



STUDY OF HALF DIALLEL AMONG GENOTYPES OF BREAD WHEAT (*TRITICUM AESTIVUM* L.) FOR YIELD AND ITS COMPONENTS

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Abstract

An experiment was conducted in Kirkuk governorate in which seven varieties of wheat were used (Sham 6, Jad, Barcelona, Adana, Abu Ghraib3, Aras and Ebaa 99). Among them Hybridization was performed, according to the second Griffing method, to study the characteristics of the plant height (cm) number of spikes. Plant⁻¹, length spike, weight spike, No. of spikelets.spike⁻¹, No. of grain.spike⁻¹, weight 1000 grain and grain yield.plant⁻¹. The results showed the significance genotypes of all the studied traits, the superiority parent Ebaa 99 in yield, as it recorded 11.24 and hybrid (Jad × Barcelona) and (Aras × Ebaa 99) in grain yield 15.12 and 14.75 respectively and there was a significant Heterosis in yield and its components, cultivar Ebaa 99 was best for the general ability to all traits and hybrids (Sham 6 × Abu Ghraib3) in yield its components. Was additive variation and dominance significant in all studied traits and environmental variation, so it was significant in all traits except for No. of grain per spikes and weight of 1000 grain. As for the values of (F), it was positive and significant in traits of spike length, spike weight, No. of spikelets per spikes No. of grains per spike and positive, but did not reach the level of significance in plant height, No. of spikes per plant and weight of 1000 grains, and values (h²) were significant in No. of spike per plant, length and weight spike, No. of spikelets per spike No. of grains per spike, the weight of 1000 grains and grain yield. The average degree of dominance was greater than one in height of the plant, No. of spikes, length and weight of spike, No. of spikelets, No. of grains, weight 1000 grains, and grain yield, reaching 1.70, 4.57, 1.23, 2.08, 1.87, 2.33, 2.04 and 3.76, respectively. The ratio a number of dominant genes to recessive KD/KR is greater than one for all traits, the values of (K) were greater than one in No. of spikes, No. of spikelets, No. of grains, grain yield and less than one in plant height, spike length, spike weight, and weight of 1000 grains. The genetic recurrence values for dominant alleles to recessive (H₂ / 4H₁) were greater than (0.25) for grain yield attribute, as it reached 0.26 and less than (0.25) in plant height, No. of spikes, length and weight of spike, No. of spikelets, No. of grains, and weight of 1000 grains. As for inheritance in a narrow sense, it was high plant height and spike length were 0.65 and 0.66, respectively and the expected genetic advance as a percentage was lower than 10% for all studied traits. The regression line cuts Wr axis along the origin point in the No. of spikes per plant, length of a spike, No. of spikelets per spike, No. of grains per spike and grain yield per plant.

Key words: wheat, genotypes, half diallel, hayman analysis, regression line

Introduction

The diallel cross is called mating design (AA), which is a system that means selecting a number of parents (P) were pure strains or varieties and conducting crosses between them, using this system as it provides important genetic information comes from the first generation obtained (Al-Zubaidi and Jabouri, 2016).

Hayman's method (1954) is important in the analysis of through which it is possible to know nature gene work and test the significance of genetic analysis and ability to test the suitability of genetic analysis model used based on results of genetic analysis and specific characteristics.

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The presence of genetic variation is essential for the selection of genotype superior to their characteristics, as it is the effective and influencing tool for efficiency to selection and its sources are in old local varieties or are the result of natural or novel mutations or a result of new genetic associations resulting from crosses. is the first to be part Genetic variation to additional genetic variation and dominance variation, inheritance in a narrow sense is an essential component in estimating expected genetic advance from a selection called in response to selection (Fisher, 1918). Comstock and Robinson (1952) determining the amount of dominant and recessive genes for each attribute in the parent, to determine which parents are best for selection in breeding programs and conducting

graphical analysis to estimate the proportion of dominant and recessive genes in each parent. (Falconer, 1981).

What we need is to develop genotypes resulting from new consortia and to select camels that are superior in their traits, by making use of the phenomenon of Heterosis that has been widely exploited in other crops. To arrive at an integrated program for breeding and devising new varieties, it is necessary to estimate basic genetic parameters related to the expected genetic improvement, as well as the degree of dominance and correlation between characteristics and heritability, as these parameters are evidence for plant breeders in the use of appropriate Al-Taweal (2009).

Materials and Methods

Seven varieties of wheat bread were used in this study, and go run hybridization was carried out according to the diallel cross-system, according to second Griffing method (1956). Was obtained (28) genotype was contained (21) first-generation hybrids, in addition to seven parents table 1.

Table 1: Name, pedigree, and Number for variety.

| Genotype | Pedigree | No. |
|-------------|--|-----|
| Sham 6 | PLo-RuFTGtos-RheL (MI2904) -IM-SM-14-OSK- GAP | 1 |
| Jad | | 2 |
| Barcelona | | 3 |
| Adana | PFAWL/seri-82/BOW | 4 |
| Abu Ghraib3 | Ajeeba * lina12* Mexico 24 | 5 |
| Aras | Elena Cement(Lermajo×Silora64) | 6 |
| Ebaa 99 | Ures/Bows/3/Jup/Bis/s//Ures | 7 |

The experiment was planted on 15/11/2019 in a mixture of soil where each experimental unit contained a matrix with a length of (4) m and distance between the experimental units (0.3) m and between plant to other (0.1) m to evaluation the genotypes (parent and hybrids) get from system Mating, using randomized complete block design with three replicates, means were analyzed between genotypes according to test the least significant difference (Dawod and Abdulyas, 1990). Nitrogen fertilizer was added at a rate of 200 kg/ha and phosphate at a rate of 100 kg/ha. Soil and crop service operations to study the traits of plant height, number of spikes per plant, spike length, spike weight, number of spikelets, number of grains per spike, weight 1000 grain and grain yield.

The data from seven cultivars and their diallel crosses (half-crossed hybridization) were analyzed according to second method - the first model (Fixed Model) proposed by Griffing (1956), in which number of genotypes under study is $n(n + 1)/2$ and equal (28) genotypes, the

mathematical model equation for general combining ability is as follows:

$Z_{i..} = Y_{i..} + Y_{ii}$; $Y_{ij.} = Y_{ji}$; $Z_{...} = 2Y_{...}$ Estimating effects of general and specific abilities on Estimating the effects of the public ability on the union for parents (g_i) $g_i = [1/r(p + 2) [Z_{i..} - (2Y_{...}/p)]$, and estimating the effects of $S_{ij} = (Y_{ij.}/r) - [1/r(n+2)] (Z_{i..} + Z_{j.}) + [2Y_{...}/r(p + 1)(p + 2)]$, general and specific effect variance $V(g_i) = [(p - 1)/2p^2] \sigma_e^2$; $V(S_{ij}) = [(p - 1)^2/p^2] \sigma_e^2$.

