تقدير كفاءة التوريث والتقدم الوراثي لصفات الغلة لبعض الهجن في القمح الطري تحت ظروف المناطق شبه الجافة والرطبه

Estimation of the Efficiency of Inheritance and the Genetic Progression of Yield Traits in some Bread Wheat Hybrids under Semi-arid and Sub-humid Conditions

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الملخص

نفذ البحث بهدف دراسة العوامل الوراثية المتحكمة بموعد طرد 50 % من السنابل (يوم)، وموعد النضج (يوم)، وارتفاع النبات (سم)، وعدد السنابل/نبات، وعدد السنيبلات/سنبلة، وعدد الحبوب في السنبلة، ووزن 1000 حبة (غ)، ووزن الحبوب في السنبلة الرئيسية (غ)، ومحصول الحبوب/نبات (غ)، ومحصول القش/نبات (غ) من خلال تطبيق نظام التهجينات الدائرية لخمسة عشر من الآباء المختلفة والمتباينة وراثياً من القمح الطري مع استبعاد الهجن العكسية، وتم إنتاج حبوب الجيل الأول (105 هجن)، والجيل الثاني (105 عائلة). قيمت نباتات الآباء والجيلين الاوّل والثاني في تجربة وضعت وفق تصميم القطاعات كاملة العشوائية، في ثلاثة مكررات، خلال الموسم الزراعي 2019/2018، ضمن موقعين في محطتى بحوث ازرع (محافظة درعا/ سورية)، وكفردان (البقاع/لبنان)، التابعتين للمركز العربى لدراسات المناطق الجافة والأراضي القاحلة (أكساد). تمّ تحليل البيانات بإستخدام طريقة الهجن التبادلية (Hayman، 1954a).

- أظهرت نتائج تحليل التباين العائد للتراكيب الوراثية (الآباء، والهجن، وتفاعلاتها) معنويةً عاليةً في الجيلين الأوّل والثانى في كلا الموقعين، ولكل الصفات المدروسة.

- أوضحت النتائج أنّ كلاً من المورثات ذات التأثير الإضافي وغير الإضافي قد أسهمت في وراثة جميع الصفات المدروسة. وأدى المكون الوراثي المضيف دوراً في وراثة معظم الصفات المدروسة في الجيلين الأوّل والثاني وموقعي الدراسة، عدا صفات موعد النضج، وإرتفاع النبات، ومحصول القش/نبات بالجيلين الأوّل والثاني وموقعي الدراسة، وأعطى المكون السيادى (H_1) تأثيراً معنوياً، وكان له دور أكبر في جميع الصفات المدروسة، وأكبر من الجزء المضيف، وكانت النسبة $(H_1/D)^{0.5}$ أكبر من الواحد لكل الصفات المدروسة، بينما بإستخدام النسبة ($4H_1/H_2$)، وقيمة (F) أظهرت الآباء عدم تساوى التكرار المورثي بالنسبة للجينات السائدة والمتنحية لكل الصفات المدروسة في الجيلين الأوّل والثاني.

- أشارت النتائج الى أنّ قيم كفاءة التوريث بمعناها الواسع كانت كبيرة جداً مقارنةً بدرجة التوريث بالمعنى الضيق، التى سجلت قيماً منخفضة الى متوسطة، ما يدل على أنّ الجزء الوراثي السيادى (السيادة الفائقة) هو الذى يتحكم فى إظهار التأثير الأكبر للصفات المدروسة كافةً.

- أظهر التحليل البياني اختلافات في مناطق السيادة والتنحي بالنسبة للآباء، إذ وجد أنّ خمسة أباء (P6, P7, P13, P14 and P15) احتوت على أكبر تكرار من الأليلات المتنحية لصفات موعد التسنبل في 50 % من النباتات، وموعد النضج التام، وارتفاع النبات، ووزن 1000 حبة،

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ووزن الحبوب في السنبلة الرئيسة، ومحصول الحبوب/نبات في كلا من الجيل الأوّل والثاني وموقعي الدراسة. لذلك، يمكن ضمن برنامج تربية القمح الطري تأجيل عمليات إنتخاب النباتات المتفوقة للأجيال اللاحقة، وفعّالية عمليات الإنتخاب في تحسين هذه الصفات والاستفادة منها لتطوير طرز وراثية مبكرة بالنضج وذات كفاءة إنتاجية عالية. تساعد تلك النتائج المربين على اختيار أفضل الآباء المرغوبة، التي يمكن من خلالها تطوير برنامج تربية فعّال للحصول على تراكيب وراثية مُحسّنة في المناطق الجافة وشبه الجافة والرطبة.
الكلمات المفتاحيّة : القمح الطري، هجن، تفاعل جيني، عوامل وراثية، التحليل البياني، الزراعة المطرية.

