GENETIC ARCHITECTURE AND DETERMINATION THE NUMBER OF DOMINANT AND RECESSIVE GENES OF WHEAT GRAIN YIELD AND IT'S COMPONENTS (*Triticum aestivum* L.).

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ABSTRACT

Six bread wheat lines and their half diallel crosses were grown by using Randomized Complete Block Design with three replications for estimating genetic parameters and the nature of gene action according to Hayman approach (1954) through graphical analysis by dividing the distance between two points of intercepted regression line and parabola curve into four parts and then estimating the amount of dominant and recessive genes exactly for each parent.

The results showed that genotypes differed significantly among themselves, other than significant additive variance components were in flag leaf area,No.spikes.plant^{-1},spike length, and 1000grain weight, while dominance significant in flag leaf area and No.grains.spike^{-1},though dominance variance (H_1) more important than (H_2). Positive F values in No.spikes.plant^{-1},spike length and 1000grains weight indicated of dominant genes than recessive which that confirm by high ratio of average degree of dominance (a^-) (more than 1 in all studied traits that means existence of over dominance, also high ratio of KD/KR refers to abundance of dominant genes more than recessive one in parents of No.spikes. plant^{-1}, spike length, No.grains. spike^{-1} and 1000grain weight. Heritability in narrow sense were in flag leaf area (0.291), 1000grain weight (0.425) , 1000 grain weight(0.425) and low in no.grains.spike^{-1} and grain yield.plant^{-1}.Parent (6) exhibited best performance in plant hieght,flag leaf area, and no.spikes.plant^{-1}, also higher in no.grains.spike^{-1} and superior in grain yield.plant^{-1} and possessing large amount of dominant genes controlling these traits.

Key Words: Type of gene action, half diallel crossing , heritability and average degree of dominance .

INTRODUCTION

Wheat is the most important cereal crop in the world. Breeding programs including crossing followed by selection contributed of improving a good and high productive genotypes. Diallel mating design is the extensive important genetically useful tool for estimating actual gene action by using Hayman approach (1954)

that illustrate the presence or absence and magnitude of additive, dominant, non allelic, maternal and reciprocal gene effects, as well as significant deviation of regression coefficient(b)from unity which confirm the stability of additive – dominance gene action (Akram *et al.*, 2009).The consequences of parental genetic diversity are not excluded on significant hybrid vigor only but also on the other genetic parameters including important of additive gene action with partial dominance for plant height ,No .tillers .plant^{-1}, spike length , grains .plant^{-1} (Khan *et al*., 2009 ;khattab *et al*., 2010; and Ul-Allah,2010) and other grain yield components (, Anwar *et al*., 2011;Erkul *et al*., 2010 , and Saeed ,2010).

 Significant values for each additive and non additive (D,H$_1$and H$_2$)were recorded in most grain yield components although dominance variances (H $_1$and H$_2$) more important than additive one (D) and (H$_1$) higher than (H$_2$) (Saeed *et al.*, 2010 ;Ahmed *et al*.,2011;and   Ul-Allah *et al*.,2011). Agronomical and physiological wheat traits controlled by additive and non additive gene effects (Farshad,2011 and Khattab *et al*.,2010). Although the latter one more important in wheat grain yield components traits in the same meaning a$^-$=√H/D > 1 referring to over dominance in many loci of grain yield components (Akram *et al*.,2008;Rabbani ,2009;Subhi, 2009 and Hamdany, 2010).

        High values of h$^2_{n.s.}$ refer to the parents ability of transmittance their genes and great genetic advance can be performed through selection, but at the low values selection should be based on pedigree method and progeny test(Subhashchandra ,2009).when the bread wheat traits showed over dominance in many loci through a$^-$=√ H/D >1, and H2 /4H1 = pq ≠0.25 which mean un equal distributions of dominant and recessive alleles among parents also KD/KR>1 referring of containing parents on surplus of dominance alleles(Al-Taweel, 2009 and Salehi, 2011).

 Negative intercepts of regression line with wr(Wr/Vr graphs) and higher in magnitude of H1and H2 indicated of importance non additive gene action, over dominance and Symmetrical distribution therefore selection in early generations more important than traits posses additive gene action (Erkul *et al*. ,2010; Erkul *et al*.,2010 and Ahmad *et al*., 2011).Many parents possesed recessive genes for grain yield.plant^{-1} and dominant in other traits suggest the use of integrated breeding strategies which can efficiently utilize the additive and non additive genetic variability.Thus use of diallel mating with recurrent selection could provide better conditions for recombination and accumulation of desirable genes and its recommended for such type of study(Nazeer *et al*. ,2011).

    The study aims to determinate the nature of inheritance and performance in genes action of grain yield and it's components by using Hayman approach and estimating the amount of dominant and recessive genes controlling parents traits by

calculating out border of parabola $(w^* = (V0l0*Vr)^{0.5}$ and the line $\bar{W} = \bar{a} + Vr$ and partition of dominant and recessive genes for each parent.

MATERIALS AND METHODS

Field trail was carried out at the research station of the Field Crops College of Agriculture / Tikrit University by using 6×6 Half . Diallel mating design of bread wheat lines for estimating genetic parameters and percent of dominance and recessive genes according to Hayman's approach(1954).After crossing in winter season,2011.F1's and their parents were grown in 2012 season by using Randomized Completely Block Design with three replications.Agricultural practices applied as recommended and the area of experimental unit were two rows(5m long)with 30cm and 20cm intra and inter plants spacing respectively.Fertilization with each 200kg N/ha and 100 kg/ha as P_2O_5.Random sample collected for recorded individual plants data of the following traits:plant height(cm),flag leaf area(cm2),No.spikes. plant^{-1}, no.grains.spike^{-1},1000 grains weight(g).and grain yield.plant^{-1}.The pedigree of genotypes is in table(1)
Data Analysis performed according to design used (Dawood and abdulyas,1990). Genetical scales and the nature performance of genes estimated by using formulas proposed by Hayman(1954)assumption of B=1 hypothesis(no epistasis)against B≠1 and the significance tested by using t-test=b-1/S_b(Chaudhry,2007 and Al-Naimy, 2006).Genetic parameters were:variance of additive gene action(D), variance of dominant effect(H_1H_2),relative gene frequency(F),whole dominant

Table1: Names and origin of studied genotypes .