The Heterosis was calculated based on the deviation of average the first generation from an average of the parents and according to the following equation (Falconer, 1989) as The variance of the Heterosis was calculated from the following equation, as shown in the following: $(H) = [F_1 - (p_i + p_j)/2]$ as that $H =$ Heterosis, $F_1 =$ mean first-generation, $p_i =$ parent means (i), $p_j =$ parent means (j) and calculated Heterosis variation in test significant Heterosis depend on t-test following equation, $t = (H/\sqrt{V(H)})$; $V(H) = (3/2) \sigma_e^2$; $\sigma_e^2 = \text{Mse}/r$.

The data were analyzed according to Jinks– Hayman method of the Diallel Crossing suggested by Jinks (1954 and 1956) and Hayman (1954 and 1958), as this analysis gives a great deal of information about a group of pure lines and their offspring after ensuring that the necessary hypotheses are fulfilled, including the estimation of the following statistical parameters: (MoLo) means parents, (VoLo) variance of parents, (MoL1) average of first generations, contrast of parent and offspring, (V1L1) averages of the variance of columns of first-generation, and (VoL1) variance of the mean of columns of the first generation and common covariation between offspring (first generation) and fathers (WoLo) average common variance of first-generation columns. All these statistics were used to calculate the genetic components in all the traits, including: E expected environmental variation component variation, D which is variation due to additional effect of genes and H1 variation due to dominance effects of genes obtain from sum of h^2 which represents sum of dominance effects of mixture sites and H2 dominance variance that obtain from increase in h^2 in all isolation genes, which equals H1 when the genetic frequency is 1/2 and F, which gives an estimate of relative frequency of dominant to recessive in parents, genetic ratios $(H1/D)^{1/2}$ expressing the average degree of dominance are calculated, and their value is denoted equal to zero on absence of dominance, and between zero and one over partial dominance, but if it exceeds one indicates superior dominance, and $H2/4H1$, and indicates the ratio of genes with positive and negative influences in parents, when ratio is equal to 0.25 indicates the symmetrical distribution of positive and negative genes, and the ratio $(4DH1)^{1/2}$

+F/(4DH1) ½ -F, which indicates ratios of dominant and recessive genes in parents, if their value is equal to one indicates equal proportions of dominant and recessive genes in the parents, and less than one indicates an increase in Recessive genes, while higher than one indicates an increase in the dominant genes, the ratio H2/ h2 indicates the number of genes groups that control the trait and have dominance behavior, estimate genetic parameter that included the average degree of dominance (\bar{a}), heritability narrow sense (H.N.S), adoption of heritability limits in narrow sense were estimated according to what he mentioned (Al-Azhari, 1999), expected genetic improvement from selection next generation, and adopted the limits of the expected genetic improvement less than (20%) is low, (20-50%) is medium, and more than 50% is high in selection as a percentage of the average quality (EGA%) Mather, Jinks (1982), Singh, and Chaudhary (2007) according to the following equations: $E = \text{Mse}/r$; $D = (Vp - E)$; $H1 = 4Vr + Vp - 4Wr - [(3n-2)/n]$; $H2 = 4Vr - 4Vr + [2(n2-1)/n2]*E$; $F = 2Vp - 4Wr - [2(n-2)/n]*E$; $h2 = 4[MF - MP]2 - [4(n-1)/n2]*E$; $KD/KR = [(4DH1)1/2 + F] / [(4DH1)1/2 - F]$; $K = h2/H2$; $\bar{a} = \sqrt{2} \sigma 2D / \sigma 2A$ H.N.S = $[1/2D] / [1/4D - 1/4F + 1/4H1 - E]$; $EGA = (i)(H.N.S)(\sigma P)$; $EGA\% = (EGA / \bar{y}) \times 100$; at this H.N.S= heritability narrow sense; i= selection value; σp = phenotypic standard deviation.

Results and Discussion

Table 2 shows the analysis of variance, notes that average squares of the genotypes including traits of yield and its components this agree with (Mohammed, *et al.*, 2019) and (Mohammed and Mohammed, 2020) these found significant in yield and its compound, as well as general and specific combining ability differed significantly for all, and general combining ability to all traits except for No. of spikes per plant and weight of spike, the significance of the general combining ability indicates to importance additive genetic, while the significance of specific combining ability to important indicates dominance

genetics. These differences between genotypes that include parents and hybrids may be due to difference of genetic factors to control in the inheritance of these traits in addition to interaction with environmental factors, this requires continuing to study genetic behavior and know nature of genes and gene action to controls inheritance of these traits, Hence the possibility of selection for superior genotype. The ratio of components to general combining ability to components of specific combining ability was less than one for all studied traits; this indicates the greater importance of dominance genetics act.

Table 3 means of significant genotypes differences in plant height superior Aras variety an average of 90.89 overall parent and hybrids (5×7) with an average of 93.43, and superiority in No. of spikes per plant variety Ebaa 99 over the rest parent an average of 5.50 and hybrids (2 × 5) over rest hybrids an average of 6.20, in spike length superior Ebaa 99 cultivar an average of 10.87 over varieties and hybrids (1 × 4) over rest of hybrids an average of 10.17, in weight of spike superior two cultivars Abu Ghraib and Aras an average of 2.33 each and hybrid (3 × 7) over rest hybrids an average of 3.55, and in No. of spikelets superior Ebaa 99 cultivar an average of 51.55 and two hybrids (1 × 7) and (3 × 7) an average it reached 53.00, in No. of grains per spike excellence Ebaa 99 an average over rest varieties an average of 49.73 and hybrid (1 × 5) over the rest of hybrids an average of 61.44, this trait is one of important correlate with grain yield that is affected by genotype and extent of its influence by environmental factors or due to different genotypes in this trait, it may be due to their different exploits growth factors, especially during the flowering stage, to form the largest No. of spikelets and grains, as well as their difference in tolerating high temperatures that may lead to weakening the vitality of pollen and drying stigma, which negatively effects of pollination, fertilization, and holding fruits (Ward Law, *et al.*, 1971).

