



Genetic Analysis in The F₁ And F₂ Cotton Generations of Diallel Crosses

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Abstract

Six divergent cotton genotypes were crossed in un-constructed to be 15 F₁ crosses then, F₂ were obtained. All genotypes were evaluated in Randomized Complete Block Design with three replicates. Genetic parameters of natural performance of genes were estimated by Hayman method (1954) for characters of Boll weight (B.W.), Seed cotton yield (S.C.Y.), Lint yield (L.Y.), Seed index (S.I.), Lint percentage (L. %), Lint index (L.I.) and oil%. The result showed that additive and dominance variance H₁ and H₂ values were significant for all traits, and the additive values were less from dominant values, that refers to the importance of dominance variance in its inheritance. Also, the H₂ values were less than H₁ which recorded that the allelic frequencies were not equal. The overall dominance effects of heterozygous loci (h²) were significant for all traits in both generations, indicating that the dominance was due to heterozygosity and was unidirectional with appreciable heterotic effect. The proportion of dominant to recessive gene in parents KD/KR were more than unity for most studied traits. The average degree of dominance (H₁/D)^{0.5} exceeded unity for all studied traits in both generations, indicating that presence of over dominance for these traits. High values for heritability in broad sense were obtained for all traits, 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 in both generations, indicating that most genetic variances were due to non-additive genetic effects. The regression line passed through the origin in boll weight in generations, seed index, lint percentage and oil% in F₁, revealed a presence of complete dominance. Meanwhile, it intersects the W_r axis above the origin in lint yield and oil% in F₂, reflecting partial dominance. The P₄, p₂, P₂, P₅, P₅, P₂ and P₅ in F₁, P₄, P₂, P₁, P₅, P₆, P₃ and P₆ in F₂ for B.W., S.C.Y., L.Y., S.I., L. %, L.I and oil%, respectively seemed to have the highest number of dominant genes.

Key words: Cotton, Diallel analysis, Gene action, Combining ability.

Introduction

Diallel crosses hybridization analysis proposed by Hayman 1954 is one of the ways to identify and test superior genotypes. As the identification of genetic structures that are characterized by suitable components of variation is one of the priorities through which it is expected to produce genetic structures within the plant breeding program for a specific crop (El Hosary 2020 and Sedhom *et al.*, 2021). The purpose of detect genetic superiority and physiological efficiency that suit the available environmental patterns in a way that can reach an increase in production per unit area. Which is among the most important objectives of the breeders of this crop. It requires identifying information related to the nature of the action of genes and the relative importance of genetic variation as it is important for

the formation of the genetic structure of the cotton crop (Abd El Samad *et al.* 2017 and Subhan *et al.*, 2002) as it helps in developing strategies which relates to sifting parents and their unions and identifying the nature of tracking isolationist generations in subsequent education programs.

To reach the goals of quantitative genetics, there are many researchers whose studies included the nature of the work of genes and the identification of the genetic mechanism for them and the components of genetic variation under different environmental conditions, including Murtaza *et al.*, (2002), Ahmed *et al.*, (2003), Murtaza (2005) and Khan *et al.*, (2007) in the cotton crop, which showed that the additional and sovereign model can suggest to cotton breeders about verifying the validity of the data and design. The inheritance of traits, as well as some genetic parameters, including the degree of

dominance (a) and hereditary in the narrow sense, and others were studied. This study also refers to the genetic analysis, which depends on estimating the action of genes and the type of inheritance after the validity of the data is investigated by relying on regression analysis and analysis of variance of some characteristics of the cotton yield and its components six genotypes of cotton in the F1 and F2 generations.

Materials and Methods

Table 1. The name, pedigree, origin, and the main characteristics of six cotton genotypes (*G. barbadense*, L.) used as parents in the present study.

Genotypes	Pedigree	Origin	Characteristics
(P ₁) Giza 85	G.67 × C.B.58	Egypt	A long staple variety, characterized by high lint strength and earliness.
(P ₂) BBB	---	Australia	The long stable characterized by big boll and black with boll weight (2.7g)
(P ₃) Giza 90	(G.83 × Dendara)	Egypt	Long staple variety for upper characterized by earliness, high No. of bolls/plant, high yielding ability and high lint percentage
(P ₄) Giza 95	[(G.83 × (G.75 × 5844)) × G.80]	Egypt	A long new staple cotton variety. Characterized by high yielding ability, high lint percentage, early maturity, and heat tolerance.
(P ₅) C.B. 58	----	USA	A medium long staple. Characterized by high lint percentage and earliness.
(P ₆) [(G.83 × G.80) × G.89] × Australy	---	Egypt	A new Promising hybrid. Characterized by high yielding ability, high lint percentage, early maturity, and heat tolerance.