Abstract

The main objective of the present investigation was to study the genetic system controlling heading date (days), maturity date (days), plant height (cm.), number of spikes/plant, number of spikelets/spike, number of grains/ spike, 1000-kernel weight (gm.), grain yield/main spike (gm.) and grain and straw yield/plant (gm.) for bread wheat (*Triticum aestivum* L.) genotypes. The diallel system for 15 genetically divergent parents of bread wheat with the exclusion of reverse hybrids was applied. F_1 and F_2 generations included 105 hybrids and 105 families, respectivley. The paternal genotypes, F_1 and F_2 generations plants were evaluated in randomized complete block design experiment with three replicates, under rainfed conditions at Izraa (Daraa governorate/ Syria) and kafrdan (Bekaa governorate/ Lebanon), Stations which belong to ACSAD. The 15 divergent parents were crossed in diallel system excluding reciprocals and evaluated with its (F_1, s and F_2, s) in 2018/2019 season. The data were analyzed by using Hayman (1954a) cross-breeding method.

Results showed high significance in F_1 and F_2 in both the experimental sites of all the investigated traits. Also, results showed that both gene actions of additive and non-additive effect contributed to the genetic system of all the investigated traits. The dominance genetic component also played a major role in the inheritance of most traits under study in both F_1 and F_2 generations and under the two sites, except for the maturity date, plant height and straw yield/plant traits in the two generations and sites. The dominant component (H_1) gave a significant effect and had a greater role for all the traits under study and greater than the additive part. The ratio $(H_1/D)^{0.5}$ derivative values which measure the average degree of dominance overall loci were greater than unity for all traits recorded, while using the ratio ($H_2/4H_1$) and the value of (F) indicated that parents had unequal genetic frequency with respect to dominant and recessive genes for all the studied traits in the first and second generations. Results indicated that the values of the inheritance efficiency in the broad sense [$h_{2(b.s.)}$] were high compared to the degree of heritability in the narrow sense [$h_{2(n.s.)}$], ranged from low to medium values, indicating that the dominant part (over dominance) controls the greatest influence for all the studied traits. The graphical analysis Wr/Vr showed differences in the regions of dominance and recessive with respect to the parents, as it was found that five parents (P_6, P_7, P_{13}, P_{14} and P_{15}) contained the largest frequency of the recessive alleles for the following traits; days to heading date, the maturity date, plant height, 1000 grain weight, grain yield/main spike and the grain yield/plant in both the F_1 and F_2 generations and under the two sites. Therefore, the selection of transgressive segregants in bread wheat breeding program, and the selection processes for improving early maturing and high-yielding genotypes could be postponed for subsequent generations. These results help ACSAD breeders to select the most desirable parents, which could be usfull for developing an effective breeding program and to obtain improved genotypes under arid, semi-arid and sub humid regions.

Keywords: Bread wheat, Hybrids, Gene action, Genetic parameters, Graphical analysis, Rainfed conditions.

Introduction

Wheat is one of the major cereal crops and is widely cultivated throughout the world under different agro-climatic conditions and provides about 20 per cent of protein to mankind (FAO, 2018). In the Arab rigon, wheat covers an area of 8.4 million hectares with 21.9 million tones production, most of the cultivated area depends on precipitation rainfall (AOAD, 2018). The wheat productivity in the Arab region compared with world was estimated at 2.82 and 3.44 tons per hectare respectivley. Egypt, Iraq, Morocco, Algeria, Syria and Tunisia considered being the highest wheat production countries in the Arab world in 2018/19 (9.34, 3.05, 2.73, 1.94, 1.73 and 0.907 MT, respectively) (World Agricultural Production, 2019).

Genetic improvement of wheat grain yield is the most desirable targeted trait by breeders to enhance wheat production under abiotic stresses (drought, salinity, temperature…etc) and meet the demand of a continuous population growth. This goal can be achieved either directly by creating variability and selecting for high grain yield in the desirable recombinant or indirectly by improving yield components and morphological traits, such as plant height, thousand-kernel weight, number of spikes per plant and number of grains per spike (Rabbani *et al.*, 2009; Hannachi *et al.*, 2013 and Nagar *et al*., 2020).

Several breeding strategies have been proposed and could be planned towards the genetic understanding of important traits of the concerned population (Mumtaz *et al*., 2015). Diallel cross technique is a good tool for identification of hybrid combinations that have the potentiality of producing maximum improvement and identifying superior lines among the progenies during early segregating generations, which be usefull in the recognition of the genetic inhertance of yield components traits and the parameters, which are mainly under polygentic control, involves the use of principles of quantitative inheritance for formulating breeding approaches in wheat (El-Hosary and Nour El Deen, 2015 and Nagar *et al.*, 2020).

The partial diallel approach developed by Hayman (1954a) and modified by Viana et al. (2000 and 2001) is a promising alternative tool to study the gene effects and inheritance of plant architecture using F_1 and/or F_2 generations obtained from crosses involving homozygous parents (Farshadfar et al., 2012; El-Hosary and Nour El Deen (2015) and Fellahi et al. (2017). It is emphasized that the proper interpretation of genotypic effects depends on the particular diallel method. Mather and Jinks (1982) procedure was practiced for partitioning the genetic variance into its components and utilizing graphical analysis to understand the genetic nature of polygentic traits and to investigate the breeding potential of parental wheat genotypes in respect to transmit or accumulate genes controlling their yielding capacity in the following generations. While, based on the High estimates of heritability resulting in high genetic progression for wheat yielding components providing greater selection opportunities in early segregating generations (Memon *et al*., 2005 and 2007). This information helps breeders to define the appropriate breeding strategy and (to) choose the most suitable parents to optimize the selection gain (Falconer and MacKay, 1996).