And excellent in weight 1000 grains Jad variety over rest cultivars with an average of 42.21 and hybrid (6 × 7)

Table 2: Analysis of variance and mean squares for genotypes, GCA and SCA for traits studies.

| S.O.V | df | height plant (cm) | No. of spike. plant ⁻¹ | spike length (cm) | spike weight (g) | No. of spikelet .spike ⁻¹ | No. of grains. spike ⁻¹ | Weight 1000 seed | grains yield g.plant ⁻¹ |
|-----------|----|-------------------|-----------------------------------|-------------------|------------------|--------------------------------------|------------------------------------|------------------|------------------------------------|
| Replicate | 2 | 195.87 | 8.36 | 10.88 | 3.56 | 67.75 | 213.93 | 34.09 | 114.78 |
| Genotypes | 27 | 69.29** | 0.76** | 1.04** | 1.08** | 46.78** | 155.10** | 44.08** | 12.75** |
| GCA | 6 | 168.37** | 0.14n.s | 0.80** | 0.91n.s | 19.15** | 80.23** | 67.38** | 7.28** |
| SCA | 21 | 40.98** | 0.94** | 1.11** | 1.13** | 54.68** | 176.49** | 37.42** | 14.32** |
| Error | 54 | 3.60 | 0.08 | 0.19 | 0.07 | 0.92 | 0.87 | 0.23 | 0.42 |
| GCA/ SCA | | 0.490 | 0.008 | 0.074 | 0.088 | 0.038 | 0.050 | 0.201 | 0.055 |

(*)(**) significant and highly significant at 0.05 and 0.01 level, respectively;

Table 3: Mean performance of the crosses and their parents for all studied traits.

| Geno- types | height plant (cm) | No. of spike. plant ⁻¹ | spike length (cm) | spike weight (g) | No. of spikelet spike ⁻¹ | No. of grains .spike ⁻¹ | weight 1000 seed | gains yield g.plant ⁻¹ |
|----------------|-------------------------|---|-------------------------|------------------------|---|--|------------------------|---|
| Sham 6 | 88.22 | 5.24 | 7.77 | 1.00 | 40.22 | 31.53 | 33.95 | 7.23 |
| Jad | 81.58 | 4.43 | 9.73 | 2.55 | 45.33 | 47.33 | 42.21 | 10.87 |
| Barcelona | 84.16 | 5.10 | 8.83 | 2.00 | 40.00 | 38.83 | 36.22 | 8.32 |
| Adana | 77.72 | 4.57 | 8.37 | 1.11 | 39.52 | 41.33 | 35.65 | 8.65 |
| Abu Ghraib3 | 80.55 | 4.67 | 8.99 | 2.33 | 40.67 | 42.17 | 32.82 | 8.04 |
| Aras | 90.89 | 5.00 | 9.85 | 2.33 | 46.44 | 38.48 | 40.80 | 9.43 |
| Ebaa 99 | 88.38 | 5.50 | 10.87 | 2.11 | 51.55 | 49.73 | 37.45 | 11.24 |
| (1×2) | 87.21 | 6.10 | 9.83 | 2.33 | 45.66 | 49.11 | 43.30 | 12.74 |
| (1×3) | 82.47 | 6.13 | 9.90 | 1.89 | 47.33 | 47.55 | 30.98 | 9.08 |
| (1×4) | 82.38 | 6.03 | 10.17 | 2.66 | 48.00 | 50.88 | 40.47 | 12.20 |
| (1×5) | 88.77 | 5.83 | 10.00 | 2.44 | 48.33 | 61.44 | 38.71 | 13.71 |
| (1×6) | 88.84 | 5.70 | 9.95 | 2.78 | 49.00 | 57.11 | 41.51 | 13.27 |
| (1×7) | 86.70 | 5.87 | 9.49 | 2.55 | 53.00 | 53.11 | 40.93 | 12.81 |
| (2×3) | 83.00 | 6.02 | 9.60 | 3.44 | 51.55 | 61.33 | 41.09 | 15.12 |
| (2×4) | 84.92 | 5.88 | 9.61 | 2.22 | 49.55 | 54.11 | 45.07 | 14.27 |
| (2×5) | 92.30 | 6.20 | 9.95 | 2.77 | 49.67 | 56.55 | 37.54 | 13.15 |
| (2×6) | 82.66 | 6.00 | 9.90 | 2.44 | 47.67 | 56.43 | 36.72 | 12.68 |
| (2×7) | 81.83 | 5.91 | 9.90 | 2.55 | 48.00 | 50.93 | 40.70 | 12.21 |
| (3×4) | 75.12 | 5.76 | 9.86 | 2.88 | 51.67 | 53.95 | 40.29 | 12.52 |
| (3×5) | 84.34 | 6.13 | 9.65 | 3.00 | 51.89 | 61.37 | 37.49 | 13.43 |
| (3×6) | 84.75 | 6.03 | 9.67 | 2.44 | 49.67 | 53.89 | 40.37 | 13.11 |
| (3×7) | 79.00 | 5.50 | 9.80 | 3.55 | 53.00 | 56.41 | 39.22 | 12.21 |
| (4×5) | 82.00 | 5.91 | 9.71 | 2.44 | 49.00 | 50.51 | 40.76 | 12.16 |
| (4×6) | 87.30 | 5.85 | 9.27 | 2.78 | 47.67 | 47.29 | 43.36 | 12.04 |
| (4×7) | 79.39 | 5.77 | 9.73 | 2.44 | 48.00 | 51.51 | 39.92 | 11.96 |
| (5×6) | 92.43 | 6.07 | 9.45 | 1.88 | 49.22 | 46.13 | 36.83 | 10.50 |
| (5×7) | 93.43 | 6.07 | 9.00 | 1.11 | 42.33 | 50.36 | 39.56 | 12.21 |
| (6×7) | 92.29 | 6.03 | 9.20 | 2.11 | 43.88 | 49.00 | 50.09 | 14.75 |
| mean parents | 84.50 | 4.93 | 9.20 | 1.92 | 43.39 | 41.34 | 37.02 | 9.11 |
| mean hybrid | 85.29 | 5.94 | 9.70 | 2.51 | 48.77 | 53.28 | 40.23 | 12.67 |
| L.S.D 5% | 3.10 | 0.36 | 0.74 | 0.41 | 1.56 | 1.52 | 0.78 | 1.06 |
| L.S.D 1% | 4.13 | 0.48 | 0.99 | 0.55 | 2.08 | 2.02 | 1.04 | 1.41 |

Means followed by a common letters are not significantly different at the 0.05 level according to L.S.D test.

over rest hybrids with an average of 50.09, this trait consider expresses in flour produced from grains which increase led to increasing the flour, which trait depends on strength output (grains), which is the recipient of photosynthesis products and on availability source and its strength by distributing photosynthetic products during the fertilization stages and physiological maturity, which depends on the susceptibility of variety and genotype (Al-Fahdawi, 2010). in yield grain superior Ebaa 99 variety on all cultivars an average of 11.24 and hybrid (2 × 3) compared to rest of hybrids on average of 15.12, the difference between genotypes in this trait are due to genetic variation and difference in (No. of spikes per

plant, No. of grains per spike and weight of 1000 grains). This result agrees with (Mohammed, 2020a) and (Mohammed, 2020 b) is found different between genotypes for traits studies.

Table 4 shows the general combining ability to parent notes in plant height the effect of general combining ability was significant to toward of desire in the parent (1), (5), (6) and (7), for No. of spikes per plant (1) and (7) were an effect of general combining ability to toward of desired, and spike length was the effect of general combining ability was significant toward of desired (2) and (7) parent, and spike weight effect of general combining ability was significant toward of desired (2) and (3) parent, for No. of spikelets was the effect of general combining ability towards an increase in the parent (2), (3) and (7), as the No. of grains per spike was the effect of general combining ability desired in (2), (3), (5) and (7), for weight 1000 grain the effect general combining ability toward desired in (2), (4), (6) and (7), but the grain yield the effect of the general combining ability toward desired in (2) and (7).