The mentioned parents were crossed in all possible combinations excluding reciprocals during 2019 growing season, giving seeds of F₁ 15 crosses. In 2020 season, hybrid seeds were sown to obtain F₂ seeds and parents were re-crossed for obtaining adequate hybrid seeds. In 2021 season, the experiment involved parents, F₁ hybrids and F₂ crosses grown at Sids Experimental Station. The experiment was set as a Randomized Complete Blocks Design (R.C.B.D.) with three replications. The plot size was two rows for parents, F₁ and F₂ hybrids. Rows were 4.0 m long with row wide of 0.65 m and hills were spaced of 0.40 m apart to give 10 hills /row, and thinned at one plant per hil. The experiment was planted on the 2nd of April. All cultural practices were followed throughout the growing season as usually done with ordinary cotton culture.

Data were recorded on individual plant basis: ten plants for F₁ and parents and 30 guarded plants for F₂ were randomly chosen from each plot. The following traits were measured: Boll weight (B.W.) (g), Seed cotton yield (S.C.Y.) (g/p.), Lint yield (L.Y.) (gp.), Seed index (S.I.) (g), Lint percentage (L. %), Lint index (L.I.) (g).

Data analysis of traits was carried out according to the experimental design method to test for

The present investigation used six divergent cotton genotypes as parents. These genotypes are Giza 85, BBB, Giza 90, Giza 95, CB58 and [(G.83 × G.80) × G.89] × Australy. The name, pedigree, origin and the main characteristics of these parent genotypes are presented in Table (1). All genotypes belong to (*G. barbadense*, L.) and the pure seeds of these genotypes were obtained from Cotton Breeding Section, Cotton Research Institute, Agricultural Research Center at Giza, Egypt.

differences between genotypes (parents and each of F₁ and F₂ generation crosses). The variances were estimated according to Hayman (1954 a and b) and Jinks (1954) methods and to test that there is no superiority and the absence of multiple alleles controlling traits and that the distribution of genes between parents is independent., So, it supports conducting Vri-Wri analysis and testing the significance of the regression coefficient to be able to conduct the analysis. The theory of cross-hybridization developed by Hayman (1954) and explained in detail by Mather and Jenks (1971) was adopted, as the components of genetic variance and their ratios and standard error for each of them were estimated as D (extra genetic variance, meaning parental variance) and H1 (dominance variance, meaning joint variance between parents and rows). P and H2=H1{1-(u-v)} (where u and v are for identifying the positive and negative genes in the parents and F = the mean Fr values across grades) the combined variance of additive and dominance effects in the only row, when F is positive it means that the dominant genes are the most frequent compared to the recessive and vice versa if it is negative, h2 (the dominance effect as an algebraic sum across all heterozygous loci in all crosses, and when the frequency of dominant and recessive alleles are

equal, the values of $H_1 = H_2 = h_2$ and its significance confirms that dominance is directed) and E (the expected component of variance) is environmental. Based on these components, the ratios of genetic constants were estimated. The most important of which is $(H_1/D)1/2$, which indicates the average degree of dominance $H_2/4H_1$ ($p:q$) and indicates the proportion of genes with positive and negative influences in the parents, and when the ratio is equal to 0.25, it indicates the first distribution similar to the positive genes that increase the trait and the negative that decrease it the equation. $\sqrt{4DH_1-F} KD/KR = \sqrt{4DH_1+F}$ and indicate the ratio of dominant and recessive genes in the parents. When the ratio is one, the dominant and recessive genes in the parents are equal and less than one indicates an increase in the recessive genes, indicating an increase in the dominant genes when they are more than one and h_2/H_2 and indicating the number of groups of genes that dominate the trait and that show dominance and estimate the dominance sequence and the mean of the trait in all the parents studied to know the parents that combine the high mean and the largest degree of dominance for use in breeding programs. Heritability in narrow sense was

estimated according to Mather and Jinks (1971) for F_1 's data, and Verhalen and Murray (1969) for the F_2 's data.

Results and Discussion

Analysis of variance of both F_1 and F_2 cotton generations for all studied characters is shown in Table 2. genotypes, parents and crosses mean squares were significant for all traits in both F_1 and F_2 generations, indicating the presence of diversity in the material and sufficient amount of genetic variability adequate for further biometrical assessment. The parents vs crosses mean squares were significant and large in magnitude in F_2 analysis than F_1 ones for all studied traits. These findings are reasonable and might be due to inbreeding depression existing the F_2 which would reduce the heterosis effects. Significant differences among genotypes for grain yield and related traits in different sets of material of cotton were reported by Iqbal *et al.* (2003), Murtaza (2005) Khan *et al.*, (2007 and 2009).

Table 2. Significance of mean squares from ordinary and combining ability analysis for all characters studied in F_1 and F_2 generations.