No	Parents	Pedigree
1	Line A-60	ACSAD875/3/TJB368.231/Buc//CUPE
2	Line 3-7	ACSAD875/TIA3
3	IPA99	Ures/Bows/3/Jup/Bl's//Ures
4	Abu-Ghraib3	Ageeba×Inia66× Maxico 24
5	Bancal	Espanish
6	Sham 6	ICARDA

effects of heterozygous loci(h2) and expected environmental variance(E) which estimated from mean parents (MP)=M0L0, parents variances(Vp)=V0I0, mean variances of arrays($\bar{v}r$)=v1L1, variance of the mean of arrays (v$\bar{r}$)=V0L1 and mean covariance between parents and their off-spring($\bar{Wr}$),and used for calculating average degree of dominance ($\bar{a} = \sqrt{H_1/D}$), percent dominant to recessive genes (KD/KR), No.of dominant genes group differ among parents controlling trait (K),

gene frequency for dominant to recessive genes ($pq^- = H_2/4H_1$) and heritability in narrow sense(h^2).Parapola drawn after calculated Wr^*values=$(V0I0 \times Vr)^{\wedge 0.5}$.Vr distances increasing gradually for adequate values of (Vr).Line regression (Wr=a+b Vr) estimated on superior(Vr) independent variable and(Wr) dependent values.The sum of squares and multiplication between them calculating according the following formulas:$Sv0 = \sum Vr^2 - (\sum Vr)^2/n$;$SWW = \sum Wr^2 - (Wr)^2/n$;$SVW = \sum VrWr - (\sum Vr)(\sum Wr)/n$. Coefficient of regression(b)=Svww/Svv;$a = \overline{W} - b\overline{V}$;predicted (Wr)= a+bVr,when Vr=0 and another big random value choosen from Vr limits for drawing regression line according to these points.$\overline{Wr} = \overline{a} + Vr$, $\overline{a} = \overline{Wr} - \overline{Vr}$.Two points($Vx_0$ and Vx_s)specify for determination the intercepted of regression line with with parabola curve(Efe,1995),where$Vx_0 = 0.5\{V_0l_0 - [V_0l_0 (V_0l_0 4a^-)]^{\wedge 0.5}\} - \overline{a}$;$Vx_s = 0.5\{V_0l_0 + [V_0l_0 (V_0l_0 4a^-)]^{\wedge 0.5}\} - \overline{a}$;Wr* should be equal to $\overline{Wr} = \overline{a} + Vr = (V_0l_0 \times Vr)^{\wedge 0.5}$. The distance between these two points divided into four equal parts for estimating the percentage of dominance and recessive genes for each parents (the first part

nearer of the origin point referring of involving parent 75-100% of dominant genes

,second part: 50-75% , third:25-50% and fourth: 0-25% of dominant genes each part and vise versa of dominant and recessive genes). Distance between intercepted points of linear regression with parabola curve calculated from the following formulas: $m = Vx_s - Vx_0$ and the later distance divided in to equal four parts by using formulas: $Vx_1 = Vx_0 + 1m/4$; $Vx_2 = Vx_0 + 2m/4$; $Vx_3 = Vx_0 + 3m/4$.where $\overline{Wx_1}$,$\overline{Wx_2}$ and $\overline{Wx_3}$ calculating depends on $\overline{W} = \overline{a} + Vr$ which used for dividing ∆s in to four equal parts through drawing line passing along till intercepted with Wr exis, where: $\overline{Wr} = \overline{a} + Vr$; $er^1 = Wr - \overline{Wr}$;$Vrr = Vr + er^1/2$; $\overline{mr} = Vii - Vx_0$;$m = Vx_s - V_0$ .The percentage of total recessive genes (Rr%)=(mr/m)×100 and the percentage of dominant genes (Dr%) will be 100-Rr%.

RESULTS AND DISCUSSIONS

Analysis of variance which revealed high significant differences among genotypes for all traits (Table2), refers to existence genetic variability that needs to further more genetic analysis for understanding type of gene action and the nature of inheritance such in traits. Similar results were recorded by Khattab *et al.*, (2010). Non significant linear regression by using t-test for all traits therefore B=(1) hypothesis excepted and genetic and statistical parameters estimated by using means, variances and covariances among parents and off-spring in Table(3).

Table 2: Analysis of variance of traits studied .

S.O.V	Replicate	Genotypes	Experimental error
d.f. Characters	2	20	40
plant hight	3.278	62.283**	10.761
flag leaf area	20.997	69.329**	6.145
no.spikes . plant^{-1}	8.829	2.824**	0.313
spike lengh (cm)	2.321	3.071**	0.392
No. graians. Spike^{-1}	165.682	157.037**	13.619
1000 grains weight	11.556	33.314**	2.217
grain yield plant^{-1}	32.088	18.622**	2.676

Table 3: Statistical parameters for the traits studied .

Characters Statistical parameters	plant height	flag leaf area	No.spikes . plant^{-1}	spike length (cm)	No. Spike^{-1}	1000 grains weight	grain yield plant^{-1}
Vp	5.266	17.045	1.574	1.218	43.504	22.133	2.595
V̄r	20.538	18.731	0.788	0.823	50.683	9.024	5.904
V r̄	4.259	3.488	0.062	0.165	2.001	2.036	0.062
W̄ r	3.043	6.650	0.137	0.333	2.794	5.505	0.265
B	0.137 0.116±	0.252 0.406±	0.690 0.531±	0.859 0.347±	0.153- 0.231±	0.145 0.590±	0.376 0.196±

(Vp):parents variances , (v̄r):mean variances of arrays, (vr̄):variance of the mean of arrays, (Wr⁻):mean covariance between parents and their off-spring, and (B):linear regression coefficient.

