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GENETIC ANALYSIS OF F_1 DIALLEL CROSS IN WHEAT (*TRITICUM AESTIVUM* L.)

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Abstract

Mean performance and nature of genetic action on earliness, yield and some quality traits were studied in a 10x10 diallel cross without reciprocals in wheat to define and select an efficient and prospective material for immediate use in hybridization programs to improve grain yield of wheat in Iraq. Parents, and F_1 were evaluated using a randomized complete block design (RCBD) with three replications for quantitative traits in 2017/2018 season. Significant genotype mean squares and its components (parents and crosses) were obtained for all traits in both generations. Significant heterosis in F_1 generation was obtained for all studied traits. Highly significant and larger (in magnitude) values of dominance component (H1) than additive were obtained for all studied traits resulting in more values of $(H1/D)^{0.5}$ which were more than unity in both generations. High heritability values (in a broad-sense) along with medium or low ones in narrow-sense were exhibited in both generations, indicating that most genetic variances were due to non-additive genetic effects. The parent 5 and 8 for days to heading; P4 for no of spike plant^{-1}, 1000-kernel weight and grain yield plant^{-1}; P3 and P8 for no of grain spike^{-1}; P10 for protein content; P7 and P8 for gluten content and P9 for dry gluten content included largest number of recessive genes for these traits. On the other hand, P3 and P10 for heading date, P1, P2 and P8 for no of spike plant-1, P1 and P6 for no of grain spike^{-1}; P2 for 1000-kernel weight and grain yield plant^{-1}; P5 and P7 for protein content; P4 for gluten content; and P1, P6 and P10 for dry gluten content, contained maximum number of dominant alleles for those traits.

***Keywords*:** Wheat, Diallel analysis, graphic analysis, Gene action, heritability

Introduction

Wheat (*Triticum aestivum* L.) is an important source of both carbohydrates and protein in human and livestock nutrition (El-Hosary, 2019 a). It is estimated to contribute as much protein as the total annual soybean crop, or 60 million tonnes of protein per year (El-Hosary, 2019b). Grain yield potential and grain protein content (GPC) of a wheat crop are crucial determinants of its profitability and product quality

Wheat is the major cereal crop in Iraq as well as several other countries due to it's an important source of both carbohydrates and protein in human and livestock nutrition (El-Hosary, 2019b). The increasing gap between production and consumption necessitates increasing wheat production in Iraq. Practically; this could not be achieved through extending the wheat cultivated area on the expense of other. So the only way to overcome this problem is to increasing the productivity of wheat through an efficient breading program. Grain proteins content (GPC) and grain yield potential of wheat crop are crucial determinants of its product quality and profitability. GPC is limiting factor in wheat, as it helps to determine milling and baking quality (El-Hosary and Nour El Deen (2015).

Success of any plant breeding program depends largely upon a better understanding of the genetic basis of yield and its contributing characters. Information about the types of gene action may help the wheat breeder of formulate the most efficient breeding procedure for achievement of maximum genetic improvement among a particular set of genotypes. Besides, to identify desirable parents and cross combinations as genetic resources for improving yield and yield contributing characters. The long-term objective of the most plant breeding programs is to increase the unit area yield of high quality crop. Development of commercial (F_1) hybrid wheat may be one way of increasing yield. Numerous genetic studies have shown the existence of major genes conferring enhanced grain protein concentration without adverse effects on yield (El-Saadoown, 2017 and 2018). Nevertheless, plant breeders' experience shows that simultaneous selection of grain protein concentration and yield is only occasionally successful at enhancing both characters (Bakhsh *et al*., 2003).

The present investigation was carried out to study the nature of gene action and determine the heritability for some important traits in wheat.

Materials and Methods

Ten parents of bread wheat were selected for this study representing a wide range of variability. The code number, names and pedigree for the genotypes are presented in Table 1.

There were crossed in all possible combinations excluding reciprocals during 2016/2017 growing season, giving seeds of F_1 45 crosses. The hybridization was made at the Agricultural Research and Experimental Station of Daily Governorate. In 15th September 2017, the experiment involved parents and F_1 hybrids was conducted in a randomized complete block design with three replications in the Agricultural Research and Experimental Station of Daily Governorate. Replicate consist of 55 rows represent parents and F_1's 2 meter long and 60 cm wide, plants within row were 10 cm apart. The recommended agricultural practices for wheat production were applied. Data were recorded on individual 10 plant basis were randomly chosen from each plot. The following traits were measured: days to heading, No. of spikes plant^{-1}, No. of grains spike^{-1}, no of grain spike^{-1}, 1000-grain weight, grain yield plant^{-1}.

Grain protein content (GPC) measured as follows: GPC%= Ng x 5.70 according to AACC (2000), where Ng is grain nitrogen content. Grain samples were ground in powder and nitrogen of grains (Ng) was determined using Kjeldahl procedure according to A.O.A.C. (1990).