Traits	generat ion	Rep.	Genoty pes	parent s	crosse s	P VS C	Err or	Source of variance			
								GCA	SCA	Err or	GC A/ SC A
DF	F1 and F2	2.00	20	5	14	1	40	5	15	40	
Boll weight (B.W.) (g)	F1	0.02	0.12**	0.08**	0.15**	0.05*	0.01	0.03**	0.05**	0.00	0.64
	F2	0.00	0.05**	0.08**	0.01**	0.42**	0.01	0.01**	0.02**	0.00	0.52
Seed cotton yield (S.C.Y.) (g/p.)	F1	10.22*	434.35*	262.43**	526.47**	9.21*	3.06	257.16**	107.32**	1.01	2.49
	F2	16.23*	411.92*	262.43**	459.65**	491.08**	3.47	211.03**	112.73**	1.15	1.876
Lint yield (L.Y.) (gp.)	F1	1.56*	105.11*	54.55*	130.49**	2.65*	0.46	59.22*	26.97*	0.15	2.22
	F2	7.50	111.49*	54.55*	112.95**	375.75**	2.54	44.44*	34.73*	0.84	1.287
Seed index (S.I.) (g)	F1	0.03	0.39**	0.36**	0.43**	0.03*	0.01	0.14**	0.13**	0.00	1.085
	F2	0.02	0.57**	0.36**	0.62**	0.9**	0.01	0.11**	0.22**	0.00	0.54
Lint percentage (L. %)	F1	0.25	23.8**	18.67*	26.28*	14.75*	0.37	10.65*	7.03**	0.12	1.513
	F2	33.70	80.52**	18.67	61.64*	654.12**	12.4	11.58*	31.93*	4.13	0.364
Lint index (L.I.) (g)	F1	0.01	1.51**	1.31**	1.63**	0.77**	0.02	0.41**	0.53**	0.00	0.777
	F2	1.02	3.89**	1.31*	2.62**	34.52*	0.44	0.41*	1.59**	0.14	0.267
oil %	F1	0.00	1.79**	1.66**	1.7**	3.76**	0.01	0.42**	0.66**	0.01	0.640
	F2	0.00	2.22**	1.66**	2.32**	3.5**	0.02	0.27**	0.9**	0.00	0.38

* and ** refer to significant if $p > 0.05$ and $p > 0.01$, respectively. P= parents, P vs C= parents vs crosses, GCA=general combining ability and SCA= specific combining ability

Genetic components and heritability

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 3). 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 in both F₁ and F₂ except Lint percentage in F₂ generation. These results indicate that the additive gene effects were involved in the inheritance of these traits in both generations. 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 Ferreira (1988), and Khan *et al.* (2009).

Highly significant values for dominance components associated with gene distribution (H2) were obtained for all traits in both generations. 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 significant for all traits in both generations, indicating that the dominance was due to heterozygosity and was unidirectional with appreciable heterotic effect.

The proportion of dominant to recessive gene in parents KD/KR were more than unity for most studied characters indicating that the dominant alleles govern these in both generations. Meanwhile, the KD/KR value was less than unity for Lint

percentage in F₂, an excess of decreasing alleles among parental genotypes. The distributions of the relative frequencies of dominant versus recessive gene (F) were not significant lint percentage in F₂ generation. 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 cases 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 in both generations, 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 low and not significant for most traits as shown in Table 3. High values for heritability in broad sense were obtained for all traits, 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 in both generations, indicating that most genetic variances were due to non-additive genetic effects. These finding support a forementioned 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. Murtaza *et al.*, (2002), Basal and Turgut (2003), Murtaza *et al.* (2006)

Table 3. Hayman's analysis for all studied traits in F₁ and F₂ generations.

Com ponent	Boll weight (B.W.) (g)	Seed cotton yield (S.C.Y.) (g/p.)	Lint yield (L.Y.) (gp.)	Seed index (S.I.) (g)	Lint percentage (L. %)	Lint index (L.I.) (g)	oil %
F1							
D	0.02*	86.35**	18.01**	0.12**	6.10**	0.43**	0.5 5**
H1	0.20*	467.93**	118.09**	0.56*	30.01**	2.41**	2.6 7**
H2	0.15*	385.07**	96.71**	0.43*	24.54**	1.77*	2.3 0**
h²	0.008*	0.28*	0.48**	0.009*	3.12**	0.16*	0.8 1**
F	0.05**	6.39**	0.65*	0.16**	5.20**	0.79**	0.7 3**
E	0.001	1.13	0.17	0.001	0.12	0.01	0.0 01
(H1/D) 0.5	3.09	2.33	2.56	2.21	2.22	2.37	2.1 9
H2/4H1	0.19	0.21	0.20	0.19	0.20	0.18	0.2 2

KD/Kr	2.29	1.03	1.01	1.95	1.48	2.26	1.86
R	0.37	-0.21	-0.14	0.66	0.34	0.64	-0.51
r²	0.14	0.04	0.02	0.44	0.12	0.41	0.26
h (b.s)	0.92	0.99	0.99	0.97	0.98	0.99	0.99
h(n.s)	0.20	0.46	0.44	0.27	0.34	0.24	0.14
t²	2.91	0.01	0.35	1.17	0.73	0.03	0.08
b	-0.15	0.38	0.34	0.18	0.28	0.44	0.11
F2							
D	0.02*	86.12**	17.26**	0.12**	1.75	0.28*	0.55*
H1	0.06**	462.01**	131.20**	0.93**	95.01**	4.99*	3.80**
H2	0.05**	397.11**	114.52**	0.71**	91.09**	4.46**	3.07**
h²	0.09**	105.34**	80.67**	0.19**	138.84**	7.37**	0.75**
F	0.04**	23.49**	6.35**	0.25**	0.21	0.57**	1.11**
E	0.0001	1.36	0.93	0.0001	4.47	0.16	0.01
(H1/D)_{0.5}	1.66	2.32	2.76	2.83	7.37	4.22	2.64
H2/4H1	0.19	0.21	0.22	0.19	0.24	0.22	0.20
KD/Kr	2.89	1.13	1.14	2.21	0.98	1.64	2.25
h (b.s)	0.87	0.99	0.98	0.98	0.85	0.89	0.99
h(n.s)	0.07	0.39	0.32	0.19	0.10	0.08	0.10
r	0.85	-0.17	0.27	0.79	0.76	0.93	0.76
r²	0.72	0.03	0.07	0.62	0.58	0.86	0.58
t²	10.51	0.02	0.01	1.61	0.03	0.25	1.96
b	0.14	0.32	0.10	0.35	0.61	1.01	-0.18