Table 5 shows estimates of effect the specific combining ability for each single hybrid for all studied traits, notes that effect of the specific combining ability for the plant height in hybrids (1 × 2), (2 × 3), (2 × 4), (2 × 5), (4 × 6), (5 × 6), (5 × 7) and (6 × 7) toward desired, No. of spikes per plant effect of specific combining ability in most crosses was recorded by the highest value of hybrid (2 × 5) value 0.57 and least effect in the hybrid (4 × 7) was record 0.17 and rest hybrids recorded values between these two values, and length of spike was significant in most of hybrids and recorded highest effect in hybrid (1 × 4) as it reached 0.95 and lowest effect in the hybrid (3 × 5) as it reached 0.22 and rest hybrids took difference between the two values, spike weight in the hybrid was recorded (3 × 7) with a value of 0.98 and the lowest effect was recorded in Hybrid (2 × 5) as its value reached 0.26, No. of spikelets record hybrid value (1 × 7) was 5.10 and least effect was recorded by hybrid (4 × 6) value was 0.89, No. of grains per spike, highest effect in hybrid (1 × 5) as it

Table 4: Estimates of parental general combining ability effects for traits studies.

| Geno- types | height plant (cm) | No. of spike. plant ⁻¹ | spike length (cm) | spike weight (g) | No. of spikelet spike ⁻¹ | No. of grains .spike ⁻¹ | weight 1000 seed | gains yield g.plant ⁻¹ |
|----------------|-------------------------|---|-------------------------|------------------------|---|--|------------------------|---|
| Sham 6 | 1.34 | 0.07 | -0.19 | -0.25 | -0.85 | -2.24 | -1.29 | -0.67 |
| Jad | -0.63 | -0.06 | 0.19 | 0.22 | 0.38 | 2.30 | 1.49 | 0.85 |
| Barcelona | -2.64 | 0.03 | -0.05 | 0.26 | 0.64 | 1.09 | -1.50 | -0.24 |
| Adana | -3.80 | -0.13 | -0.17 | -0.14 | -0.72 | -1.27 | 0.64 | -0.20 |
| Abu Ghraib3 | 1.51 | 0.00 | -0.09 | -0.07 | -0.85 | 0.92 | -2.10 | -0.33 |
| ARAS | 3.25 | 0.02 | 0.06 | 0.02 | 0.07 | -1.73 | 1.67 | 0.11 |
| Ebaa 99 | 0.96 | 0.07 | 0.25 | -0.04 | 1.33 | 0.93 | 1.10 | 0.48 |
| S.E(gi) | 0.34 | 0.05 | 0.08 | 0.05 | 0.17 | 0.17 | 0.09 | 0.12 |

Means followed by a common letters are not significantly different at the 0.05 level according to L.S.D test.

Table 5: Mean performance of the crosses and their parents for all studied traits.

| Geno- types | height plant (cm) | No. of spike. plant ⁻¹ | spike length (cm) | spike weight (g) | No. of spikelet spike ⁻¹ | No. of grains .spike ⁻¹ | weight 1000 seed | gains yield g.plant ⁻¹ |
|----------------|-------------------------|---|-------------------------|------------------------|---|--|------------------------|---|
| (1×2) | 1.41 | 0.40 | 0.26 | 0.00 | -1.29 | -1.26 | 3.67 | 0.77 |
| (1×3) | -1.33 | 0.34 | 0.56 | -0.48 | 0.12 | -1.60 | -5.65 | -1.80 |
| (1×4) | -0.25 | 0.40 | 0.95 | 0.69 | 2.14 | 4.09 | 1.69 | 1.28 |
| (1×5) | 0.82 | 0.07 | 0.71 | 0.39 | 2.60 | 12.46 | 2.67 | 2.93 |
| (1×6) | -0.85 | -0.08 | 0.50 | 0.64 | 2.36 | 10.78 | 1.70 | 2.05 |
| (1×7) | -0.69 | 0.04 | -0.14 | 0.48 | 5.10 | 4.11 | 1.69 | 1.21 |
| (2×3) | 1.17 | 0.36 | -0.11 | 0.60 | 3.12 | 7.64 | 1.68 | 2.73 |
| (2×4) | 4.25 | 0.38 | 0.02 | -0.22 | 2.47 | 2.78 | 3.52 | 1.84 |
| (2×5) | 6.33 | 0.57 | 0.29 | 0.26 | 2.71 | 3.03 | -1.28 | 0.85 |
| (2×6) | -5.06 | 0.35 | 0.08 | -0.16 | -0.20 | 5.56 | -5.87 | -0.06 |
| (2×7) | -3.59 | 0.21 | -0.11 | 0.01 | -1.13 | -2.61 | -1.32 | -0.91 |
| (3×4) | -3.54 | 0.17 | 0.50 | 0.41 | 4.33 | 3.84 | 1.73 | 1.18 |
| (3×5) | 0.37 | 0.41 | 0.22 | 0.44 | 4.67 | 9.06 | 1.66 | 2.22 |
| (3×6) | -0.96 | 0.30 | 0.08 | -0.20 | 1.54 | 4.23 | 0.78 | 1.46 |
| (3×7) | -4.42 | -0.29 | 0.02 | 0.98 | 3.61 | 4.10 | 0.20 | 0.18 |
| (4×5) | -0.80 | 0.35 | 0.40 | 0.29 | 3.14 | 0.56 | 2.79 | 0.91 |
| (4×6) | 2.75 | 0.27 | -0.20 | 0.53 | 0.89 | 0.00 | 1.62 | 0.36 |
| (4×7) | -2.87 | 0.14 | 0.08 | 0.26 | -0.03 | 1.56 | -1.24 | -0.11 |
| (5×6) | 2.57 | 0.36 | -0.09 | -0.43 | 2.58 | -3.36 | -2.17 | -1.06 |
| (5×7) | 5.86 | 0.30 | -0.73 | -1.15 | -5.57 | -1.80 | 1.13 | 0.28 |
| (6×7) | 2.98 | 0.26 | -0.69 | -0.24 | -4.93 | -0.50 | 7.89 | 2.38 |
| S.E(Sij) | 0.84 | 0.12 | 0.19 | 0.11 | 0.42 | 0.41 | 0.21 | 0.29 |

Means followed by a common letters are not significantly different at the 0.05 level according to L.S.D test.

reached 12.46 and lowest effect recorded in the hybrid (4 × 5) when effect recorded at 0.56, in weight of 1000 grains, effect of highest value recorded in hybrid (6 × 7) with a value of 7.89 and lowest recorded effect in hybrid (3 × 6) its value was 0.78 and grain yield recorded the highest value in hybrid (1 × 5), as value was 2.93 and lowest in hybrid (4 × 6) was 0.36.