Additive type of gene action was significant in flag leaf area(17.04),no.spikes .plant^{-1}(1.57),spike length(1.21) and 1000 grain weight(22.13)(table 4).While significant dominance variances (H_1) in flag leaf area(47.09),No.grains.spikes^{-1},(179.45) and 1000grains weight(29.10) that refer to important additive and non additive type of gene action in inheritance flag leaf area and 1000grains weight, these results are adequate with Saeed(2010).Also flag leaf area exhibited significant (H_2)(47.27) and 1000 grains weight(22.62) that means allo distribution of gene frequency in these traits, which need for concentrate favourable genes by using recurrent selection and pedigree selection(Salehi ,2011 and Nazeer *et al.*,2011). Although the no. of dominant genes higher than recessive in No.spikes.plant^{-1},spike length, and 1000grains weight, but were not significant as a result of positive F values, while negative non significant F in plant height, leaf area and grain yield indicating of surplus negative genes for these traits(Al-Taweel ,2009).All traits showed significant positive h^2N.S. except 1000 grains weight was negative non significant which indicate of negligible effects of dominant

heterozygous loci(Anwar *et al.*,2011).Data in Table (4) showed genetic parameters estimates including average degree of dominance (H_1/D) which were more than one in that confirm that over dominance type of gene action is effect amajor role of inheritance of such traits(Rabbani, 2009 ;Al-Hamdany ,2010; and Ul-Allah ,2010).The portion of positive effect genes (increasing trait) and negative effect (decreasing trait) ($\bar{p}\bar{q}$ =H_2/$4H_1$) less than 0.25 of dominant loci appeared which means irregular distribution of alleles (Salehi , 2011).One group of dominant genes(H_2/h^2) appeared controlling plant height(0.92) and No.grains.spike^{-1}(1.42) two groups in flag leaf area(2.72), No.spikes.plant^{-1} (2)and spike length(2.28), three groups in grain yield.plant^{-1}(2.73). Many traits (plant height, flag leaf area and grain yield.plant^{-1})exhibited KD/KR less than(1)which perhaps reflected from high ratio of recessive

Table 4: Genetic parameters for the traits studied .

Genetic parameters	plant height	flag leaf area	No.spikes . plant^{-1}	spike lengh (cm)	No. spike	1000 grains weight	grain yield plant^{-1}
E	10.40 ±8.70	6.85 ±6.36	0.71 ±0.37	0.48 ±0.28	20.86 ±26.41	2.66 ±3.42	4.07 ±2.71
D	5.26 ±23.03	17.04 ±16.83	1.57 ±0.98	1.21 ±0.76	43.50 ±69.88	22.13 ±9.06	2.59 ±7.18
F	-15.51 ±56.27	-1.64 ±41.13	1.64 ±2.14	0.45 ±1.86	48.02 ±170.71	18.69 ±22.13	-1.30 ±17.55
H1	47.50 ±58.47	47.09 ±42.74	2.26 ±2.50	1.88 ±1.93	179.43 ±177.39	29.10 ±22.99	14.27 ±18.23
H2	44.30 ±52.33	47.27 ±38.18	1.46 ±2.24	1.66 ±1.72	153.00 ±158.47	22.62 ±20.54	15.21 ±16.29
h^2	41.04 ±35.15	130.41 ±25.69	2.94 ±1.50	3.80 ±1.16	218.47 ±106.66	-0.12 ±13.82	41.56 ±10.96
$\bar{a}$	3.00	1.66	1.19	1.24	2.03	1.14	2.34
$\bar{p}\,\bar{q}$	0.23	0.25	0.16	0.22	0.21	0.19	0.26
H2 / 4H	0.92	2.75	2.00	2.28	1.42	-0.01	2.73
KD / KR	0.34	56.66	3.77	3.03	176.70	50.76	12.17
h^2 N. S	0.36	0.33	0.29	0.36	0.17	0.42	0.15

(E):environmental variance , (D)variance of additive gene action , (F):relative gene frequency ,(H_1):variation due to dominant effect of genes ,(H_2):variation due dominant effect of genes correlated for gene distribution , (h^2):overall dominant effects of heterozygous loci , ($\bar{a}$):average degree of dominance , ($\bar{p}\,\bar{q}$):gene frequency for dominant to recessive genes, (H2 / 4H):proportion of genes with positive and negative effects in the parents ,(KD/KR):percent dominant to recessive genes, (K):No.of dominant genes groups differ among parents controlling trait, and ($h^2_{N.S.}$):heritability in narrow sense.

genes in their parents(Al-Taweel ,2009 ; Salehi , 2011).While other traits (no.spikes.plant^{-1},spike length, no.grains.spike and 1000grains weight possessing dominant genes higher than recessive one of the parent under investigation. High heritability in narrow sense (0.425) for 1000grains weight represents 42.5% of variances belong to additive type of gene action, also moderate values(0.367,0.331 and0.291) in plant height, flag leaf area, No.spikes.plant^{-1} and spike length respectivilly.Other traits were low in the heritability estimates, because of increasing dominance variance (Al-Naiymi ,2006 ;Salehi , 2011) as a result of that, selection will be efficient in 1000 grain weight, No.spikes.plant^{-1} , and spike length in early segregating generations.