* 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, h²= Overall dominance gene effects of the heterozygous loci in all crosses, (H1/D)^{0.5} = mean degree of dominance at each locus over all loci, H2/4H1 = measures the average frequency of positive versus negative alleles at loci exhibiting dominance, KD/KR = the ratio of total number of dominant to receive alleles in the parents, h² (b.s) = broad sense heritability and h² (ns) = narrow sense heritability.

Graphical (wr/vr) analysis.

Graphical presentation (Vr,Wr) of different traits in both generations are given in Figures from 1 to 7. The regression coefficient significantly differed

from zero but not from unity for F₁ and in F₂, indicating that the genetic system could be deduced to be additive without the complication of non-allelic interaction. For the other cases, regression slope

differed from unity, indicating that a complementary type of epistasis was involved.

The regression line passed through the origin in boll weight in both generations, seed index, lint percentage and oil% in F1, revealed a presence of complete dominance. Meanwhile, it intersects the Wr axis above the origin in lint yield and oil% in F2, reflecting partial dominance. The presence of over dominance, however, was obtained from computing the ratio of H1 to D for these cases (Table 3). 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 parental genotypes.

The rank of parents according to their average values and the degree of dominance in the studied traits in F1 and F2 generations are presented in table 4.

The parent no 1 showed high values for all studied traits followed by no 4 for boll weight and lint yield, no 3 for seed cotton yield and no 6 for seed index, lint percentage, lint index and oil% (Table 4).

The P4 and P3 for boll weight, P1 and P2 for seed cotton yield and lint yield in both generations, P5 for seed index in both generation in both generation, P5 and P6 for lint percentage in F1 and F2, respectively, P2 and P3 for lint index in F1 and F2, respectively and P5 and P6 for oil% in F1 and F2, respectively included largest number of recessive genes for these cases (Table 4) and Fig (1:8) . On the other hand, P1 , P5, P5, P1, P2, P5, P2 in F1 and P2, P5, P5, P2, P5, P6 and P4 in F2 for boll weight, seed cotton yield, lint yield, seed index, lint index and oil% , respectively seemed to have the highest number of recessive genes (Table 4) and Fig (1:8).

Table 4. The sequence of parents according to their average values and the degree of dominance in the studied traits in F1 and F2 generations

Traits	Sequence of parents according to average traits higher → lower	F1	F2
		Sequence of parents according to the degree of dominance dominant → recessive	Sequence of parents according to the degree of dominance dominant → recessive
Boll weight (B.W.)	P1, P4, P3, P6, P2, P5	P4,P3,P5,P2,P6,P1	P4,P3,P6,P1,P5,P2
Seed cotton yield (S.C.Y.)	P1, P3, P4, P5, P6, P2	P2,P1,P4,P3,P6,P5	P2,P1,P3,P6,P4,P5
Lint yield (L.Y.)	P1, P4, P3, P6, P5, P2	P2,P1,P4,P3,P6,P5	P1,P2,P3,P4,P6,P5
Seed index (S.I.)	P1, P6, P5, P2, P3, P4	P5,P4,P2,P6,P3,P1	P5,P6,P4,P1,P3,P2
Lint percentage (L. %)	P1, P6, P4, P3, P5, P2	P5,P3,P1,P4,P6,P2	P6,P2,P4,P1,P3,P5
Lint index (L.I.)	P1, P6, P4, P5, P3, P2	P2,P6,P4,P3,P1,P5	P3,P5,P2,P1,P4,P6
oil %	P1, P6, P2, P3, P5, P4	P5,P6,P3,P4,P1,P2	P6,P3,P2,P1,P5,P4