Table 6 shows variation of influence of general and

specific combining ability for each parent for all traits, the importance of this lies in knowing how parents achieve values of their impact as well as determining which of the parents under study is more beneficial in improving the trait, in plant height parents were (1) (5) and (6) have a general combining ability this indicates the parent (5) has transferred a portion of his genes to his hybrids, while (6) parent transferred his genes to hybrids on a regular, the No. of spikes per plant it appears that parents (1) and (7) had transferred their genes to hybrids on a regular, the spike length the parent (7) transferred his genes to hybrids on a regular, and weight of spike it appears the parents (2) and (3) have transmitted his genes to hybrids on a regular, No. of spikelets notes that the parents (3) and (7) have transferred a portion of its genes to its hybrids, grain per spike it appears that parent (7) has transmitted its genes to its hybrids on a regular unlike the parents (2), (3) and (5) have Transferring their genes to hybrids on an irregular, and weight 1000 grain (1) and (4) he inherited his genes to his hybrids on a regular, unlike parents (6) and (7) who showed that their genes were transferred to the irregularly or a part of their genes, grain yield, the parent (2) transferred a part of his genes to his hybrids, unlike the parent (7), who inherited most of his genes to his hybrids.

The Heterosis calculated on the deviation of the first generation from the average parents was noted in table 7 the values of Heterosis of the studied traits are shown in height of plant There is a significant Heterosis for hybrid (2 × 5), (5 × 6) and (5 × 7) amounted to 11.24, 6.71 and 8.96 each, respectively, No. of spike per plant, most of the crosses were significant and recorded the highest value in hybrid (2 × 5) was 1.65 and lowest value in hybrid (6 × 7) was 0.78 and rest of the crosses it lies between two values.

For spike length, superior some hybrids their hybrid (1 × 4) recorded a value of 2.10 and lowest value of hybrid (1 × 2) was 1.08, and spike weight also excelled some hybrids highest value in there is a hybrid (1 × 4)

Table 6: Estimation of (σ^2_{gi}) and (σ^2_{sij}) for the parents of the studied traits.

| Parents | Variance | height plant (cm) | No. of spike. plant ⁻¹ | spike length (cm) | spike weight (g) | No. of spikelet spike ⁻¹ | No. of grains .spike ⁻¹ | weight 1000 seed | gains yield g.plant ⁻¹ |
|-------------|--------------|-------------------|-----------------------------------|-------------------|------------------|-------------------------------------|------------------------------------|------------------|-----------------------------------|
| Sham 6 | σ^2_g | 0.77 | -0.02 | -0.02 | 0.04 | 0.45 | 4.75 | 1.60 | 0.32 |
| | σ^2_S | -0.62 | 0.32 | 1.74 | 1.39 | 42.95 | 307.71 | 60.81 | 18.96 |
| Jad | σ^2_g | -0.63 | -0.02 | -0.02 | 0.03 | -0.12 | 5.06 | 2.15 | 0.60 |
| | σ^2_S | 93.68 | 0.79 | -0.15 | 0.39 | 24.56 | 113.11 | 66.13 | 12.23 |
| Barcelona | σ^2_g | 5.93 | -0.02 | -0.05 | 0.05 | 0.14 | 0.93 | 2.20 | -0.06 |
| | σ^2_S | 29.90 | 0.48 | 0.30 | 1.84 | 64.11 | 190.99 | 40.78 | 18.43 |
| Adana | σ^2_g | 13.43 | -0.01 | -0.03 | 0.00 | 0.25 | 1.38 | 0.34 | -0.08 |
| | σ^2_S | 40.77 | 0.42 | 1.03 | 1.00 | 38.46 | 40.49 | 29.77 | 6.65 |
| Abu Ghraib3 | σ^2_g | 1.26 | -0.02 | -0.05 | -0.01 | 0.45 | 0.60 | 4.34 | -0.01 |
| | σ^2_S | 76.05 | 0.70 | 1.01 | 1.89 | 81.93 | 259.80 | 24.91 | 15.54 |
| ARAS | σ^2_g | 9.56 | -0.02 | -0.05 | -0.02 | -0.26 | 2.75 | 2.73 | -0.11 |
| | σ^2_S | 44.01 | 0.35 | 0.46 | 0.89 | 38.13 | 175.04 | 107.14 | 12.48 |
| Ebaa 99 | σ^2_g | -0.11 | -0.02 | 0.01 | -0.02 | 1.50 | 0.62 | 1.14 | 0.11 |
| | σ^2_S | 78.02 | 0.17 | 0.72 | 2.50 | 94.11 | 44.89 | 69.27 | 7.31 |
| | σ^2_e | 3.60 | 0.08 | 0.19 | 0.07 | 0.92 | 0.87 | 0.23 | 0.42 |

Table 7: Heterosis over mid-parent (M.P.) in the F₁ generation for all studies traits.

| Genotypes | height plant (cm) | No. of spike. plant ⁻¹ | spike length (cm) | spike weight (g) | No. of spikelet spike ⁻¹ | No. of grains .spike ⁻¹ | weight 1000 seed | gains yield g.plant ⁻¹ |
|-----------|-------------------|-----------------------------------|-------------------|------------------|-------------------------------------|------------------------------------|------------------|-----------------------------------|
| (1×2) | 2.31 | 1.26** | 1.08* | 0.55 | 2.89* | 9.68** | 5.22** | 3.69** |
| (1×3) | -3.72 | 0.96** | 1.60** | 0.39 | 7.22** | 12.37** | -4.11** | 1.30 |
| (1×4) | -0.59 | 1.13** | 2.10** | 1.61** | 8.13** | 14.45** | 5.67** | 4.26** |
| (1×5) | 4.38 | 0.88* | 1.62** | 0.78* | 7.89** | 24.60** | 5.32** | 6.07** |
| (1×6) | -0.71 | 0.58 | 1.14* | 1.11** | 5.67** | 22.10** | 4.13** | 4.94** |
| (1×7) | -1.60 | 0.50 | 0.18 | 1.00** | 7.11** | 12.48** | 5.23** | 3.57** |
| (2×3) | 0.13 | 1.25** | 0.32 | 1.17** | 8.89** | 18.25** | 1.87** | 5.53** |
| (2×4) | 5.27* | 1.38** | 0.56 | 0.39 | 7.13** | 9.78** | 6.14** | 4.51** |
| (2×5) | 11.24** | 1.65** | 0.59 | 0.33 | 6.67** | 11.80** | 0.02 | 3.69** |
| (2×6) | -3.58 | 1.28** | 0.11 | 0.00 | 1.78 | 13.52** | -4.79** | 2.53** |
| (2×7) | -3.15 | 0.94** | -0.40 | 0.22 | -0.44 | 2.39* | 0.87 | 1.16 |
| (3×4) | -5.82* | 0.93** | 1.26* | 1.33** | 11.91** | 13.87** | 4.36** | 4.04** |
| (3×5) | 1.98 | 1.25** | 0.74 | 0.83* | 11.55** | 20.87** | 2.96** | 5.25** |
| (3×6) | -2.78 | 0.98 | 0.32 | 0.28 | 6.45** | 15.23** | 1.86** | 4.23** |
| (3×7) | -7.27** | 0.20 | -0.05 | 1.50** | 7.22** | 12.13** | 2.38** | 2.43** |
| (4×5) | 2.87 | 1.29** | 1.03 | 0.72* | 8.91** | 8.76** | 6.52** | 3.81** |
| (4×6) | 3.00 | 1.07** | 0.16 | 1.06** | 4.69** | 7.38** | 5.14** | 3.00** |
| (4×7) | -3.66 | 0.73* | 0.12 | 0.83* | 2.47* | 5.98** | 3.38** | 2.02* |
| (5×6) | 6.71** | 1.23** | 0.03 | -0.45 | 5.67** | 5.80** | 0.02 | 1.76* |
| (5×7) | 8.96** | 0.98** | -0.93 | -1.11** | -3.78** | 4.41** | 4.42** | 2.58** |
| (6×7) | 2.66 | 0.78* | -1.16* | -0.11 | -5.12** | 4.89** | 10.96** | 4.41** |
| (S.E) | 1.34 | 0.25 | 0.30 | 0.18 | 0.67 | 0.65 | 0.34 | 0.45 |