Graphical figures(1,2,3,4,5,6 and 7)explain the relationship between Wr* and Vr which refer to the type of gene action according to the intercepted points of line regression with Wr axis..The distribution of parents along regression line in Figure1 for plant height trait state parent 6 was the nearest to the origin point and located at the first part of regression line which contains 75-100% of dominant genes and exactly 97.8%, while 3 , 4 and 5 parents located at the third part which contains 25-50% of dominant genes and exactly 42.59,52.28 and 52.96% for the last parents respectively(table 5). Parents 1 and 2 possessing 75-100% of recessive genes for being located at fourth part and contained exactly 84.29 and 74.4% of recessive genes respectively and possessing the lesser percentage of recessive genes but didn't decrease mean performance this trait.Parents differed genetically among others in flag leaf area according to Fig.2, parents 3 and 6 were the nearest to the origin point through being located at the first part and have 75-100% of dominant genes which are complement with the results of Table 5 for the percentage of dominant genes (81.52 and 80.79% respectivilly).Estimated percentage of dominant genes for flag leaf was 45.46% for the parent 2 for being located at the second part of regression line.The third part regression line involved parents 4 and 5 which have possessed 57.8 and 62.16% of dominant genes respectively, besides the last parent 1 which possessed lowest percentage of dominant genes (24.67%) and the highest recessive genes.The No.of spikes.plant^{-1} controlled by dominant genes larger than recessive in parents 1, 3, 4 and 6 and ranged from 73.25% in parent 6 to 88.88% in parent 1 concentrated in the first part of regression line, on the other hand the parents 2 and 5 possessed dominant genes 61.13 and 53.12% respectively as a result of their location at the second part of line regression.These results were adequate between table (5) data and the outputs of Figure 3.Parents differ in spike length through distribution along regression line parts(Fig.4), parent 5 located at the first part of regression line and possess high amount of dominant genes (80.97%) (Fig.4), while the ratio of dominance to recessive genes of spike length were moderate(50-70%) in 1,2,3 and 6 parents and

low in parent 4 which possessed 38.32% and was the lesser parent in spike length mean (8.94cm) that confirm the important dominance of genes controlling this trait.Drawing Vr against Wr* line regression of no.grains.spike^{-1} in Figure 5 refers to the possessing of most parents (1,3 and 5) 75-100% of dominant genes affecting inheritance such trait and estimating the exact percentage of dominant genes were 73.38,79.53 and 81.58% for the last parents respectively (table 5). Comparing the output of Figure 5 with the means of these trait exhibited the superiority of parent 5 followed by parent 3 as a reflectance of dominant genes effects of increasing No.grains.spike^{-1} Other than 2 and 6 parents have 61.55 and 73.6% of dominant genes respectively, while parent 4 has the lesser amount of dominant genes (37.83%) which is located at the third part of regression line, is parallel with the lowest mean of No.grains.spike^{-1} referring to importance dominant genes in selection for improving No.grains.spike^{-1} of wheat lines. Graphical analysis of 1000grains weight (fig.6) revealed possessing parents (2 and 4) dominant genes larger than recessive (95.22 and 80.4%respectivilly) ,though non significant differences their means of 1000grains weight traits.Second part of regression line contain 1,3 and 5 parents that possessed 71.88,74.47 and 63.86% of dominant genes respectively. On the opposite direction parent 6 has a large amount of recessive genes (46.48) than others and located at the third part of regression line and gave the lower mean of No.grains.spike^{-1} which clarifying the vital role of dominant genes in increasing No.grains.spike^{-1}.Graphical analysis of grain yield.plant^{-1}showed that the parent 6 has a large percentage of dominant genes (99.82) (table 5) and located at the first part of regression line(Fig.7), while other parents 3 and 5 located on the second part of regression line and possessed 72.8 and 82.52% of dominant genes respectively. Moderate percentage of dominant genes controlling inheritance grain yield were in parent 1 (49.61%) and parent 4 48.26% at the third part of regression line. The last part of regression line contain parent 2 which indicated of possess low amount of dominant genes and the high amount of recessive genes (67.21%). Regression line were under origin point for all traits which indicated of existence over dominance type of gene action (Singh and Chaudhary, 2007) and these results are complement with the findings of table (4) about over dominance more than (1) for all studied traits.The output of graphical analysis of grain yield indicates the importance of dominant genes in increasing grain yield mean and selection would be effective of improving such traits. The importance of dominant genes and sloping upper to down or ascending arrangement of recessive genes will give accurate evaluation of parents that should be selected in breeding through crossing program depending on possessing high percentage of dominant genes controlling such traits(Efe,1996).

Table 5: Means of traits studied and the percentage of recessive (R%) and dominant (D%)genes .

Traits		Parents					
		1	2	3	4	5	6
plant height(Cm)	Mean	70.23	70.33	74.1	67.57	72.16	72.66
	Ri(%)	84.29	71.44	57.41	47.72	52.96	-2.86
	Di %	15.70	28.55	42.59	52.28	47.03	102.86
flag leaf area	Mean	24.82	19.65	25.36	19.04	30.25	24.43
	Ri %	75.32	53.54	18.47	42.19	37.83	19.20
	Di %	24.67	46.45	81.52	57.80	62.16	80.79
No.spikes. plant-1	Mean	5.96	5.43	6.56	6.33	4.56	8.30
	Ri %	11.11	38.86	16.78	24.01	46.87	26.74
	Di %	88.88	61.13	83.22	75.99	53.12	73.25
spike length (cm)	Mean	10.07	10.21	10.08	8.94	12.22	9.57
	Ri %	30.96	26.39	20.3	61.67	19.03	36.54
	Di %	69.03	73.60	79.7	38.32	80.97	63.45
No. grains.Spike	Mean	41.67	41.81	48.44	37.83	55.64	40.20
	Ri%	26.61	38.45	20.46	50.38	18.41	26.40
	Di%	73.38	61.55	79.53	49.61	81.58	73.60
1000 grains weight(g)	Mean	43.2	37.32	34.74	35.57	44.82	33.49
	Ri %	28.11	4.77	25.52	19.59	36.13	46.48
	Di %	71.885	95.228	74.477	80.40	63.86	53.51
grain yield. plant^{-1}(g)	Mean	10.83	8.5	11	8.333	11.3	12.33
	Ri %	50.38	67.21	27.11	51.74	17.47	0.71
	Di %	49.61	32.78	72.88	48.26	82.52	99.28