1- Wet Gluten Percentage of wheat samples were calculated using AACC method (using the gluten index (Glutomatic device of the Swedish origin of the General Company for Grain Manufacturing, General Center in Baghdad in the quality control department) by weighing (10) of flour for each sample (model) separately. A special bowl was added (4.8) of the brine and a mixture of flour for (20-22) seconds, then it was carried out automatic washing for (5) minutes and after the completion of the washing process transferred the eye (piece of gluten) and weighed in a sensitive balance after confirmation Parts of them are not kept in the bowl and the results are taken and recorded in grams.

2- Dry gluten (g). After calculating the percentage of wet gluten is dried sample in an oven and temperature (105 C) for four minutes using the device (Glutork, 2020) and the sample is weighed in a sensitive balance and then record the results.

The genetic parameters were estimated using the procedure described by Hayman (1954 a and b). Heritability in narrow-sense was estimated according to Mather and Jinks (1971) for F_1's data.

The variance and covariance statistics across replications were used to obtain estimates of the components of variation and their respective standard errors. The validity of the assumptions of diallel analysis was tested by the following formula (Sharma *et al*., 2004): t 2 ={(n2)/4[(MSS(Vr)- (MSS(Wr)]2 /{MSS(Vr)x[MSS(Wr)-MSP(Wr.Vr)2]}Where: Wr = covariance between parents and American Research Journal of Agriculture, Volume 1, Issue 4, 2015 ISSN 2378-9018 www.arjonline.org 15 their off-spring and Vr = variance of each array in which a particular parent is involved. Significance of calculated ‘‘t” value was tested against the tabulated ‘‘F” value with 4 and (n-2) degrees of freedom. Significant value indicates failure of the assumptions (Hayman, 1954 a and b). Another test was done by estimating the regression coefficient ‘‘bWr.Vr” of Wr on Vr as follows: bWr.Vr=[cov(Wr.Vr)/var Vr]=[MSP(Wr.Vr)/MSS(Vr]. The standard error (SE) for the regression coefficient (b) value was estimated as follows: SEb=[MSS(Wr)-bMSP(Wr.Vr)(n-2)]1/2 Where: n = number of parents.The significance of (b) different from zero (t1) and from unity(=1) (t2) can be tested by t-test as under: t1 = (b-0)/SEb and t2 = (1-b)/SEb The foregoing values were tested against the ‘‘t” tabulated value for (n-2) degrees of freedom according to (Mather and Jinks, 1971). If all the assumptions were valid, the regression coefficient would be significantly different from zero but not from unity. Hayman (1954 a and b), derived the expectations for the statistics calculated from the F1 diallel table and the expected values of the component variations using least squares. The notations of Mather and Jinks (1971) are used and described as follows: V0L0 (Vp) (variance of the parents) = D + Ê, V1L1(Vr)(mean of all the Vr values) = ¼ D - ¼ F + ¼ H1 + ¼ H2 + [Ê + Ê (n-2)/2n2], Vr (variance of all the progenies in each parental array) = ¼ D + ¼ H1- ¼ H2 - ¼ F + (n+1)/2n2 Ê, W0L01(Wr) (mean of all the Wr. values)= ½ D - ¼ F + Ê/n, (ML1 - ML0) 2 = dominance relationship = ¼ h2 + [(n -1) Ê/n2)]. The components of Ê, D, H1, H2, h2 and F were estimated in F1as follows: Ê = [(Errors S.S. + Reps S.S.)/r]/[(r-1) + (c-1) (r-1)]. D =V0L0 – Ê, F = 2 V0L0 - 4W0L01 - [2Ê (n-2)/n], H1 = V0L0 + 4 V0L1 - 4W0L01 - [Ê (3n-2)/n], H2 = 4 V1L1 - 4 V0L1 - 2Ê h 2 = 4(ML1 - ML0) 2 - [4Ê (n-1)/n2] Where: n = number of parents. Ê = expected environmental component of variance. D = variance due to additive effects of the genes. F = mean of the covariance of additive and dominance effects across all arrays. H1= variance component due to dominance deviation. H1=[1-(u-v)2], where, u and v are the proportions of positive and negative genes, respectively in the parents. h 2 = algebraic sum of dominance effects across all loci in heterozygous phase in all crosses. The following genetic parameters were also calculated: Average degree of dominance is estimated as (H1/D)1/2 1. If the of this ratio is zero, there is no dominance. 2. If it is greater than zero, but less than one, there is partial dominance. 3. If it is equal to 1, there is complete dominance. 4. If it is greater than 1, it indicates over dominance. Ratio of dominant and recessive genes in the parents (KD/KR) is estimated as follows: KD/KR = [(4DH1) 1/2+ F]/[(4 DH1) 1/2 - F] If KD/KR ≈1.0, it means nearly equal proportion of dominance and recessive alleles in parents, i.e. symmetrical distribution; p = q = 0.5. Any deviation from 1.0 indicates asymmetry of distribution (p # q). Thus: Ratio > 1 refers to excess of dominant alleles and minority of recessive alleles (p > q). Ratio < 1 means minority of dominant alleles and excess of recessive alleles (p < q). The ratio of dominant genes with positive or negative effects in parents (H2/4H1) was determined. The maximum theoretical value of 0.25 for this ratio arises when, p = q = 0.5 at all loci. A deviation from 0.25 would stem when p ≠ q Thus: if this ratio ≈ 0.25, it means symmetrical distribution of positive and negative dominant genes in parents, while if this ratio ≠ 0.25, it means asymmetry of distribution. Narrow-sense heritability (h2 n) was estimated using the following equation: h2 n = [1/4D / (1/4D + 1/4H1– 1/4F + Ê]. Expected genetic advance from selection (GA). The expected genetic advance (GA) from direct selection as a percentage of the mean (x) was calculated according to Singh (1990) based on 1% selection intensity as follows: GA = 100 [(k.h2 n δph)/x] Where: k = 2.64 (selection differential for 1% selection intensity), and δph= square root of the dominator of the narrow sense heritability.