The main objectives of this investigation are: 1) to determine the inheritance of gene action for grain yield and its components of bread wheat in a population of the 15×15 half diallel crosses under two different environmental sites. 2) to detect non-allelic interactions and gene distribution in the 15 parental genotypes through graphical analysis, and 3) to partition phenotypic variation into genotypic and environmental components as well as subdivididing genetic parameters as outlined by Hayman (1954b) in F_1 and F_2 generations.

Materials and methods

Fifteen divergent parents of bread wheat has been used in this study were crossed during the growing season2016/2017 to form a non-reciprocal diallel set of 105 F_1 hybrids. Names, source, pedigree and/or selection history of the parental lines are presented in Table (1). In 2017/2018 season, hybrid seeds were sown to obtain F_2 seeds and parents were re-crossed to obtaining adequate quantity of hybrid seeds. In 2018/2019 season, the experiment involved parents, F_1 hybrids and F_2 crosses was conducted in a randomized complete block design with three replications at two environmentally different sites; Izraa in Syria (32.8449° N, 36.2251° E), which is classifies as a semi-arid site and kafrdan in Lebanon (34.017° N, 36.050° E), which is classifies as a sub-humid site. The plots were consisted of two rows for each of the parents and F_1's and F_2 consisted of four rows (3.5 meter long and 30 cm wide for each cross), plants within row were 20 cm apart. The recommended agricultural practices for wheat production were applied and sowing date was 15, 13 and 18 November in the three growing seasons, respectively for both locations. The recommended dose of phosphatic fertilizer (120 kg P_2O_5/ha) was added during seed bed preparation, whereas nitrogen fertilizer (150 kg N/ ha) was applied as ammonium sulfate (20.5% N) at three splits, where 1/3 of the amount was incorporated in dry soil before sowing, 1/3 was added one week before panicle initiation growth stage 18 and the rest was added at grain filling period growth stage 50 of Zadoks' scale (Zadok *et al.*, 1974).

Table 1. Names, source, pedigree and/or selection history of the parental genotypes.

Genotype	Source	Pedigree and/or selection history
Line-1	ICARDA	SHUHA-7/SHUHA-14/3/ALTAR 84/AEGILOPS SQUARROSA (TAUS)//OPATA ICW04-0241-9AP-0AP-0AP-12AP-0AP
Line-2	ICARDA	ATTILA-3//NESMA*2/261-9/3/JOHAR-10 ICW01-21212-3AP-10AP-0AP-0AP-5AP-2AP-0AP
Line-3	ICARDA	PAURAQUE CGS01B00055T-099Y-099M-099Y-099M-2WGY-0B
Line-4	CIMMYT	TRCH//PRINIA/PASTOR
Line-5	ACSAD	QUAIU CGS01B00046T-099Y-099M-099Y-099M-10WGY-0B
Line-6	ICARDA	IRQIPAW35 S5B-9B-98/ABUZIG-4
Line-7	ICARDA	KAUZ›S›/BOCRO-3//ANGI-2 ICW04-0154-8AP-0AP-0AP-1AP-0AP
Line-8	CIMMYT	PRL/2*PASTOR//DANPHE#1 CMSS07B0010S-099M-099Y-099M-16WGY-0B
Line-9	CIMMYT	ONIX/ROLF07
Line-10	ICARDA	ND643/2*WBLLI//VILLA JUAREZ F2009 CMSS08Y00233S-099Y-099M-099NJ-7WGY-0B
Line-11	ICARDA	SAAR/3/C80.1/3*BATAVIA//2*WBLL1/4/C80.1/3*BATAVIA//2*WBLL1 CGSS04Y00035T-099M-099Y-099ZTM-099Y-099M-9WGY-0B
Line-12	ACSAD 1196	TEVEE7/ SHUHA19/3/ CHILERO-3// TSI/SNB's' ACS-W-9925(2003)-14IZ-3IZ-1IZ-0IZ
Line-13	ACSAD 1236	GIZA164/SAKHA34//SIEF-7 ACS-W-10121(2005)-0IZ-0IZ-2IZ-OIZ
Line-14	ACSAD 1254	HAAMA-11//KARAWAN-1/TALLO-3 ACS-W-10303(2006)-0IZ-8IZ-1IZ-0IZ
Line-15	ACSAD 1280	PASTOR/DHARWAR DRY /4/ RL6043/4*NAC//PASTOR/3 /BABAX ACS - W- 10408 (2007)- 1IZ -1IZ-1IZ-0IZ

CIMMYT; Centro International de Mejoramiento de Maize Y Trigo (Mexico) = International maize and wheat improvement center.
ICARDA ; International Center of Agricultural Research in the Dry Areas.
ACSAD ; Arab Center for the Studies of Arid Zones and Dry Lands.