was 1.61 and lowest value in Hybrid (4 × 5) was 0.72, No. of spikelets per spike significantly outperformed most of the hybrids the highest value of hybrid (4 × 3) was 11.91 and lowest value in hybrid (4 × 7) was 2.4, as for No. of grains per spike all hybrids exceeded the highest hybrid value (1 × 5) with a value of 24.60 and lowest value of 2.39 for hybrid (2 × 7), the weight of 1000 grains,

most of the hybrids significantly outperformed, and lowest value for hybrid (3 × 6), where it recorded 1.86, and for grain yield of exceeded most of the hybrids, where it recorded the highest value of hybrid (1 × 5) with a value of 6.07 and lowest value recorded by the hybrid (5 × 6) if it recorded a value of 1.76.

Table 8 shows data of the statistical constants that were calculated, the estimation of the average parents (MoLo) and variance of parents (VoLo) and the average of the column variance (V1L1) and average column variation (VoL1) and average common variation of the first generation columns (WoLo) that was used to estimate the genetic components of the traits Studied.

Table 9 shows results the analysis of variance by the Hayman method (1954a), it shows that additional variation (D) was significant from zero for a plant height 19.83, spike length 0.879, spike weight 0.317, number of spikelets 19.51, number of grains per spike 33.46 and

weight 1000 grains 11.34 this indicates that the additional genetic variation is important in determining these characteristics, and selection for them can be made because inheritance is expected to be high in it.

But values of (H1 and H2), they were significant for all traits, indicating the presence of dominance effects

Table 8: Estimation of some genetic parameters for the studied characters.

| Genetic parameter | height plant (cm) | No. of spike. plant ⁻¹ | spike length (cm) | spike weight (g) | No. of spikelet spike ⁻¹ | No. of grains .spike ⁻¹ | weight 1000 seed | gains yield g.plant ⁻¹ |
|-------------------|-------------------|-----------------------------------|-------------------|------------------|-------------------------------------|------------------------------------|------------------|-----------------------------------|
| MoLo | 84.50 | 4.930 | 9.201 | 1.918 | 43.390 | 41.345 | 37.015 | 9.112 |
| VoLo | 23.31 | 0.151 | 1.070 | 0.380 | 20.617 | 36.289 | 11.824 | 2.200 |
| VILl | 18.69 | 0.193 | 0.258 | 0.337 | 13.479 | 43.211 | 13.416 | 3.574 |
| VoLl | 7.59 | 0.003 | 0.009 | 0.034 | 0.530 | 2.802 | 2.675 | 0.219 |
| WoLo | 7.82 | 0.010 | 0.064 | 0.047 | 0.778 | 4.794 | 4.231 | 0.637 |

that control these traits, this indicates that the frequency of dominant and recessive genes is not equal to these traits and when considering the values of additional and dominant variance it is clear that the dominance genetic variance (H1 and H2) was greater in its value than the additional variation of all studied traits, and thus it can be concluded that the dominance genetic variation is the most important in the inheritance of all studied traits, this indicates the possibility of benefiting from Heterosis in this study.

The values of (F) that are taken as a guide for the relative frequency of dominant and recessive genes in parents, if they are positive, they indicate an increase in the dominant genes and if are negative they indicate an increase in recessive genes were positive and significant in spike length, spike weight, No. of spikelets per spike and No. of grain per spikes, and positive but did not reach the height of the plant, No. of spikes per plant, the weight of 1000 grains this is evidence of the prevalence of genes prevalent in parents for these characteristics.

For the values of (h²) which (express sum of the dominance effects of the mixture sites), they were significant in No. of spikes per plant, length and weight

Table 9: Estimation of some genetic parameters for the studied traits.

| Genetic Parameter | height plant (cm) | No. of spike. plant ⁻¹ | spike length (cm) | spike weight (g) | No. of spikelet spike ⁻¹ | No. of grains .spike ⁻¹ | weight 1000 seed | gains yield g.plant ⁻¹ |
|-------------------|-------------------|-----------------------------------|-------------------|------------------|-------------------------------------|------------------------------------|------------------|-----------------------------------|
| D | 19.83 | 0.026 | 0.87 | 0.317 | 19.516 | 33.464 | 11.344 | 0.699 |
| S.E | 7.73 | 0.050 | 90.171 | 0.194 | 6.452 | 21.538 | 6.533 | 0.922 |
| H1 | 57.35 | 0.544 | 1.328 | 1.367 | 68.432 | 182.291 | 47.262 | 9.871 |
| S.E | 9.70 | 0.063 | 0.215 | 0.244 | 8.089 | 26.999 | 8.190 | 1.155 |
| H2 | 37.42 | 0.508 | 0.615 | 1.086 | 49.596 | 155.988 | 42.001 | 10.416 |
| S.E | 6.56 | 0.043 | 0.145 | 0.165 | 5.475 | 18.276 | 5.544 | 0.782 |
| F | 10.36 | 0.085 | 1.611 | 0.480 | 36.548 | 49.366 | 6.040 | -0.294 |
| S.E | 15.56 | 0.102 | 0.344 | 0.391 | 12.978 | 43.322 | 13.141 | 1.854 |
| h ² | 0.12 | 2.951 | 0.630 | 0.997 | 84.386 | 417.579 | 30.178 | 36.530 |
| S.E | 4.60 | 0.030 | 0.102 | 0.116 | 3.837 | 12.807 | 3.885 | 0.548 |
| E | 3.49 | 0.125 | 0.191 | 0.063 | 1.101 | 2.825 | 0.480 | 1.501 |
| S.E | 1.09 | 0.007 | 0.024 | 0.027 | 0.913 | 3.046 | 0.924 | 0.130 |
| b = | 0.49± | 0.611± | 0.696± | 0.174± | 0.686± | 0.439± | 0.151± | 0.603± |
| | 0.27 | 0.096 | 0.306 | 0.438 | 0.422 | 0.213 | 0.332 | 0.132 |

b = regression coefficient

of spike, No. of spikelets per spikes, No. of grains per spikes, the weight of 1000 grains and grain yield, this indicates the effect of dominance mixture location but not significant in length height this breeding throe Heterosis in excellent in the trait, and selection can be efficient in its isolation generations and in improving it genetically. But environmental variance

(E), it was significant in all traits this indicates the environmental effect is significant in these traits except No. of grains per plant and weight of 1000 grains were not significant.