Results and Discussion

Analysis of variance of F_1 generation for all studied characters is shown in Table 2. Genotypes, parents, crosses and parent *vs* crosses mean squares were significant for all traits in F_1 generation, indicating the presence of diversity in the material and sufficient amount of genetic variability adequate for further biometrical assessment. Significant differences among genotypes for grain yield and related traits in different sets of material of wheat were reported by Joshi *et al.* (2004), Seleem and Koumber (2011) and El-Saadoown (2018).

Mean performance values of the parents and F_1 generations for all traits are presented in Table 3. For days to heading the parent no 7 (Millan) and the crosses P1xP8 and P5xP8 gave the lowest mean value for heading.

The parent no 9 (IPA 99) and the cross P4xP7 had the highest number of spikes plant^{-1}. For No. of grains spike^{-1};

the P9 (IPA 99) and the three F_1 hybrid P1xP10, expressed the highest values for this trait. The parent no 4 (Site mall) and F_1 hybrids P2xP6, P3xP5 and P3xP10 was the highest hybrid for No of spikelets spike-1. For no of kernels spike^{-1}, the highest no of kernels were found by the parent no 2 (Kawz) and the cross P3xP4. As for 1000-grain weight, the parent no 4 (Site mall) and F_1 hybrids P2xP5, P2xP6, P3xP5 and P3xP10 exhibited the highest weight. Regarding, grain yield plant^{-1}, P5 (Florka) and the cross combination P6xP9 expressed the highest value for this trait. On the other hand, the high grain yield plant^{-1} were detected also, by the crosses P2xP9, P6xP9 and P3xP9 could be attributed to the high values of No. of spikes plant, No. of grains spike^{-1} and grain yield plant^{-1}. As for protein content six parents (P1, P3, P4, P5, P7 and P10) exhibited high protein content, however the crosses P4xP8, P4xP9, P5xP8 and P6xP8 give the highest values for this trait. For wet gluten content the highest values were detected by two parents P3 and P7 and the crosses P3xP10, P4xP8 P7xP8, P7xP10, and P9xP10. As for dry gluten content, P4 and the crosses P2xP5, P2xP6, P2xP8, P3xP5, P3xP10 and P4xP9 gave the highest value of this trait. Therefore, these crosses could be efficient for prospective wheat breeding programs aiming at improving wheat grain yield.

The half diallel analysis of Hayman method (Hayman 1954 a and b) provided six genetic statistical parameters. They are D, H1, H2, h^2, F and E (Table 4). Several ratios were derived as given by method of Hayman (1954b) and Jinks (1954) to provide further genetic information about each trait. The additive component (D) reached the significant level of probability for all studied traits except, days to heading and 1000-kernel weight and gluten content. These results indicate that the additive gene effects were involved in the inheritance of these traits. Significant values for the dominance component (H1) were obtained for all traits in both generations and large of magnitude than D one, indicating that the dominance type of gene action was the most prevalent genetic component in inheritance of these traits. These results are in agreement with those reported by Ashoush (2006), Seleem and Koumber (2011) and Farshadfar *et al.* (2012).

Highly significant values for dominance components associated with gene distribution (H2) were obtained for all traits. The H2 values were smaller than the H1 values for most traits indicating unequal allele frequency in the parents. These agree with findings obtained by Hayman (1954 b). The overall dominance effects of heterozygous loci (h^2) proved insignificant for all traits in both generations, indicating that the dominance was due to homozygosity indicating that the additive type of gene action was the most prevalent genetic component in inheritance of these traits. These results are in agreement with those reported by Arunachalam, (1976), Ashoush (2006), Seleem and Koumber (2011) and Farshadfar *et al.* (2012).

Highly significant values for dominance components associated with gene distribution (H2) were obtained for all traits. The H2 values were smaller than the H1 values for most traits indicating unequal allele frequency in the parents. These agree with findings obtained by Hayman (1954 b). The proportion of dominant to recessive gene in parents KD/KR were more than unity for all studied characters indicating that the dominant alleles govern these in both generations. The distributions of the relative frequencies of dominant versus recessive gene (F) were not significant for days to heading, no of spikes plant-1, no of grain spike-1 and dray gluten content. Thus, it could be concluded that an equality of the relative frequencies of dominant and recessive alleles were present in parents for studied traits. For other traits significant F values were obtained indicating a symmetry of gene frequency among the parental population were detected. The same conclusion was obtained for proportion of genes with positive and negative effects by H2/4H1. The weighted measure of average degree of dominance $(H1/D)^{0.5}$ exceeded unity for all studied traits, indicating that presence of over dominance for these traits. Consequently, selection for any of these traits in the early segregating generations will be of little use.