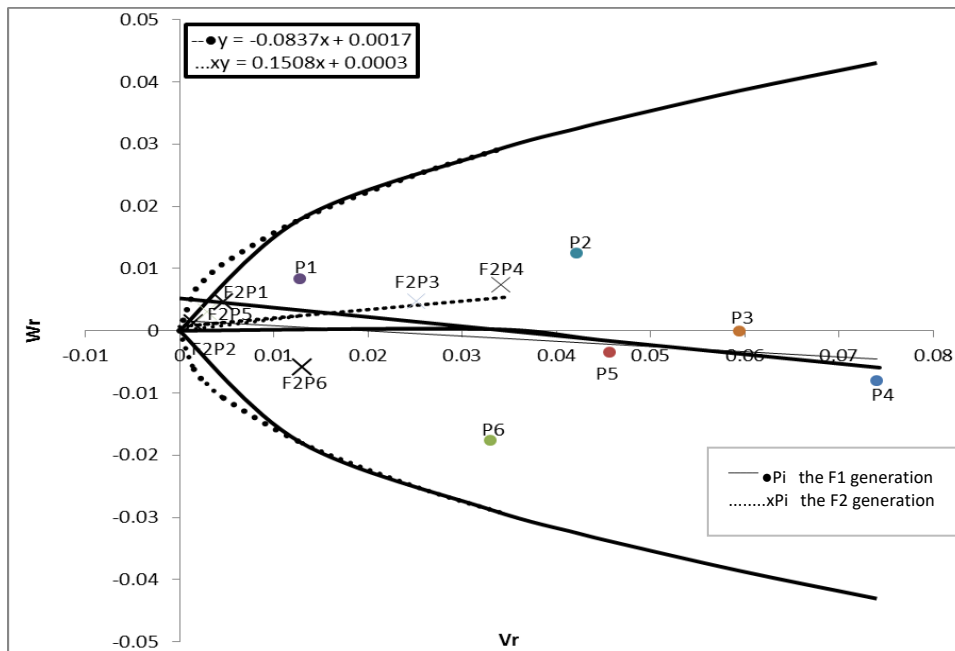


Fig 1. W_r/V_r graph for boll weight in F₁ and F₂ generations.

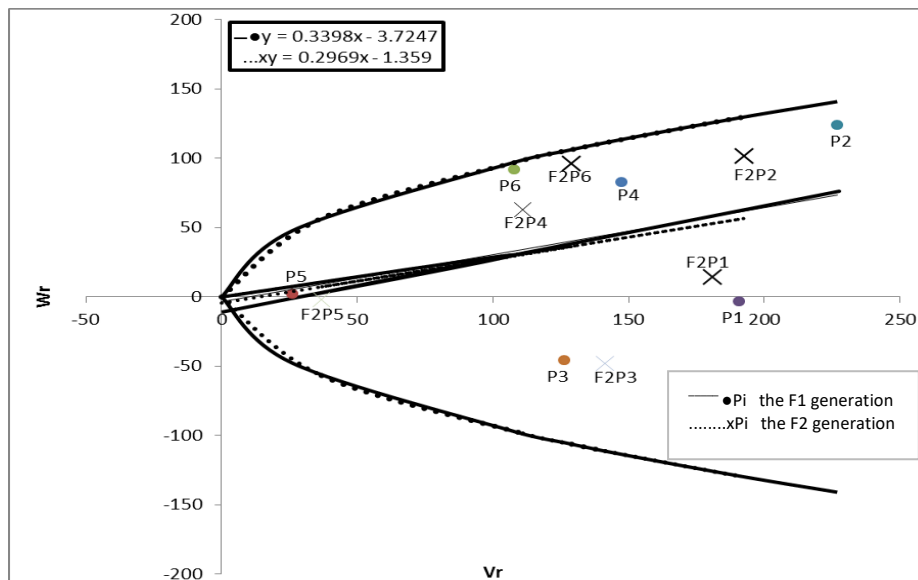


Fig 2. W_r/V_r graph for seed cotton yield in F₁ and F₂ generations.

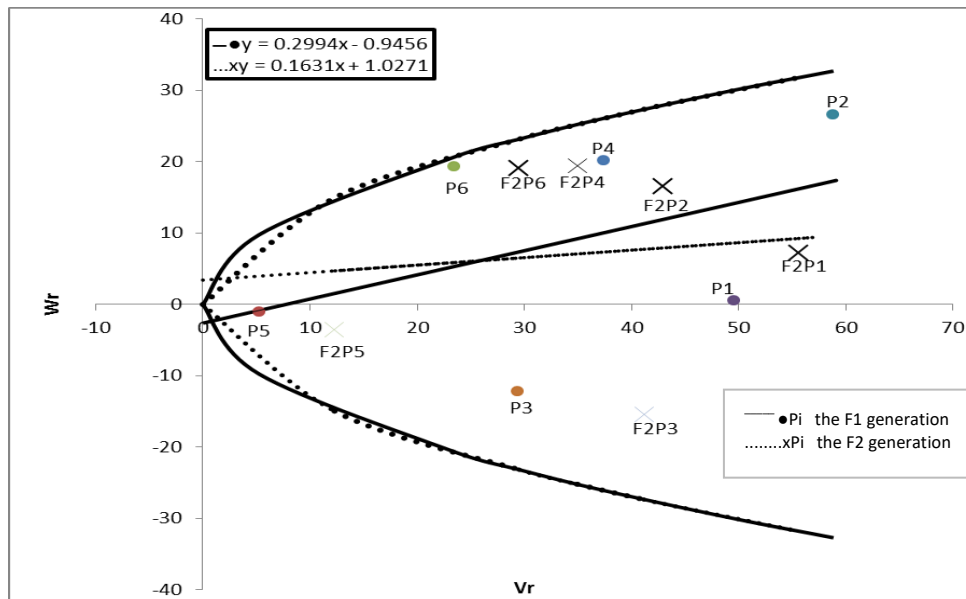


Fig 3. W_r/V_r graph for lint yield in F_1 and F_2 generations.