Conclussion:Parent 6 which regarded the best parents exceeded all the others and realable depend directly and using directly in wheat breeding programs for possessing large amount of dominant genes controlling grain yield and some of it's components that is parallel with a good performance in most traits studied (plant height,flag leaf area and No.spike.plant^{-1}.Also parent 6 give a good results at No.grains.spike^{-1} and grain yield.plant^{-1}).
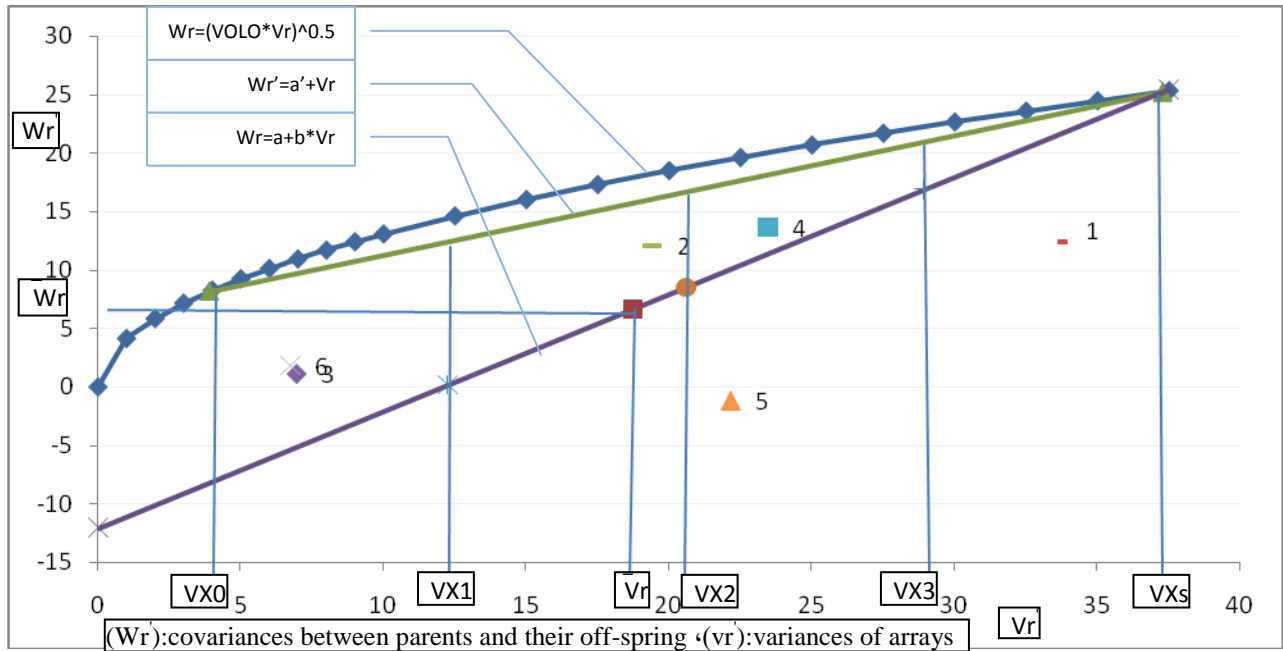
Fig.1:Wr-Vr Graph of plant height.