Heritability estimates in both broad and narrow sense for the studied attributes were computed according to Mather and Jinks (1971) In addition, the computed t^2 was not significant for all traits as shown in Table 4. High values for heritability in broad sense were obtained for all traits except protein content and dry gluten content, revealing that most phenotypic variability in each trait was due to genetic causes. High heritability values in broad sense along with medium or low ones in narrow sense were exhibited, indicating that most genetic variances were due to non- additive genetic effects. These finding support the aforementioned results on genetic components in which H1 estimates played a greater role in the inheritance of these characters. Therefore, the bulk method program for improving such traits might be promising Bakhsh *et al.* (2003); Allah *et al.* (2010); Kumber (2011).

Graphical (wr/vr) analysis

Graphical presentation (Vr, Wr) of different traits in both generations are given in Figures from 1 to 8. The regression coefficient significantly differed from zero but not from unity for F_1 diallel cross, indicating that the genetic system could be deduced to be additive without the complication of non-allelic interaction. Also, For all trait, regression slope differed from unity, indicating that a complementary type of epistasis was involved.

The regression line passed through the origin in no of spike plant^{-1}, revealed a presence of complete dominance. Meanwhile, it intersects the Wr axis above the origin in days to heading and no of grain spike^{-1} reflecting partial dominance. The presence of over dominance was found by other traits, however, was obtained from computing the ratio of H1 to D for these cases (Table 4). This contradiction between the two types of analysis might be an expected result of the presence of complementary type of non-allelic interaction which inflated the ratios of H1 to D and distorted the Vr,Wr (Hayman, 1954 b and Mather and Jinks, 1971). However, the regression line intersected the Wr below the point of origin in the remaining cases, indicating an over dominance in the inheritance of these cases. The array points scattered along the regression line for all traits in both generations indicating genetic diversity among the parents. The low magnitude of correlation coefficient between parental mean (Yr) and the (Wr+Vr) might be due to a presence of nonallelic interaction in some genotype. The parent 5 and 8 for days to heading; P4 for no of spike plant^{-1}, 1000-kernel weight and grain yield plant^{-1}; P3 and P8 for no of grain spike^{-1}; P10 for protein content; P7 and P8 for gluten content and P9 for dry gluten content included largest

number of recessive genes for these traits. On the other hand, P3 and P10 for heading date, P1, P2and P8 for no of spike plant^{-1}, P1 and P6 for no of grain spike^{-1}; P2 for 1000-kernel weight and grain yield plant^{-1} ; P5 and P7 for protein content; P4 for gluten content; and P1,P6 and P10 for dry gluten content, contained maximum number of dominant alleles for those traits.

Table 1 : The code number, name and pedigree of the studied parental bread wheat varieties and lines.

Code No.	Name	Pedigree
Pa1	Abu-Graib	Ajeeba* Lian 12 * Mexico 24
Pa2	Kawz	Kauz 2 \ yaco \\ Kauz \ 3 \ Ousis
Pa3	Osais	Ousis\ Kauz \\ 4 BUC
Pa4	Site mall	El-Solimania research center
Pa5	Florka	El-Solimania research center
Pa6	Kalak	El-Solimania research center
Pa7	Millan	El-Solimania research center
Pa8	Hithab	El-Solimania research center
Pa9	IPA 99	Ures \ Rows \ 3 \ Jup \ B \ S \ Ures
Pa10	Sham 6	Plo - Ruft GTOS - RHel (M12904) – IM – SM – 14 – OSK – GAP

Table 2 : Significance of mean squares from ordinary analysis for all characters studied in F_1 generation.

SOV	Df	Mean squares							
		days to heading	No. of spike plant^{-1}	No. of grains spike^{-1}	1000-grain weight	Grain yield plant^{-1}	Protein content	Wet Gluten content	dry Gluten content
		F_1 diallel cross							
Blocks	2	193.58**	21.69*	57.91**	329.82**	0.83	37.53**	689.47**	329.82**
Genotypes	54	37.29**	102.17**	56.60**	42.37**	75.28**	1.09**	30.87**	42.36**
Parent (P)	9	29.28**	94.58**	63.83**	25.65**	68.07**	2.67**	28.78**	25.66**
F_1 hybrid (h)	44	38.78**	101.58**	55.04**	46.56**	78.11**	0.73**	31.96**	46.56**
P *vs* h (heterosis)	1	43.88**	196.72**	60.28*	8.09	10.21*	2.54**	2.12**	8.09**
Error	108	4.85	4.71	4.48	3.14	2.21	0.08	4.89	3.143

* p< 0.05; ** p< 0.01

Table 3 : Mean performance of all studied genotypes (parents and F_1 generation) for all studied traits.