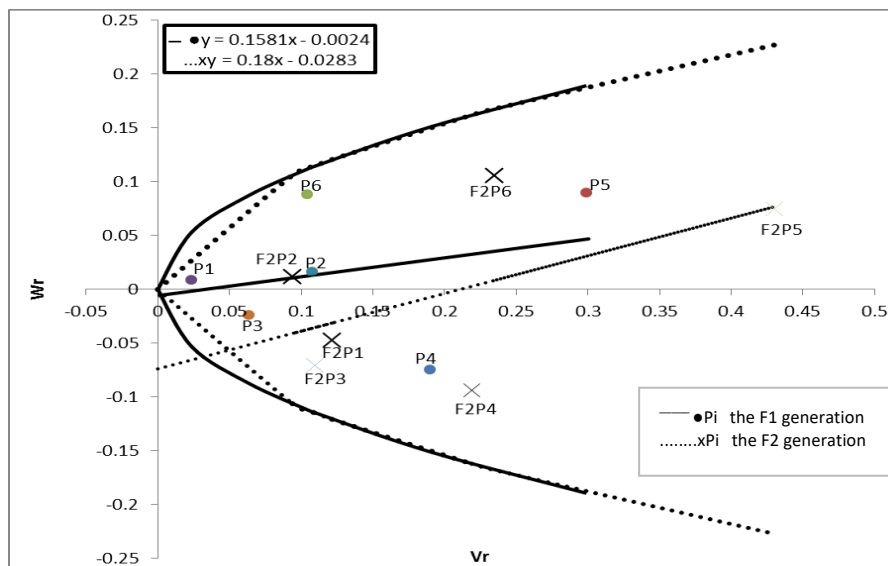


Fig 4. W_r/V_r graph for seed index in F_1 and F_2 generations.

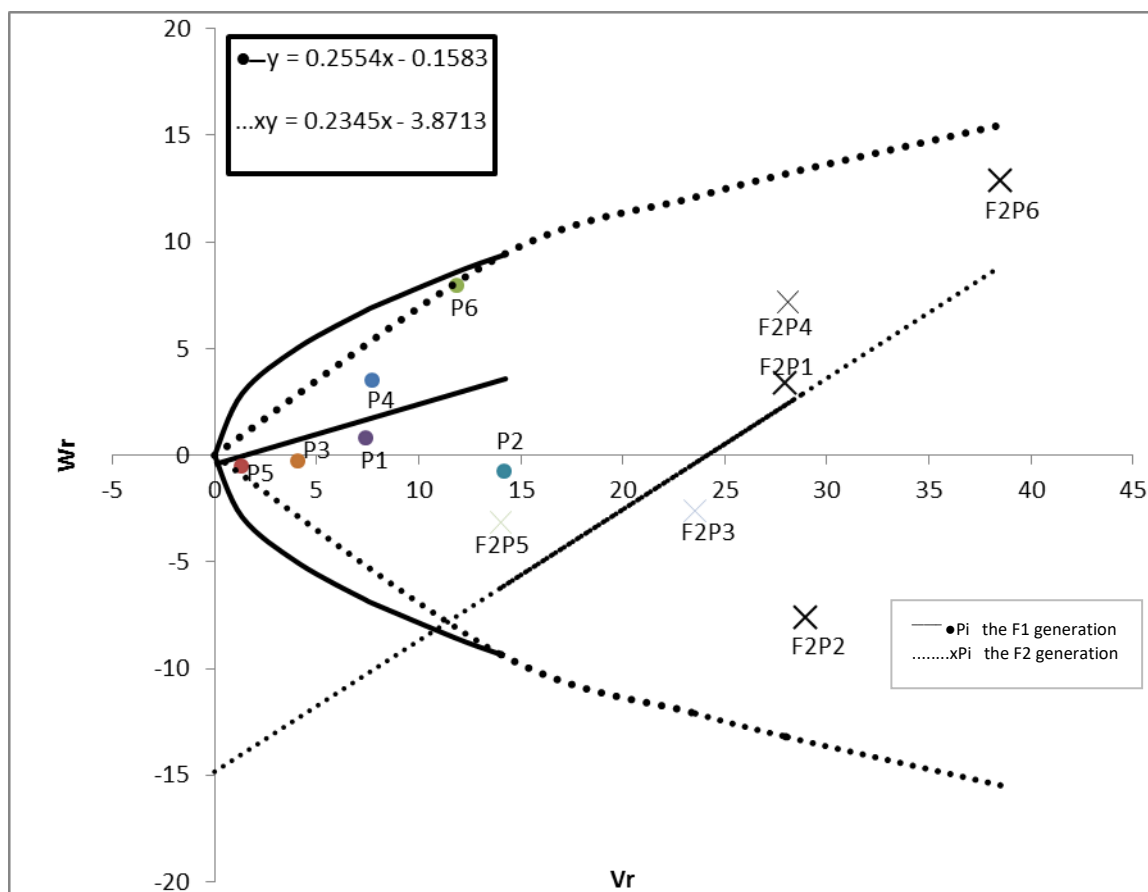


Fig 5. W_t/V_r graph for lint percentage in F_1 and F_2 generations.