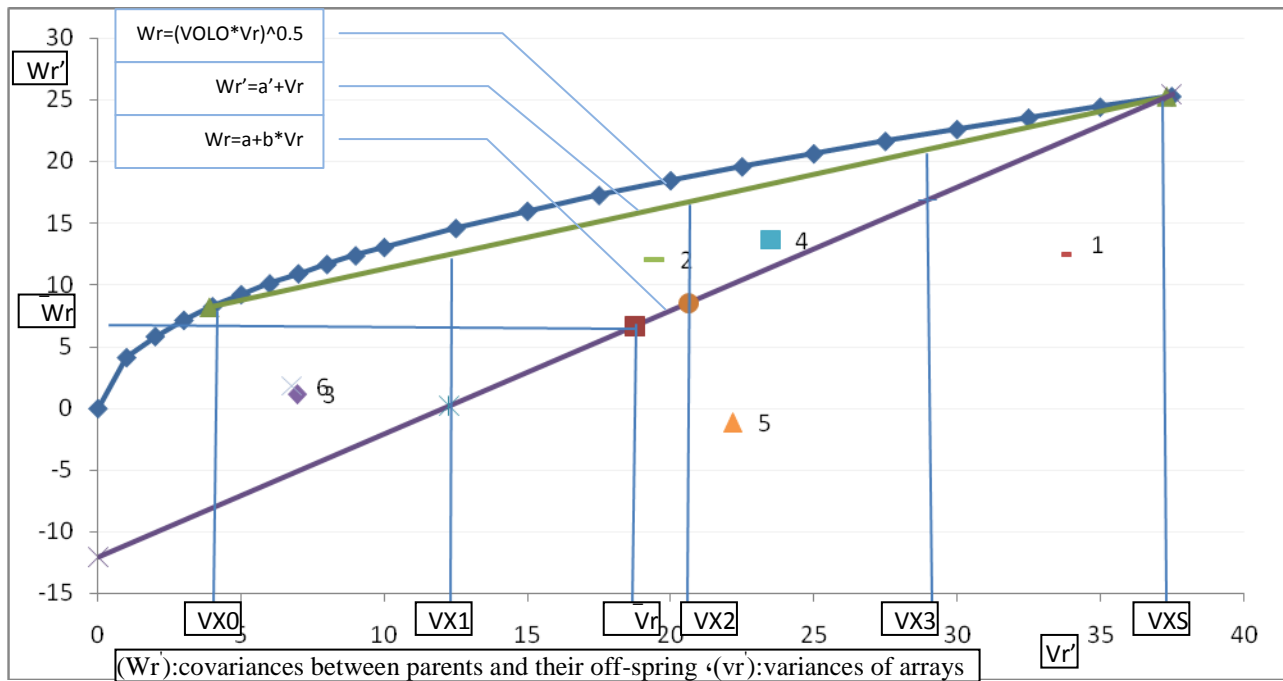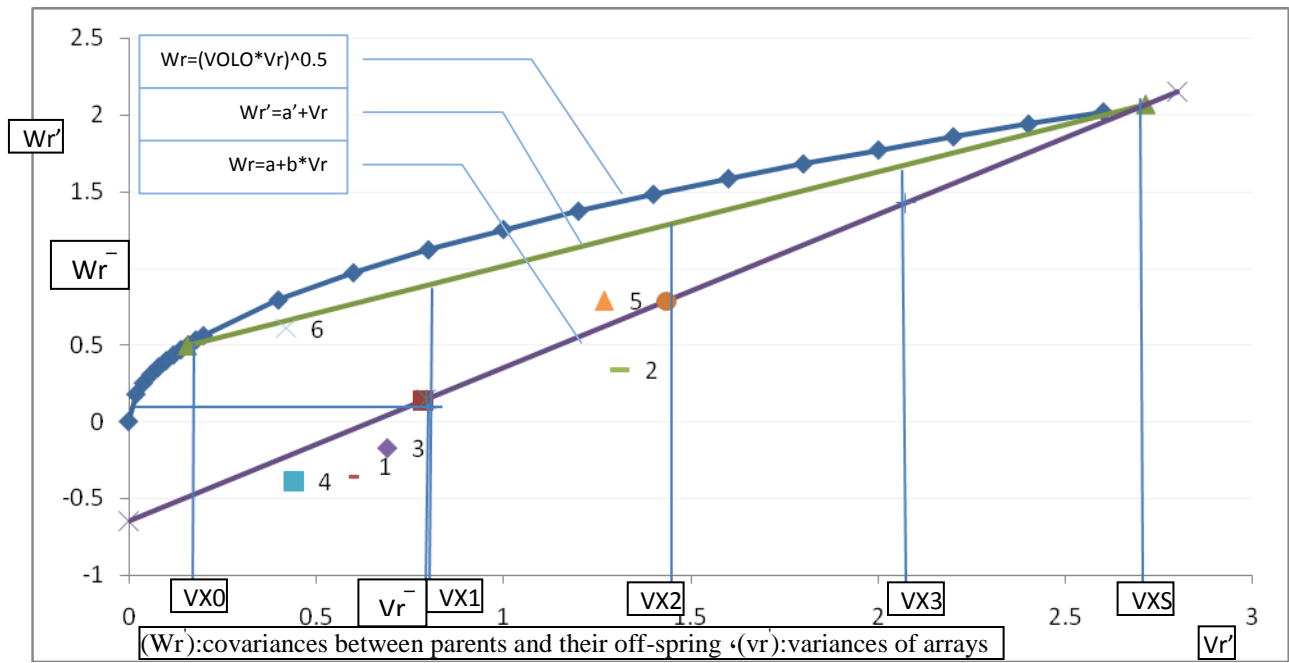Fig. 2: W r- V $_r$ Graph of flag leaf area
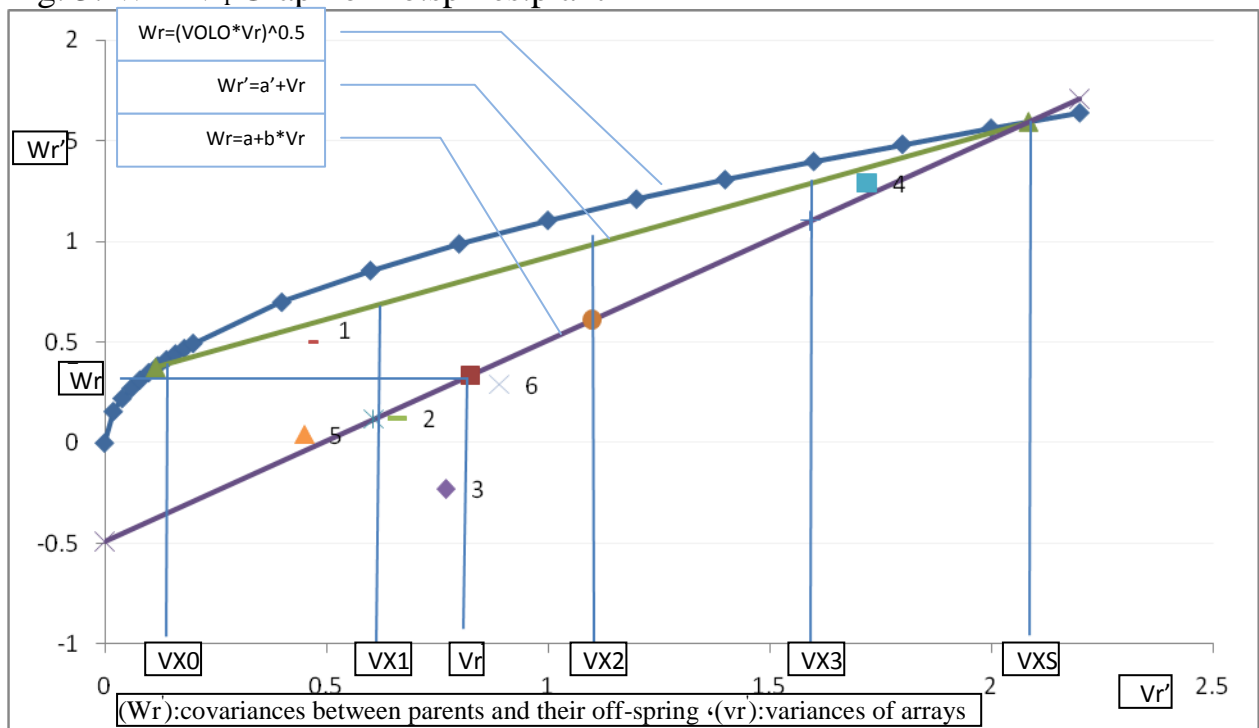
Fig. 3: W r- V $_r$ Graph of no.spikes.plant $^{-1}$