Genotype	days to heading day	No. of spikes plant-1	No of kernel spike-1	1000-grain weight (g)	Grain yield plant-1 (g)	Protein content	Wet Gluten content	dry Gluten content
Abu-Graib (P1)	99.67	19.77	43.21	37.03	45.59	14.44	13.20	37.03
Kawz(P2)	107.00	20.44	59.78	38.00	38.88	13.73	15.33	38.00
Osais (P3)	105.67	28.66	49.73	35.80	42.92	14.28	20.33	35.80
Site mall(P4)	101.33	24.55	47.00	44.50	41.06	14.50	18.00	44.50
Florka(P5)	106.67	23.44	51.69	36.70	48.41	14.62	15.67	36.70
Kalak (P6)	103.00	25.44	45.00	36.33	37.26	13.77	18.00	36.33
Millan(P7)	97.33	28.22	50.12	34.17	31.11	14.57	22.00	34.17
Hithab(P8)	101.33	31.55	51.67	39.73	37.82	13.49	17.00	39.73
Ibaa 99(P9)	102.00	37.77	47.02	37.17	41.53	14.68	11.67	37.17
Sham 6 (P10)	104.33	32.17	51.51	40.47	39.05	11.56	15.67	40.47
P1xP2	99.00	24.33	49.02	35.10	44.46	13.66	14.30	35.10
P1xP3	100.33	15.44	41.89	37.53	34.93	13.86	15.67	37.53
P1xP4	101.00	23.33	44.01	31.00	46.93	13.79	16.00	31.00
P1xP5	98.33	25.88	46.12	38.80	37.43	14.62	18.33	38.80
P1xP6	107.00	28.44	51.79	40.37	41.52	14.45	17.00	40.37
P1xP7	105.67	17.44	44.10	31.67	36.42	13.33	17.33	31.67
P1xP8	96.33	25.22	47.67	40.50	47.92	13.22	10.27	40.50
P1xP9	107.00	24.89	45.57	34.90	37.43	13.40	15.67	34.90
P1xP10	105.67	22.77	47.87	36.80	41.06	14.41	14.67	36.80
P2xP3	102.33	31.22	46.34	37.07	38.87	14.50	18.00	37.07
P2xP4	101.67	28.55	47.88	41.20	44.91	14.28	14.00	41.20
P2xP5	109.00	27.66	49.88	43.00	35.82	14.92	19.33	43.00
P2xP6	105.00	30.13	44.30	44.90	42.81	13.80	19.67	44.90
P2xP7	107.00	21.89	48.89	38.80	42.53	14.57	8.67	38.80
P2xP8	100.33	23.55	47.33	40.60	39.90	14.39	18.00	40.60
P2xP9	106.67	17.55	50.65	38.73	48.08	14.21	11.47	38.73

P2xP10	105.67	22.62	53.39	38.57	38.54	13.96	13.67	38.57
P3xP4	102.67	33.33	57.77	31.13	36.50	13.54	16.00	31.13
P3xP5	106.67	35.88	52.13	44.77	39.44	14.86	17.33	44.77
P3xP6	107.00	25.11	42.33	36.93	42.21	14.19	18.33	36.93
P3xP7	102.67	21.11	48.45	38.90	42.60	13.99	21.67	38.90
P3xP8	101.67	17.55	41.65	40.57	47.03	14.08	18.67	40.57
P3xP9	106.67	29.44	52.33	33.43	48.03	13.91	14.67	33.43
P3xP10	104.00	27.55	50.44	44.77	40.18	14.68	22.33	44.77
P4xP5	105.00	13.00	51.87	39.47	41.67	14.23	19.00	39.47
P4xP6	105.00	17.55	46.65	36.50	34.02	14.12	16.00	36.50
P4xP7	110.00	40.99	46.59	32.53	27.49	14.21	17.73	32.53
P4xP8	113.00	22.78	55.55	31.20	30.37	15.25	20.67	31.20
P4xP9	105.67	27.66	52.55	41.83	44.45	15.17	16.67	41.83
P4xP10	101.67	19.00	50.58	37.57	35.95	14.62	18.33	37.57
P5xP6	98.33	17.55	46.20	39.83	42.74	14.32	12.00	39.83
P5xP7	105.67	26.11	55.78	30.93	40.75	13.78	14.33	30.93
P5xP8	97.67	26.77	41.53	38.07	45.53	15.18	14.77	38.07
P5xP9	99.00	19.77	48.87	40.23	39.95	14.71	13.00	40.23
P5xP10	107.00	26.11	50.01	40.17	45.34	14.49	18.00	40.17
P6xP7	103.00	21.89	50.22	39.30	34.11	14.30	15.07	39.30
P6xP8	107.00	20.33	47.61	36.07	44.16	15.13	14.67	36.07
P6xP9	106.33	36.00	45.01	31.70	50.37	14.62	17.33	31.70
P6xP10	105.67	20.00	42.75	31.83	46.06	14.54	19.33	31.83
P7xP8	104.33	18.11	50.09	32.70	47.15	14.23	20.33	32.70
P7xP9	108.67	27.77	53.57	40.03	45.18	14.57	17.33	40.03
P7xP10	100.33	22.77	44.75	31.93	34.10	14.36	21.33	31.93
P8xP9	106.67	19.22	42.43	36.63	42.04	14.42	10.00	36.63
P8xP10	101.67	22.33	38.12	39.00	34.88	13.52	10.33	39.00
P9xP10	106.67	30.11	52.21	36.13	43.44	14.49	20.40	36.13
LSD 5%	1.06	1.03	0.22	0.68	0.48	0.45	3.54	2.84

Table 4 : Hayman's analysis for all studied traits in F_1 diallel cross.