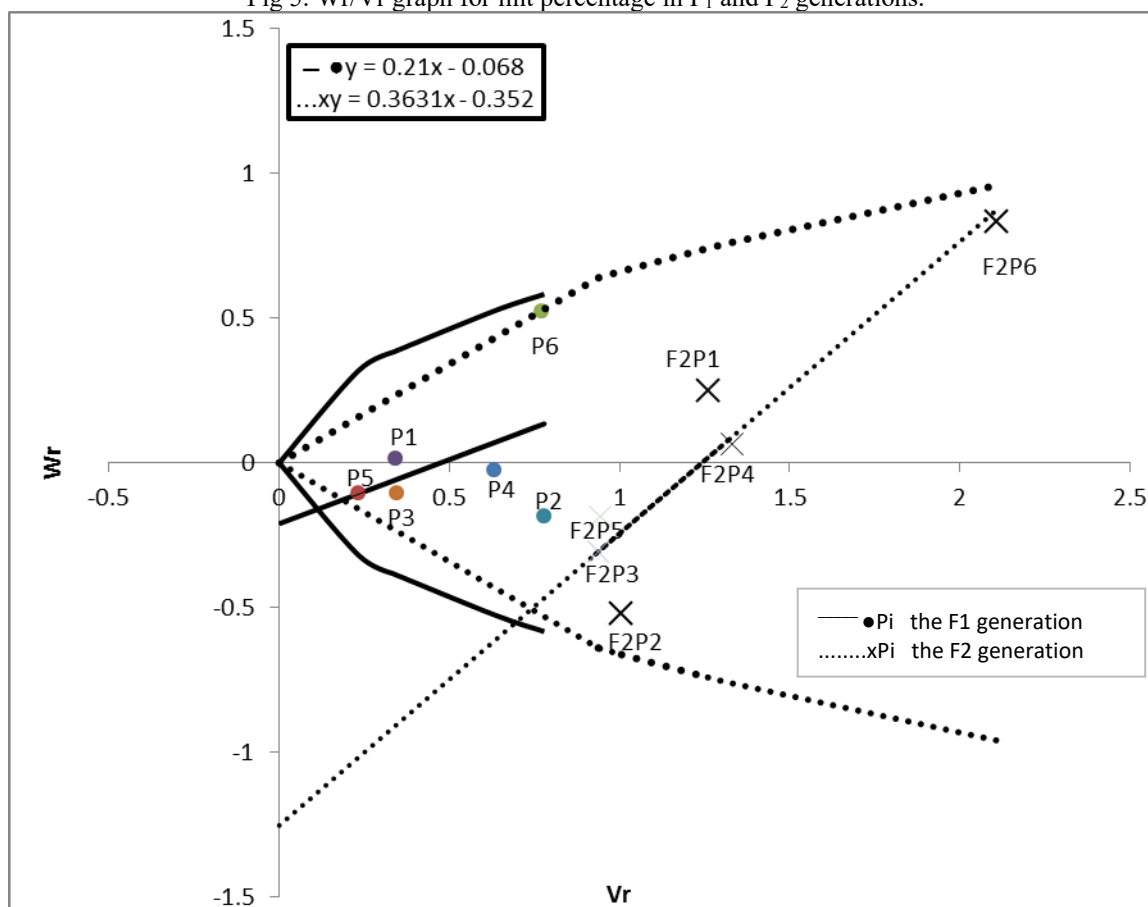


Fig 6. W_t/V_r graph for lint index in F_1 and F_2 generations.