Fig.4:Wr-Vr Graph of No.grains.spike^{-1}.
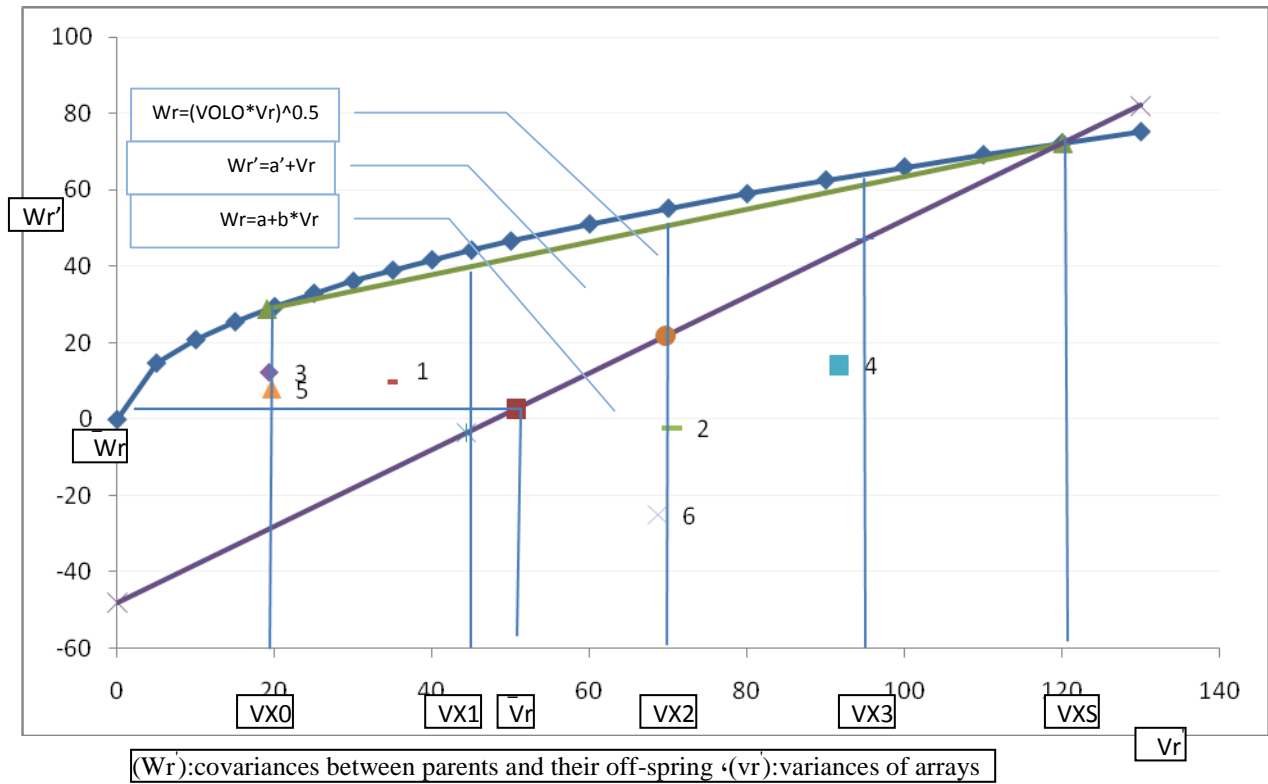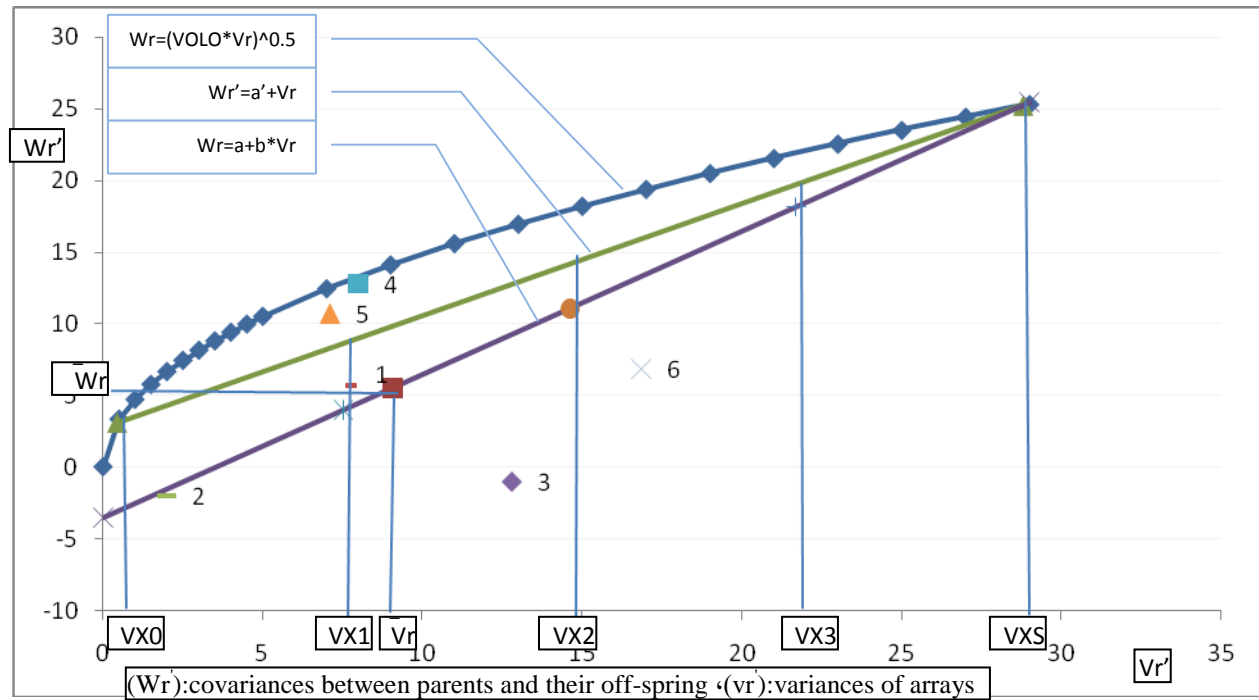
Fig.5:Wr-Vr graph of no.grains.spike^{-1}.
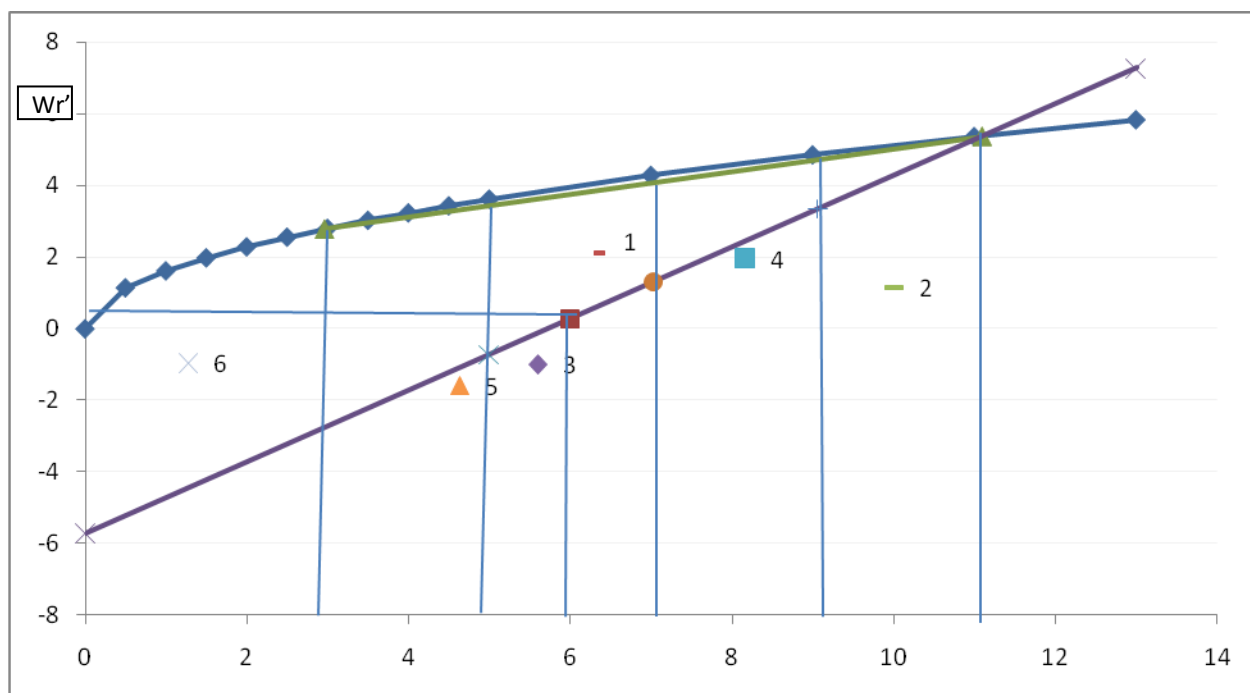