Component	Days to heading	No of spikes plant $^{-1}$	No of gains spike^{-1}	1000-grain weight	Grain yield plant^{-1}	Protein content	Wet Gluten content	Dry Gluten content
D	6.99	29.85*	19.46**	5.52	22.17**	0.42**	3.81	5.52**
H1	75.25**	163.89**	106.92**	51.07**	119.61**	1.01**	28.13**	51.07**
H2	41.45**	129.84**	59.19**	44.37**	85.26**	0.13	22.49**	44.37**
h^2	4.79	25.37	7.3	-0.02	1.09	0.17	-1.8	-0.02
F	37.25	56.71	58.34	11.07	44.44*	1.25**	4.87**	5.92
E	2.76	1.67	1.82	3.03**	0.73	0.47	5.78**	3.03**
$(H1/D)^{0.5}$	3.28	2.34	2.34	3.04	2.32	1.55	2.71	3.04
H2/4H1	0.14	0.198	0.14	0.22	0.18	0.03	0.19	0.22
KD/KR	9.61	2.36	4.55	1.43	2.52	54.15	1.61	1.43
r	0.11	0.15	0.43	0.59	-0.39	-0.87	0.51	-0.37
r^2	0.01	0.02	0.18	0.35	0.15	0.76	0.26	0.14
h^2 (b.s)	81.14	95.57	91.37	82.47	97.41	10.3	57.79	0.48
h^2 (n.s)	11.92	9.54	21.04	18.26	22.5	0.04	0.17	18.26
t^2	23.14	9.24	30.47	0.63	4.42	12.56	0.67	0.63
b	0.59	0.05	0.59	0.05	0.90**	1.35	0.41	0.05

* $p< 0.05$; ** $p< 0.01$

Where: E= the expected environmental component of variation, D= Variation due to additive effect, F= Refers to relative frequencies of dominant *Vs* recessive genes in the parents, H1 = component of variation due to dominance effects, H2 = Component of variation due to non-additive effects, h^2= Overall dominance gene effects of the heterozygous loci in all crosses, $(H1/D)^{0.5}$ = mean degree of dominance at each locus over all loc, H2/4H1 = measures the average frequency of positive versus negative allels at loci exhibiting dominance, KD/KR = the ratio of total number of dominant to receive allels in the parents, h^2 (b.s) = broad sense heritability and h^2 (ns) = narrow sense heritability.

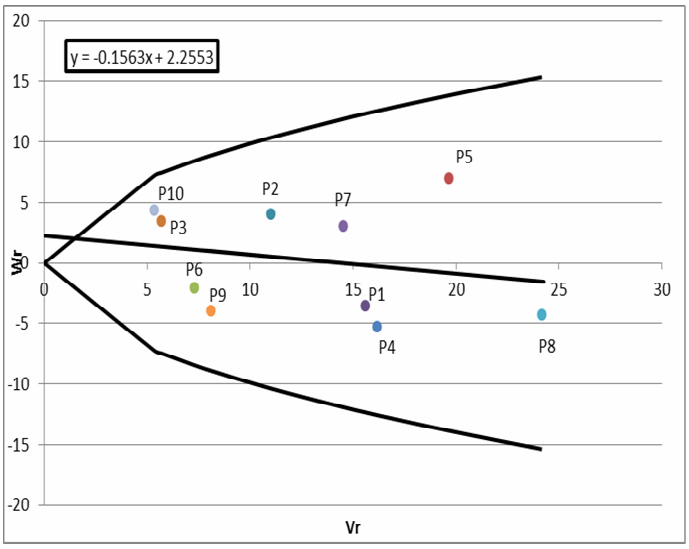

Fig. 1 : Wr/Vr graph for days to heading in F_1 diallel cross.