Meteorological data presented in Table (2) show that the annual precipitation during the three consecutive growing seasons were 163.45, 181.60 and 215.45mm under the first site and 427.80, 475.33, and 590.51mm, respectively.The following traits were recorded and statistically analyzed; Number of days to heading and maturity (days), plant height (cm), number of spikes/plant, number of spiklets/spike, number of grains/spike, 1000 kernel weight (g), grain yield/main spike (g), grain yield/plant (g) and straw yield/plant (g) for each genotype and cross.

Table 2. Monthly average weather data at the two sites Izraa and kafrdan during three growing seasons 2016/ 2017, 2017/ 2018 and 2018/ 2019.

Site	Month	Season (2016-2017)			Season (2017-2018)			Season (2018-2019)		
		T.† (C°)		Amount Rainfall (mm)	T.† (C°)		Amount Rainfall (mm)	T.† (C°)		Amount Rainfall (mm)
		Max.	Min.		Max.	Min.		Max.	Min.	
Izraa	November	21.42	11.34	2.08	23.80	12.60	2.31	21.64	11.70	4.17
	December	15.40	8.87	6.30	17.11	9.86	7.00	16.90	10.28	11.00
	January	11.14	6.08	34.68	13.10	7.15	40.80	11.25	8.14	35.00
	February	13.15	4.59	35.70	15.47	5.40	42.00	14.19	3.22	67.28
	March	19.30	5.87	2.55	22.70	6.90	3.00	18.63	5.81	45.00
	April	22.07	8.93	12.75	25.96	10.50	15.00	23.62	11.15	34.00
	May	25.95	11.86	64.35	28.83	13.18	71.50	29.44	15.09	19.00
	June	32.51	15.61	0.00	36.12	17.34	0.00	35.65	18.70	0.00
	Mean	**20.60**	**9.33**	**Tot. =163.45**	**22.89**	**10.37**	**Tot. =181.60**	**21.41**	**10.51**	**Tot. =215.45**
Kafrdan	November	27.85	13.61	6.24	30.94	15.12	6.93	25.97	14.04	12.51
	December	18.90	10.06	17.85	22.24	11.832	21	20.28	12.34	33.00
	January	14.48	7.29	104.04	17.03	8.58	122.4	13.50	9.77	105.00
	February	17.09	5.51	107.10	20.11	6.48	126	17.03	3.86	187.00
	March	25.08	7.04	7.65	29.51	8.28	9	22.36	6.97	94.00
	April	30.38	11.34	40.50	33.75	12.6	45	28.34	13.38	102.00
	May	33.73	14.23	130.50	37.48	15.816	145	35.33	18.11	57.00
	June	42.26	18.73	0.00	46.96	20.808	0	42.78	22.44	0.00
	Mean	**26.78**	**11.20**	**Tot. =427.80**	**29.75**	**12.44**	**Tot. = 475.33**	**25.70**	**12.61**	**Tot. =590.51**

†T. = Temperature

The components of variation for diallel crosses were estimated according to Hayman(1954a) and Jinks (1956). In this model, the genetic parameters are; *D* (the variation due to additive effects), *H1* (the variation due to dominance effects), *F* (the covariance of dominance and additive effects involving a particular parent), and H2 (a dominance measure indicating asymmetry of positive and negative effects of genes). The previous components were used for computation of the other derived ratios included (i) average degree of dominance $(H1/D)^{1/2}$, (ii) proportion of genes with positive and negative effects in the parents (H_2/4 H1), (iii) proportion of dominant and recessive genes in the parents, *F* being insignificantly different from zero $[(4D\ H1)^{0.5}+F]/[(4DH1)^{1/2}–F]$ and (iv) number of groups of genes controlling the traits and exhibited dominance (h^2/H_2) to work out gene action for various traits under study. The genetic interpretation of this diallel approach is based on statistical models with fixed genotypic effects. The significance of various statistics is tested by t. test at n -2 d.f. as t = parameter/S.E of parameter. The variance, covariance (Vr, Wr) graphical analysis was used to illustrate gene action and other genetic properties of parents for different traits recorded in addition to heritability in narrow-sense ($h^2_{n.s}$) and broad-sense ($h^2_{b.s}$) for F_1's data as outlined by Mather and Jinks (1982) and Verhalen and Murray (1969) for the

F_2's data. All statistical analyses were performed using the program Genes, version 2018.25 (Cruz, 2013).
To test the validity of diallel cross assumptions, two main tests were employed; 1) The uniformity of Wr, Vr by using Hayman's (1954a andb) formula as shown in Table (3), t^2 value is not significant), 2) The regression coefficient of Wr/Vr is expected to differ significantly from zero but not from unity (absence of non-allelic interaction with independent distribution of the genes among the parents) if all assumptions are valid (Jinks and Hayman, 1953). Simple correlation coefficient between ($\bar{Y_r}$) and (W_r + V_r) was computed to determine whether the increasing or decreasing genes are the dominant one's

Results and discussion

Analysis of variance

The analysis of variance (ANOVA) due to wheat parental genotypes, crosses and parents vs crosses were highly significant for all the studied traits under each site in both the generations (F_1 and F_2) (Table 3). Indicating sufficient differences in their genetic constitution, the presence of diversity and sufficient amount of genetic variability adequate for further biometrical assessment. The parents vs crosses mean squares were large in magnitude in F_2 analysis than F_1 for all the studied traits which might be due to inbreeding depression existing in the F_2 generation reducing the heterosis effects. Similar findings were reported in F_1 and/or F_2 generatin by Joshi *et al*. (2004); Rabbani *et al*. (2009); Seleem and Kumber (2011); EL-Hosary and Nour El Deen (2015); Fellahi *et al*. (2017); Ljubičić *et al*. (2017); El-Gammaal and Yahya (2018) and Al-Timimi *et al*. (2020).