Table 10 shows the values of ratios of hereditary features and heredity and notes the average degree of dominance was greater than one in height of plant the No. of spikes per plant length and weight of spike No. of spikelets per spike No. of grains per spike weight of 1000 grains and grain yield this indicating presence of over dominance this another evidence of the possibility of benefiting from Heterosis for obtaining hybrids is described in this study.

The ratio of a number of dominant genes to recessive KD/KR was greater than one for all traits, which indicates an increase in dominance genes in parents for all studied traits these indicators all confirm the importance of dominance genes in parents and possibility of obtaining superior hybrids by benefiting from the Heterosis unlike grain yield was less than one.

The values of (K = h²/H²) were greater than one in No. of spikes per plant, No. of spikelets per spike, No. of

Table 10: The ratios of genetic components for the studied traits.

| Genetic parameter | height plant (cm) | No. of spike. plant ⁻¹ | spike length (cm) | spike weight (g) | No. of spikelet spike ⁻¹ | No. of grains .spike ⁻¹ | weight 1000 seed | gains yield g.plant ⁻¹ |
|-------------------|-------------------|-----------------------------------|-------------------|------------------|-------------------------------------|------------------------------------|------------------|-----------------------------------|
| H1/D | 1.70 | 4.57 | 1.23 | 2.08 | 1.87 | 2.33 | 2.04 | 3.76 |
| KD/KR | 1.36 | 2.11 | 6.85 | 2.15 | 3.00 | 1.92 | 1.30 | 0.89 |
| h ² H2 | 0.00 | 5.80 | 0.55 | 0.92 | 1.70 | 2.68 | 0.72 | 3.51 |
| H2/4H1 | 0.16 | 0.23 | 0.12 | 0.20 | 0.18 | 0.21 | 0.22 | 0.26 |
| Heritability | 0.65 | 0.03 | 0.66 | 0.18 | 0.09 | 0.32 | 0.35 | 0.05 |
| E.G.A. | 4.01 | 0.014 | 0.10 | 0.157 | 0.526 | 1.273 | 2.075 | 0.377 |

Table 11: Parents' order according to average and degree of dominance for all studied traits.

| Characters | Parent sequences according to their averages high to low | Parent sequences according to degree of dominance to recessive |
|---------------------------|--|--|
| height plant (cm) | 4' 5' 2' 3' 1' 7' 6 | 7' 5' 4' 6' 2' 3' 1 |
| No. of spike per plant | 2' 4' 5' 6' 3' 1' 7 | 2' 5' 4' 6' 3' 1' 7 |
| spike length (cm)ý | 1' 4' 3' 5' 2' 6' 7 | 1' 7' 4' 3' 5' 6' 2 |
| spike weight (g)ý | 1' 4' 3' 7' 5' 6' 2 | 7' 3' 1' 4' 5' 2' 6 |
| No. of spikelet per spike | 4' 3' 1' 5' 2' 6' 7 | 3' 1' 7' 4' 5' 2' 6 |
| No. of grains per spike | 1' 5' 3' 4' 5' 2' 7 | 1' 3' 5' 6' 4' 2' 7 |
| Weight 1000 seed | 5' 1' 4' 3' 7' 6' 2 | 1' 6' 7' 3' 4' 2' 5 |
| grains yield per plant | 1' 5' 3' 4' 6' 2' 7 | 3' 1' 5' 6' 4' 2' 7 |

grains per spike and grain yield this indicates the number of dominant gene groups controlling these traits that show

dominance and less than one in plant height, spike length, spike weight and weight of 1000 grains.

The values of gene frequency for dominant alleles to recessive (H2/4H1) were greater than (0.25) for grain yield this indicates the distribution of alleles between these parents was uniform while they were less than (0.25) in plant height, number of spikes per plant, length and weight of spike, number of spikelets,

number of grains per spike and weight of 1000 grains this indicates that distribution of these alleles among parents was irregular and this is due to unequal estimates of the two components (H1 and H2) this is consistent with results that found (Al-Taweel 2009).

As for heritability in the narrow sense was high in height of the plant, length of the spike, this results from an increase in the percentage of additional variation in these traits and its formation of a high percentage of phenotypic variation, and a medium average of No. of grains per spike and weight of 1000 grains, and low No. of spikes per plant weight of spike, No. of spikelets, and grain yield.

The expected genetic advance as a percentage was low (less than 10%) for all traits studied.

It appears from table 11 the parent (7) excelled in

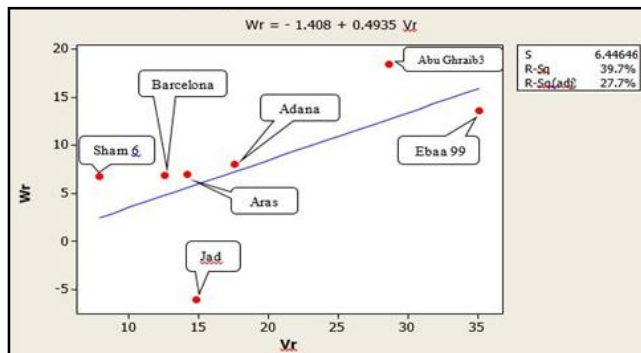


Fig. 1: Height Plant (cm).

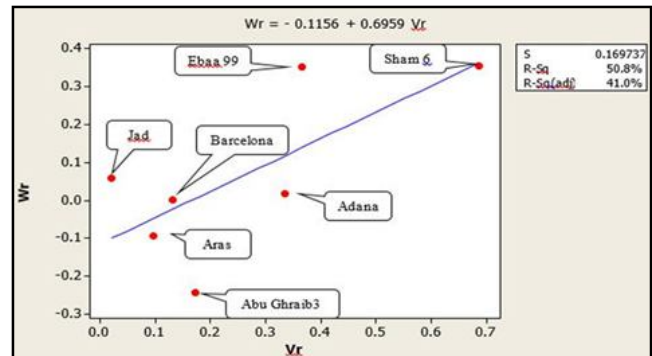


Fig. 3: Spike Length.

