agric. Sci. 43(1): 49-57.
[21] Janno, F.O. and M.M.Elsahookie 2009. Improvement of some maize traits by honeycomb selection. The Iraq J. of Agric. Sci. 40(2): 194-200.
[22] Mostafavi, Kh., M.Ghaemi, S.Kh. Khorasani. 2013. Using correlation and some genetics methods to study of morphological traits in corn (Zea mays L.) yield and yield components under drought stress condition. International Res. J. of Applied and Basic Sci. 4(2): 128-139.
[23] Muhmud ,I.,and H. H. Kramer.1951. Segregation for yield ,high, and maturity following a soybean cross.Agron,J.43:605-609.
[24] Allard,R.W.1960.Priniples of Plant Breeding. 2nd edition John Wiley and Sons Inc, New York.
[25] Mather, K. and J.L. Jinks.1982. Biometrical Genetics 3rd Edition Chapman and Hall London P 396.
[26] Chen,X.M.,and Line,R.F.1995. Gene number and heritability of wheat cultivars with durable , high –temperature , adult –plant(HTAP)resistance to puccinia striiforms. Phytopathology 85:573 578.
[27] Dehgani, H., M. Moghaddam, M.R. Ghannadha, M. Valizasdeh and M.Torabi 2002 Inheritan ce of the latent period of strip rust in wheat. Journal of Genetic and Breeding 56:155-163.
[28] Baktash,F.Y and A.Y.AL-Younis.1994.Advance generations of maize .Iraqi J.of Agric.Sci.25(2):49-52.
[29] Singh, R.K., and B.D. Chaudhary.1985.Biometrical Methods in Quantitative genetic Analysis.Kalyani Publishers, New Delhi- Ludhiana.pp.318.
[30] Shahrokhi, N., S.Kh. Khorasani and A. Ebrahimi. 2011. Generation mean analysis for yield and yield components in maize (Zea mays L.). J. of Plant Physiology and Breeding. 1(2) : 59-72.
[31] Abed, N.Y. 2012. Estimation of gene action and number of genes for several growth characters in maize. The Iraq J. of Agric. Sci. 43(1): 49-57.
[32] Janno, F.O. and M.M.Elsahookie 2009. Improvement of some maize traits by honeycomb selection. The Iraq J. of Agric. Sci. 40(2): 29-47.
[33] Elsahookie, M.M. and K.M. Wuhaib. 1990. Heritability and homeostasis of maize populations derived by different selection schemes. Mesopotamia J. of Agric. 22(4): 7-16.
[34] Wannows, A.A., M.Y.Sabbooh, and S.A.AL-Ahmad. 2015. Generation mean analysis technique for determining genetic parameters for some quantitative traits in two maize hybrids (Zea Mays L.). Jordan J. of Agric. Sci. 11(1): 59-72.
[35] Wannows, A.A., H.K.Azzam and S.A.AL-Ahmad. 2010. Genetic variances, heritability, correlation and path coefficient analysis in yellow maize crosses (Zea mays L.). Agric. Biol. J. of North America, 1(4) : 630-637.
[36] Moualla, M.Y., S. ALAhmad and R.M.Hayas. 2011. Genetic variance, Heritability, phenotypic correlation coefficient and path analysis for single crosses of maize (Zea mays L.) Tishreen Univ. J. for Res. Sci. studies- Biol. Sci. series 33(1) 128-139.
[37] Abed, N.Y., B.H.Hadi, W.A.Hassan and K.M.Wuhaib. 2017. Assessment yield and its components of Italian Maize inbred lines by full diallel cross. AL-Anbar J. of Agric. Sci. (special No. of 5th Sci. conf. of the Faculty of Agric. Univ. of Anbar (part 1), 15: 114-128.
[38] Mostafavi, Kh., M.Ghaemi, S.Kh. Khorasani. 2013. Using correlation and some genetics methods to study of morphological traits in corn (Zea mays L.) yield and yield components under drought stress condition. International Res. J. of Applied and Basic Sci. 4(2): 252-259.
[39] Alhadi,R.A.,M.Sabbouh and S.AL-Ahmad.2013.Genetic analysis of some traits in segregation generation of two maize(Zea maysL.) hybrids. Damascus Journal of Agriculture Sciences 29(2):117-135.
[33] Hadi, B. H. and K.M. Wuhaib. 2015. Estimation of genetic parameters of growth and yield characters of yellow maize (Zea mays L.) under tow levels of nitrogen and plant density. Egypt. J. of Appl. Sci. 30(2) 114-129.

[34] Hassan, W. A., K.M. Wuhaib and B.H.Hadi. 2017. Heritability and genetic gain to a selective of maize under sufficient and insuffieient water, nitrogen and potassium. Al-Anbar J. of Agric. Sci. (Special No. of 5th Scientific Conference of the faculty of Agric. Univ. of Anbar (part 1) 15 156-165.

[35] Wuhaib, K.M. 2012(a). Testing introduced germplasm of maize by line x tester mating system :: I- yield and yield components . The Iraqi J. of Agric. Sci. 43(1): 38-48.

[36] Hadi, B.H. and K.M.Wuhaib. 2010. Heritability and genetic gain in maize. AL-Anbar J. of Agric. Sci. 8(1): 96-107.

[37] Murtaza, N.G.Shabbir, T. Mahmood, M.Ansar. M.I.Tabassum and M.Ilyas. 2014. Criterion for the selection of high yielding maize (Zea mays L.) genotypes. J Agric. Res. 52(2): 177-183.