Mean performance of bread wheat genotypes

The heighest mean performance values for different selected crosses of F_1 and F_2 generations for all traits under the two sites Izraa and kafrdan conditions are presented in Tables 4 and 5. For Heading and maturity dates, the two crosses P9×P15 and P10×P14 in F_1 and F_2 generations under both the sites as well as the three crosses; P9×P12, P9×P_{15} and P_{10}×P_{12} in F_2 under Izraa conditions and the four crosses P1×P6, P10×P14, P12×P13 and P12×P14 under kafrdan conditions were the erliest in heading and maturity dates similar findings was obtained by Kheiralla and El-Defrawy (1994). Meanwhile, for plant height and straw yield/plant the cross P6×P14 recorded the highest vlues in F1 (138.00 and 141.36 cm), for plant height and (34.21 and 38.50 g) for straw yield/plant as well as in F2 (142.32 and 147.53 cm) for plant height and (32.57 and 37.67 g) for straw yield/plant under Izraa and kafrdan, respectivley. While, for No. of spikes/plant and no of spikelets/spike the two crosses P9×P13 and P12×P13 exhibited the heighest values (6.80 spikes and 23.83 sipkelets) in F_1 and (6.37 spikes and 24.46 sipkelets) in F_2 under Izraa conditions and 6.93 spikes and 23.83 sipkelets in F_1 6.95 spikes and 43.51 in F_2 under kafrdan conditions.
Furthermore, for 1000 kernel weight the eight crosses P6×P13, P6×P14, P6×P15, P8×P14, P11×P15, P12×P13 and P14×P15 in F1 and the four crosses P6×P14, P7×P12, P12×P13 and P12×P14 in F2 under Izraa conditions, as well as the nine crosses P6×P13, P6×P14, P6×P15, P8×P15, P11×P15, P12×P13, P12×P14, P12×P15 and P14×P15 in F1and the ten crosses P1×P5, P1×P8, P6×P13, P7×P10, P9×P14, P12×P13, P12×P14, P13×P14, P13×P15 and P14×P15 in F2 under kafrdan conditions exhibited the highest weight (Table 4).
For no. of grains/spike, grain yield/main spike (g) and grain yield/plant (g) the six crosses (P6×P13,P7×P13, P8×P10, P9×P15, P10×P12 and P11×P15) in F_1 and the three crosses (P8×P10, P9×P11 and P10×P12) in F2 under Izraa conditions recorded the heighest values, as well as the five crosses (P6×P13, P6×P15, P11×P15,P12×P15) and (P14×P15) in F_1 and the three crosses (P8×P14, P9×P15, P12×P15) and (P14×P15) in F2 under kafrdan conditions expressed the highest values for these traits. Therefore, these crosses may be utilized for obtaining transgressive segregants in the next generations resulting from dominance gene interaction for different characters and could be efficient for prospective wheat breeding programs aiming to improving bread wheat grain yield. Similar results were obtained by Joshi *et al*. (2004); Rabbani *et al*. (2009); Hannachi *et al*. (2013); Khaled (2013); Aglan and Farhat (2014); EL-Hosary and Nour El Deen (2015); Fellahi et al. (2016); El-Gammaal and Yahya (2018) and Al-Timimi *et al*. (2020).

Table 3. Significance of mean squares from diallel crosses analysis for all studied traits in F_1 and F_2 generations under the tow sites Izraa and Kafrdan.