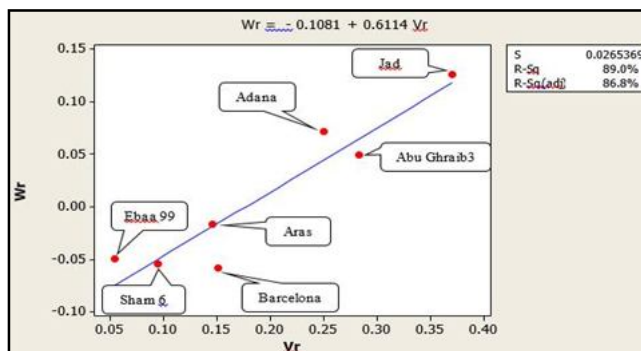


Fig. 2: No. of Spike. Plant.

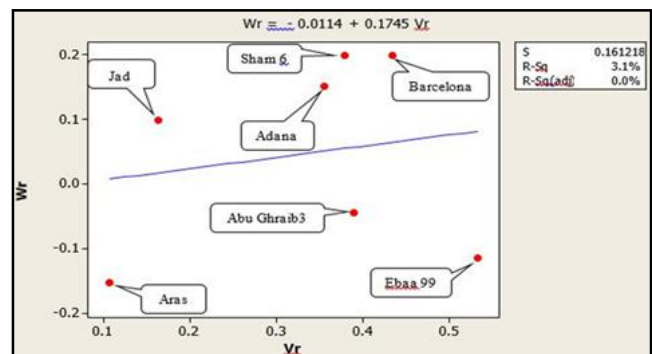


Fig. 4: Spike Weight.

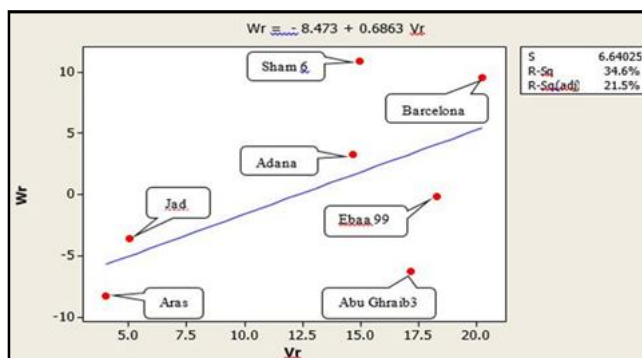


Fig. 5: No. of Spikelet.Spike.

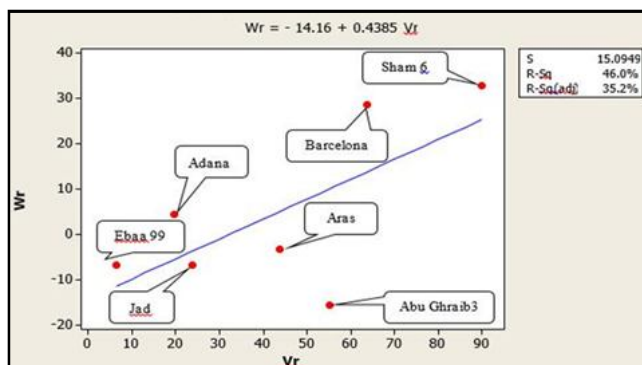


Fig. 6: No. of Grains. Spike.

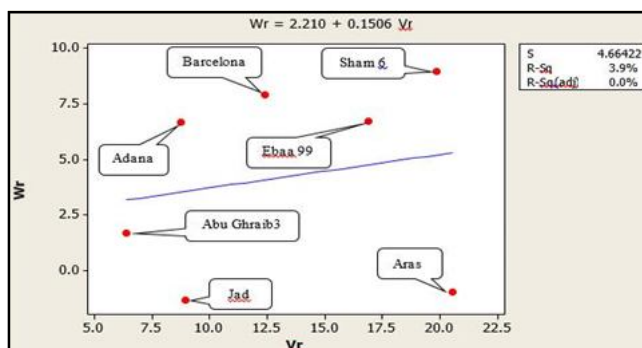


Fig. 7: Weight 1000 Seed.

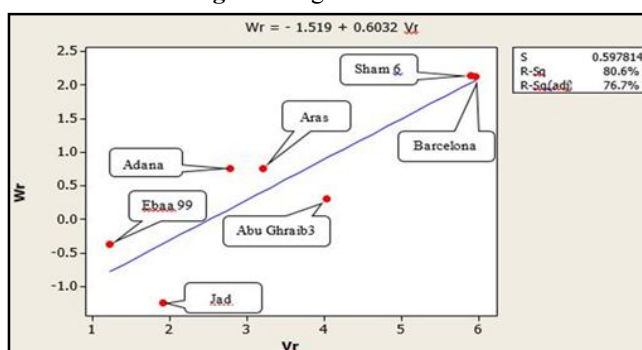


Fig. 8: Grains Yield g. Plant.

the number of dominant genes that control traits, as well as in taking averages highest degree of dominance in No. of spikes per plant, No. of grains per spike and grain yield, followed by parent (2) spike weight and weight of 1000 grains Then parent (6) followed it in height of the

plant, the weight of spike and the number of spikelets per spike the rest parent varied in order high average and degree of dominance.

The regression line on simple Hayman-Jenkins model Vr graphs have been plotted against Wr showing the slope of regression line indicating a lack of interest in genetic interfering effects, regression analysis can be used to identify the degree of dominance rate (which is measured by the distance between the point of intersection of the regression line with axis and point of origin) the ratio of dominant and recessive genes in parents through the distribution of parents along the regression line, and it can also be a measure of genetic variation between parents do this by spacing the parents along the regression line. It is clear from these graphs height of plant and weight of 1000 grains, because regression line cut Wr axis on top of original point indicating partial dominance state, while regression line cut Wr axis under the origin point in No. of spikes per plant, length of the spike, No. of spikelets per spike, No. of grains per spike and yield grains but spike' weight, it appears complete dominance because slope line passed through origin point this is consistent with what he got the regression line crossed the Vr axis in all traits they studied, while found this result with Al-Azzawi (2015) in No. of spikes per plant and No. of grains per spike reverse result in yield grain.

The regression line cut the Wr axis to all studied traits. While the distribution of parent around the regression line, the distribution of these parent around it indicates in order to the degree of dominance parent that contain a greater number of dominant genes occupy positions closer to the point of origin, while parent that contains a greater number of recessive genes occupy sites farthest from a point of origin and it is noted there is a genetic variation between parents for most of the traits, while parent that have equal proportions of the dominant and recessive genes occupy intermediate positions.

Conclusion

Superior Ebaa 99 in grain yield and general combining ability, hybrids (Jad × Barcelona) and (Aras × Ebaa 99) in grain yield. There was an increase in dominance genes in parents of all traits, by the presence of over dominance, and presence of dominance influences to control these traits. Heritability narrow sense was high in plant height and spike length expected genetic advance as a percentage was lower than 10% for all studied traits. While cutting regression line Wr axis under origin point in No. of spikes per plant, length of the spike, No. of spikelets per spike, No. of grains per spike and grain yield per plant.

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