Where, Abu-Graib (P1), Kawz(P2), Osais (P3), Site mall(P4), Florka(P5), Kalak (P6), Millan(P7), Hithab(P8), Ibaa 99(P9) and Sham 6 (P10)

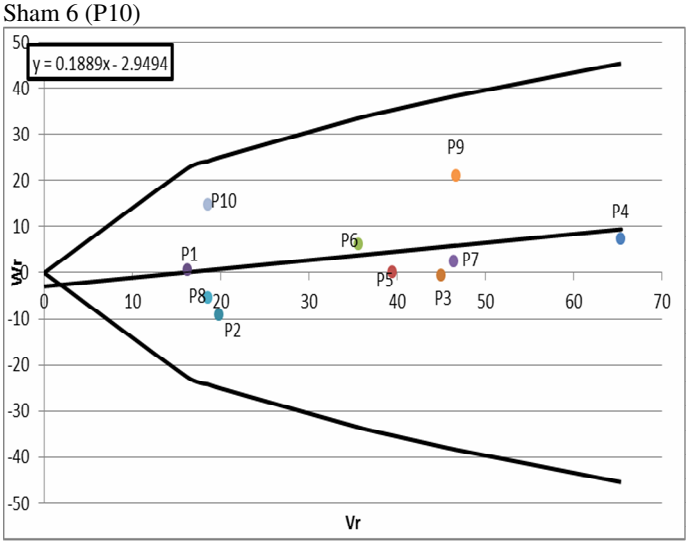

Fig. 2 : Wr/Vr graph for no of spike plant-1 in F_1 diallel cross.

Where, Abu-Graib (P1), Kawz(P2), Osais (P3), Site mall(P4), Florka(P5), Kalak (P6), Millan(P7), Hithab(P8), Ibaa 99(P9) and Sham 6 (P10)

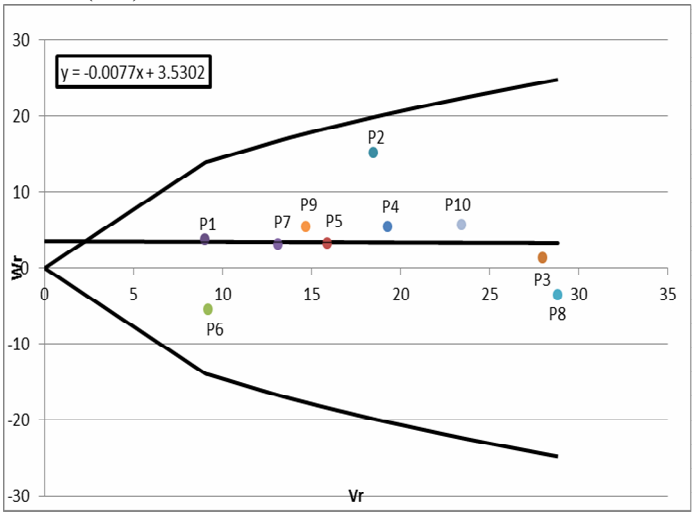

Fig. 3 : Wr/Vr graph for no of grain spike-1 in F_1 diallel cross.

Where, Abu-Graib (P1), Kawz(P2), Osais (P3), Site mall(P4), Florka(P5), Kalak (P6), Millan(P7), Hithab(P8), Ibaa 99(P9) and Sham 6 (P10)

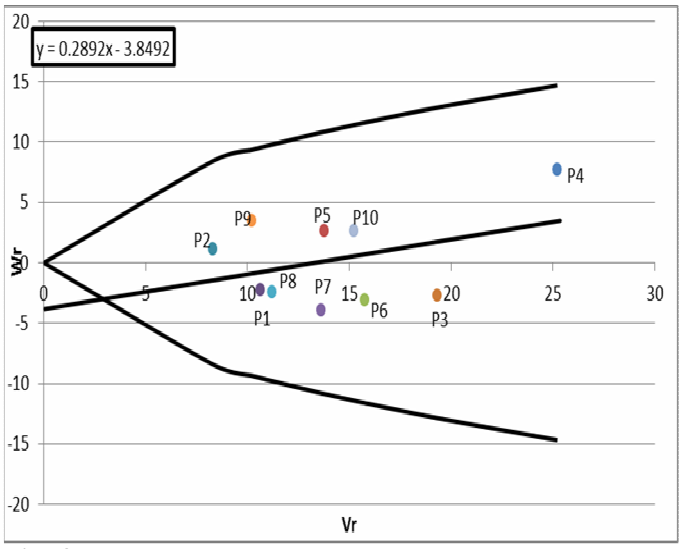

Fig. 4 : Wr/Vr graph for 1000 kernel weight in F_1 diallel cross.

Where, Abu-Graib (P1), Kawz(P2), Osais (P3), Site mall(P4), Florka(P5), Kalak (P6), Millan(P7), Hithab(P8), Ibaa 99(P9) and Sham 6 (P10)

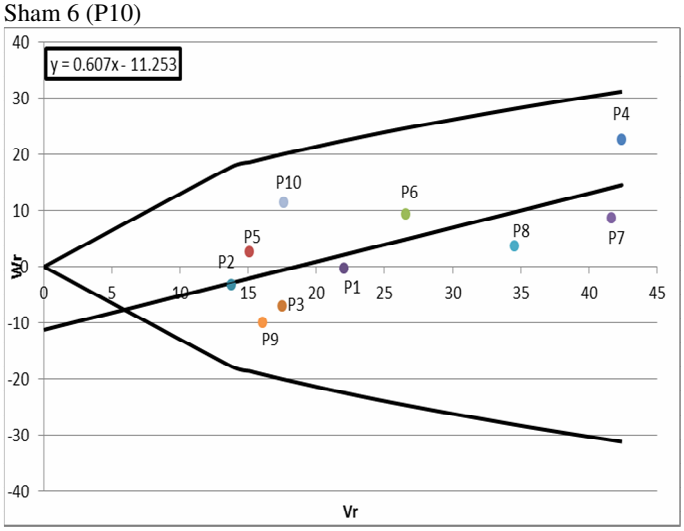

Fig. 5 : Wr/Vr graph for grain yield plant-1 in F_1 diallel cross.