Location	Generation	Source	d.f.	Heading date (days)	Maturity date (days)	plant height (cm.)	No. of spikes/ plant	No. of spikelets /spike	1000 kernel weight (g)	No. of grains/ spike	Grain yield/ main spike (g)	Grain yield/ plant (g)	Straw yield/ plant (g)
Izraa	F_1	Blocks	2	1.56	4.28	29.14	0.09	3.68	0.01	10.74	0.08	8.19	1.27
		Genotyes	120	153.99**	432.15**	3169.18**	1.16**	137.31**	0.34**	359.98**	1.07**	213.42**	103.59**
		Parents (P)	14	140.18**	372.31**	2860.57**	0.85**	116.54**	0.27**	314.96**	0.96**	188.76**	96.95**
		Crosses (C)	104	150.91**	423.51**	3105.80**	1.14**	134.56**	0.33**	352.78**	1.05**	209.15**	101.52**
		P vs c	1	202.11**	553.76**	4327.64**	1.88**	191.04**	0.47**	495.98**	1.48**	294.76**	133.95**
		Erorr	242	6.32	78.2	269.36	0.15	11.91	0.04	79.58	0.17	23.4	7.36
		t^2		0.57	7.08	24.38	0.06	1.07	0.004	7.20	0.01	2.11	0.66
	F_2	Blocks	2	1.95	5.18	35.26	0.11	4.45	0.01	13	0.1	10.24	1.54
		Genotyes	120	192.49**	522.90**	3834.71**	1.45**	166.15**	0.43**	435.58**	1.29**	266.78**	125.34**
		Parents (P)	14	184.88**	487.63**	3577.23**	1.13**	157.24**	0.34**	411.94**	1.12**	253.72**	111.21**
		Crosses (C)	104	188.64**	512.44**	3758.02**	1.42**	162.83**	0.42**	426.87**	1.26**	261.44**	122.83**
		P vs c	1	161.69**	449.05**	3826.45**	1.20**	152.77**	0.37**	379.14**	1.12**	233.46**	117.87**
		Erorr	242	7.9	94.62	325.93	0.19	14.41	0.05	96.29	0.21	29.25	8.91
		t^2		0.52	6.48	21.31	0.02	0.06	0.003	6.71	0.01	1.95	0.70
Kafrdan	F_1	Blocks	2	2.45	6.63	45.17	0.14	5.7	0.02	16.65	0.12	12.84	1.97
		Genotyes	120	241.48**	669.83**	4912.23**	1.82**	212.83**	0.53**	557.97**	1.66**	334.68**	160.56**
		Parents (P)	14	223.59**	631.39**	4543.56**	1.24**	196.22**	0.42**	545.98**	1.38**	252.71**	151.09**
		Crosses (C)	104	236.65**	656.43**	4813.99**	1.78**	208.57**	0.52**	546.81**	1.63**	327.99**	157.35**
		P vs c	1	313.55**	803.32**	6157.84**	2.50**	284.11**	0.78**	713.77**	2.83**	468.15**	276.62**
		Erorr	242	9.91	121.21	417.51	0.24	18.46	0.06	123.35	0.26	36.70	11.41
		t^2		0.61	7.49	26.14	0.07	1.15	0.004	7.76	0.01	2.28	0.71
	F_2	Blocks	2	3.06	8.03	54.65	0.18	6.9	0.02	20.14	0.15	16.05	2.38
		Genotyes	120	301.86**	810.50**	5943.80**	2.27**	257.52**	0.67**	675.14**	2.01**	418.35**	194.28**
		Parents (P)	14	284.20**	763.30**	5688.60**	1.86**	245.16**	0.52**	650.82**	1.61**	397.29**	179.01**
		Crosses (C)	104	295.82**	794.29**	5824.92**	2.22**	252.37**	0.66**	661.64**	1.97**	409.98**	190.39**
		P vs c	1	266.95**	751.03**	5740.99**	2.10**	243.27**	0.54**	642.65**	1.51**	360.19**	183.71**
		Erorr	242	12.39	146.66	505.18	0.29	22.34	0.08	149.25	0.32	45.87	13.8
		t^2		0.55	6.84	22.86	0.02	0.84	0.004	7.19	0.01	2.09	0.74

*,** denote significant difference at 0.05 and 0.01 probability levels, respectively.

Table 4. Mean performance of the best suerior 19 selected crosses for all studied genotypes in each of F_1 and F_2 generations under Izraa conditions.