Fig. 6: W r- V $_r$ of 1000 grains weight.

Fig. 7: W r- V $_r$ Graph of grain yield. Plant $^{-1}$.

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البنية الوراثية وتحديد ازواج الجينات السائدة والمتنحية في حاصل حبوب الحنطة مكوناته (*Triticum aestivum* **L.**).

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المستخلص

زرعت ستة تراكيب من الحنطة وهجنها دون العكسية باستخدام تصميم القطاعات العشوائية الكاملة وبثلاث مكررات لتقدير بعض المعالم الوراثية والتعرف على طبيعة عمل الجينات وفقا لطريقة Hayman عام 1954 وايجاد الجزء المحصور من خط الانحدار الواقع بين نقطتي تقاطعه مع منحني القطع المكافئ وتقسيمه الى أربعة أقسام متساوية وتقدير نسب الجينات السائدة والمتنحية في كل أب. أوضح تحليل التباين للتراكيب الوراثية أن هناك اختلافات معنوية بينهما،وأن الفعل الجيني الإضافي معنوي في صفات مساحة ورقة العلم وعدد السنابل.نبات[-1] وطول السنبلة ووزن 1000حبة بالغم ، كما كانت التباينات السيادية معنوية للصفات السابقة عدا صفة عدد السنابل.نبات[-1]، وان التباين السيادي(H_1) أكثر أهمية من(H_2) وان قيم (F) موجبة في عدد السنابل وطول السنبلة ووزن 1000حبة، فضلا على ذلك فان معدل درجة السيادة$(\bar{a})$ اكثر من واحد صحيح في جميع الصفات المدروسة دليلاً على وجود السيادة الفائقة، كما أن متجهة (KD/KR) تشير الى زيادة الجينات السائدة في الاباء في صفات عدد السنابل.نبات[-1]وطول السنبلة وعدد حبوب السنبلة ووزن 1000حبة، وكانت درجة التوريث بالمعنى الضيق متوسطة(0.291) في مساحة العلم ووزن 1000حبة بينما كانت منخفضة في الصفات الاخرى. أظهر الاب (6) اداءا متميزا في ارتفاع النبات ومساحة ورقة العلم وعدد سنابل النبات وكان جيدا في عدد حبوب السنبلة ومتفوقا في حاصل النبات وكانت تحت تأثير اعداد كبيرة من ازواج الجينات السائدة التي تحكم هذه الصفات.

الكلمات المفتاحية: طبيعة عمل الفعل الجيني ، التهجين التبادلي النصفي ، نسبة التوريث ، معدل درجة السيادة .