Where, Abu-Graib (P1), Kawz(P2), Osais (P3), Site mall(P4), Florka(P5), Kalak (P6), Millan(P7), Hithab(P8), Ibaa 99(P9) and Sham 6 (P10)

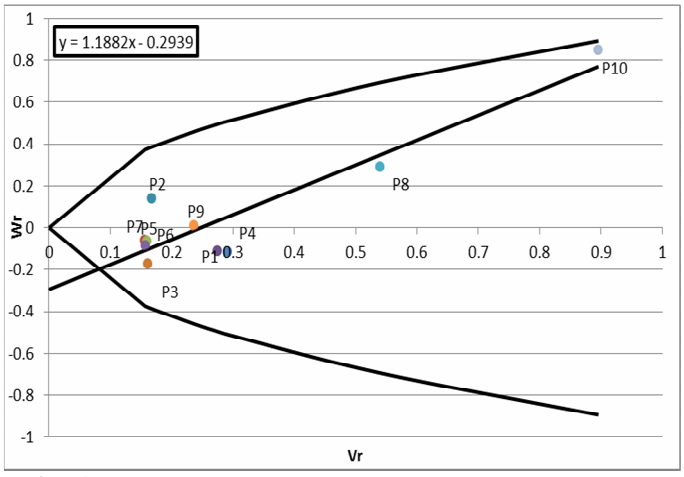

Fig. 6 : Wr/Vr graph for protein content in F_1 diallel cross.

Where, Abu-Graib (P1), Kawz(P2), Osais (P3), Site mall(P4), Florka(P5), Kalak (P6), Millan(P7), Hithab(P8), Ibaa 99(P9) and Sham 6 (P10)

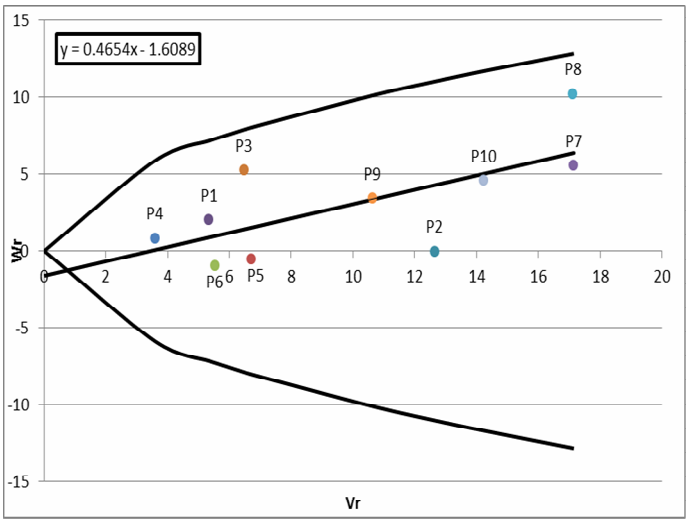

Fig. 7 : Wr/Vr graph for wet gluten content in F_1 diallel cross.

Where, Abu-Graib (P1), Kawz(P2), Osais (P3), Site mall(P4), Florka(P5), Kalak (P6), Millan(P7), Hithab(P8), Ibaa 99(P9) and Sham 6 (P10)

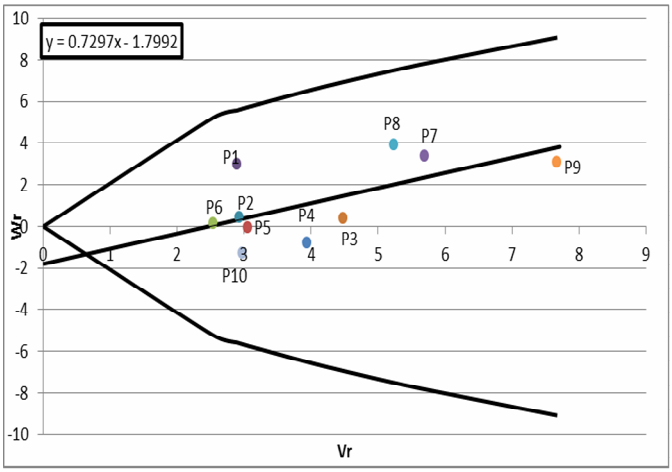

Fig. 8 : Wr/Vr graph for dry gluten content in F_1 diallel cross.

Where, Abu-Graib (P1), Kawz(P2), Osais (P3), Site mall(P4), Florka(P5), Kalak (P6), Millan(P7), Hithab(P8), Ibaa 99(P9) and Sham 6 (P10)

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