Generation	Crosses	Heading date (days)	Maturity date (days)	plant height (cm)	No. of spikes/ plant	No. of spikelets/ spike	1000 kernel weight (g)	No. of grains/ spike	Grain yield/ main spike (g)	Grain yield/ plant (g)	Straw yield/ plant (g)
F_1	$P_6 \times P_{13}$	100.80	164.03	118.48	6.33	19.33	34.20	89.45	2.62	17.52	26.36
	$P_6 \times P_{14}$	100.00	163.40	138.00	6.25	14.67	33.18	63.73	2.32	14.10	34.21
	$P_6 \times P_{15}$	105.20	162.13	126.33	6.00	16.83	34.02	74.41	2.28	14.88	25.99
	$P_7 \times P_{10}$	101.20	162.13	115.67	6.17	18.50	31.92	80.22	2.41	15.44	30.01
	$P_7 \times P_{12}$	98.80	150.23	122.67	6.00	15.33	30.78	81.23	2.45	13.30	28.55
	$P_7 \times P_{13}$	105.60	163.90	115.00	6.12	16.00	31.68	90.82	2.65	17.30	25.55
	$P_7 \times P_{14}$	100.40	162.00	105.48	6.05	21.67	31.14	85.42	2.48	14.48	27.57
	$P_7 \times P_{15}$	98.80	155.80	92.00	6.10	18.17	30.78	83.15	2.30	15.00	27.82
	$P_8 \times P_{10}$	101.60	157.07	84.33	6.00	16.83	30.90	91.56	2.69	17.76	23.58
	$P_8 \times P_{14}$	100.40	166.43	81.78	5.83	21.33	33.00	85.75	2.50	15.11	27.79
	$P_8 \times P_{15}$	99.20	177.97	102.67	6.00	19.33	30.36	87.54	2.48	13.45	23.36
	$P_9 \times P_{13}$	98.40	160.23	92.00	5.65	22.17	31.98	82.42	2.46	14.75	25.88
	$P_9 \times P_{15}$	91.40	133.77	86.51	5.83	18.50	30.36	88.75	2.61	17.20	30.68
	$P_{10} \times P_{12}$	96.80	157.20	69.00	5.33	16.17	30.90	93.00	2.63	17.62	26.87
	$P_{10} \times P_{14}$	94.00	142.63	79.15	5.67	15.50	30.42	87.06	2.47	14.58	24.27
	$P_{11} \times P_{15}$	105.20	160.87	105.67	6.30	19.00	33.90	91.88	2.69	18.05	21.01
	$P_{12} \times P_{13}$	107.60	172.27	117.24	6.80	23.83	34.56	75.26	2.33	14.71	33.51
	$P_{13} \times P_{15}$	106.80	171.00	126.33	6.25	18.17	32.16	65.87	2.32	15.07	24.81
	$P_{14} \times P_{15}$	108.40	173.53	108.67	6.15	21.67	34.62	72.74	2.37	14.41	25.04
L.S.D		4.04	14.22	16.40	0.23	1.55	2.04	11.35	0.38	7.78	4.36
F_2	$P_6 \times P_{13}$	98.78	160.75	115.29	6.01	18.55	32.04	77.86	2.48	15.00	25.83
	$P_6 \times P_{14}$	98.00	160.13	142.32	6.13	17.97	33.54	72.25	2.29	14.61	32.57
	$P_6 \times P_{15}$	103.10	158.89	122.81	5.68	16.10	32.52	72.92	2.35	12.39	25.67
	$P_7 \times P_{10}$	104.24	157.27	111.30	5.98	20.21	33.36	75.40	2.29	14.29	24.11
	$P_7 \times P_{12}$	101.76	155.43	108.99	5.82	16.85	33.84	80.11	2.34	14.19	26.84
	$P_7 \times P_{14}$	103.41	157.44	101.55	6.02	19.97	32.64	80.30	2.37	14.36	25.91
	$P_8 \times P_9$	105.26	153.75	92.66	5.86	18.53	33.06	81.73	2.28	14.59	25.11
	$P_8 \times P_{10}$	103.63	146.64	86.86	6.00	17.17	31.56	94.31	2.79	16.92	24.99
	$P_8 \times P_{14}$	98.39	153.30	82.65	5.72	20.91	32.10	84.03	2.56	15.24	27.23
	$P_8 \times P_{15}$	97.22	174.41	120.21	5.88	18.75	31.34	85.79	2.44	14.95	22.89
	$P_9 \times P_{10}$	103.22	163.44	118.45	5.51	22.44	29.76	87.93	2.52	14.49	27.12
	$P_9 \times P_{11}$	96.70	164.08	98.94	5.72	19.14	33.06	93.57	2.74	17.74	28.09
	$P_9 \times P_{12}$	93.84	155.31	102.66	5.47	20.78	32.88	87.61	2.50	14.28	31.12
	$P_9 \times P_{13}$	96.43	157.03	90.16	5.64	22.44	31.38	80.77	2.42	14.25	25.36
	$P_9 \times P_{15}$	92.51	133.93	85.24	5.72	18.13	31.38	86.98	2.47	14.70	30.06
	$P_{10} \times P_{12}$	94.86	149.58	67.62	5.23	18.84	29.76	91.14	2.75	18.45	26.33
	$P_{12} \times P_{13}$	105.45	168.82	122.81	6.37	23.85	35.30	83.55	2.59	14.15	33.24
	$P_{12} \times P_{14}$	106.62	170.68	112.37	6.03	16.00	33.90	75.69	2.48	15.80	22.38
	$P_{12} \times P_{15}$	110.42	166.48	121.04	6.06	16.75	30.44	79.94	2.56	16.11	24.16
$LSD_{0.05}$		3.86	13.61	14.68	0.29	1.35	1.98	13.86	0.66	7.47	4.50

Table 5. Mean performance of the best 25 selected crosses for all studied genotypes in each of F_1 and F_2 generations under Kafrdan conditions.