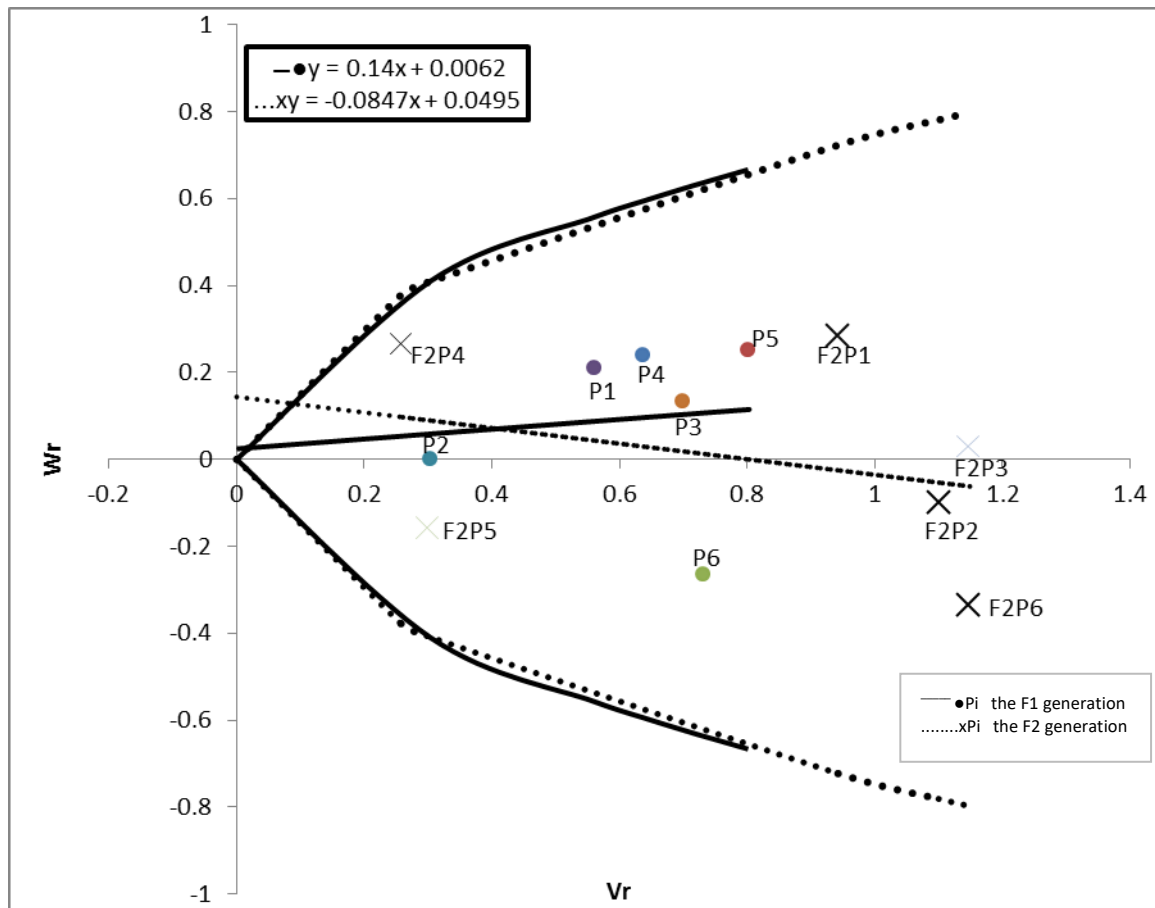


Fig 7. W_r/V_r graph for oil % in F_1 and F_2 generations.

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التحليل الوراثي للجيل الاول و الثانى فى الهجن التبادلية للقطن

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اجرى التهجين بين ستة طرز تراكيب وراثية متباينة من القطن في شكل نصف دائرى و تم تكوين ١٥ هجين فى الجيل الاول وتم الحصول على الجيل الثانى. وقيمت جميع التراكيب الوراثية في تصميم القطاعات العشوائية الكاملة بثلاث مكررات. تم تقدير الفعل الجينى بطريقة هابمن ١٩٥٤ لجميع الصفات المدروسة. أظهرت النتائج وجود قيم معنوية للفعل الجينى المضيف و السيادة لجميع الصفات , وأن قيم التباين الإضافي اقل من قيم التباين السيادة مما يدل على أهمية التباين السيادة في توريثها . كما ان قيم H2 اقل من H1 مما يشير الى ان التكررات الاليلية غير متساوية فيه. تجاوز متوسط درجة السيادة $(H1 / D)^{0.5}$ الوحدة لجميع الصفات المدروسة في كلا الجيلين , مما يشير إلى وجود هيمنة على هذه الصفات. تجاوز متوسط درجة السيادة الوحدة لجميع الصفات المدروسة في كلا الجيلين , مما يشير إلى وجود فوق سيادة لهذه الصفات. تم الحصول على قيم عالية للكفاءة الوراثية بالمدى الواسع لجميع الصفات , مما يدل على أن معظم التباين الظاهري في كل صفة راجع الى التباين الوراثي. و تم الحصول على قيم كفاءة وراثية متوسطة أو منخفضة بالمعنى الضيق في كلا الجيلين , مما يشير إلى أن معظم التباينات الجينية كانت بسبب تأثيرات وراثية غيرمضيفة. كان خط الانحدار ماراً عبر نقطة الأصل في وزن اللوز فى كلا الجيلين و دليل البذور ونسبة الالياف ونسبة الزيت في الجيل الاول مما يدل وجود سيادة تامة. بينما يقطع خط الانحدار محور Wr فوق الأصل في محصول الالياف ونسبة الزيت في الجيل الثانى , مما يعكس السيادة الجزئية. كان الاب الرابع, الثانى, الثانى, الخامس, الثانى و الخامس فى الجيل الاول و الاب الرابع, الثانى , الاول, الخامس, السادس, الثالث و السادس فى الجيل الثانى لصفات وزن اللوز, محصول البذور , محصول الالياف, دليل البذره, معامل الشعر و نسبة الزيت على الترتيب تحتوي على اعلى القيم للجينات السائدة.