Generation	Crosses	Heading date (days)	Maturity date (days)	plant height (cm)	No. of spikes/ plant	No. of spikelets / spike	1000 kernel weight (g)	No. of grains/ spike	Grain yield/ main spike (g)	Grain yield/ plant (g)	Straw yield/ plant (g)
	$P_1 \times P_5$	105.42	169.60	109.60	6.14	19.81	34.02	88.84	2.65	17.14	28.67
	$P_1 \times P_6$	100.78	168.92	95.68	6.34	21.51	33.58	86.47	2.57	16.65	28.93
	$P_1 \times P_8$	103.63	166.64	87.71	6.04	21.60	33.71	75.22	2.46	15.86	24.52
	$P_3 \times P_{12}$	97.92	153.75	117.57	5.75	22.18	35.97	88.21	2.65	15.90	29.42
	$P_6 \times P_{13}$	102.82	167.31	115.41	6.59	20.15	37.36	96.72	2.99	19.33	27.41
	$P_6 \times P_{14}$	105.00	171.57	141.36	6.50	18.36	36.23	76.67	2.48	16.76	38.50
	$P_6 \times P_{15}$	107.30	165.38	113.39	6.24	26.02	37.17	97.38	2.85	19.52	26.62
	$P_7 \times P_{10}$	103.22	165.38	101.49	6.41	17.43	34.90	73.43	2.47	15.08	25.61
	$P_7 \times P_{12}$	100.78	163.44	97.57	6.24	18.55	33.64	88.63	2.52	16.96	29.70
	$P_7 \times P_{13}$	110.88	161.60	110.48	6.41	16.21	34.59	90.29	2.72	17.52	26.57
	$P_8 \times P_{14}$	102.41	159.56	97.71	6.07	19.23	36.04	89.18	2.58	17.48	28.90
	$P_8 \times P_{15}$	101.18	181.53	107.57	6.24	17.20	33.14	91.04	2.65	17.14	24.29
F_1	$P_9 \times P_{11}$	99.54	168.91	103.65	6.07	19.16	34.52	73.31	2.81	17.67	27.56
	$P_9 \times P_{13}$	100.37	163.44	95.68	5.98	22.48	34.97	85.71	2.63	16.34	26.92
	$P_9 \times P_{14}$	102.90	158.27	99.73	5.46	16.99	34.27	86.74	2.76	15.68	25.47
	$P_9 \times P_{15}$	93.29	140.21	87.71	6.07	18.24	33.20	90.30	2.67	15.85	31.90
	$P_{10} \times P_{12}$	101.64	160.27	81.76	5.55	17.60	33.71	82.63	2.81	16.21	27.95
	$P_{10} \times P_{14}$	94.88	140.54	91.76	5.89	18.24	33.20	90.54	2.63	16.13	25.24
	$P_{11} \times P_{15}$	107.30	164.08	98.58	6.33	20.45	37.35	94.48	2.80	19.34	21.43
	$P_{12} \times P_{13}$	109.75	175.71	119.86	6.93	23.83	36.04	86.96	2.45	16.88	33.78
	$P_{12} \times P_{14}$	110.98	177.65	115.43	6.36	20.37	37.67	78.78	2.55	17.04	23.29
	$P_{12} \times P_{15}$	109.34	175.07	119.56	6.38	19.98	37.11	94.99	2.84	19.63	26.21
	$P_{13} \times P_{14}$	109.75	175.71	93.32	6.55	18.70	35.28	70.83	2.33	15.90	23.46
	$P_{13} \times P_{15}$	108.94	174.42	129.86	6.40	17.12	34.46	77.39	2.44	16.21	25.31
	$P_{14} \times P_{15}$	113.82	182.21	117.10	6.56	16.78	38.12	96.37	2.96	18.40	26.29
L.S.D		4.18	14.64	17.33	0.26	1.74	0.35	14.90	0.70	8.07	4.52
	$P_1 \times P_5$	101.13	156.82	112.46	5.52	20.99	38.56	81.78	2.69	15.49	20.11
	$P_1 \times P_6$	95.96	150.67	105.02	5.44	21.70	33.28	86.45	2.71	15.36	28.84
	$P_1 \times P_8$	100.76	163.97	121.91	6.45	22.62	36.60	80.97	2.65	15.70	26.86
	$P_3 \times P_{12}$	102.90	168.14	127.53	6.37	19.83	33.47	75.14	2.45	16.21	32.83
	$P_6 \times P_{13}$	105.16	162.07	119.72	5.22	18.49	36.41	75.84	2.51	15.97	26.29
	$P_6 \times P_{14}$	103.56	165.23	147.53	6.12	18.99	34.27	78.16	2.46	15.66	37.67
	$P_6 \times P_{15}$	103.80	158.53	93.75	6.05	19.96	35.66	83.32	2.50	15.73	27.91
	$P_7 \times P_{10}$	114.21	156.75	86.01	6.22	19.20	36.67	84.88	2.59	16.75	24.98
	$P_7 \times P_{12}$	108.58	154.81	106.29	6.05	20.17	36.10	83.51	2.53	15.92	26.95
	$P_7 \times P_{13}$	107.37	156.82	90.76	6.00	19.12	34.46	85.00	2.55	16.22	26.11
	$P_8 \times P_{14}$	105.70	149.57	90.34	6.24	18.56	33.09	98.08	2.87	19.17	25.99
	$P_8 \times P_{15}$	100.71	161.44	80.70	5.85	16.89	31.70	88.72	2.53	15.66	31.56
F_2	$P_9 \times P_{11}$	100.36	156.37	85.95	6.05	17.70	35.28	87.39	2.73	16.88	28.32
	$P_9 \times P_{13}$	99.16	177.90	115.02	6.12	23.76	32.51	89.22	2.61	16.58	23.80
	$P_9 \times P_{14}$	105.29	166.71	113.19	5.52	20.27	36.10	91.44	2.79	16.04	28.21
	$P_9 \times P_{15}$	91.53	142.29	104.25	5.95	21.14	35.91	97.32	2.92	18.98	29.22
	$P_{10} \times P_{12}$	98.72	168.61	106.76	5.69	22.99	33.27	91.12	2.67	15.83	32.37
	$P_{10} \times P_{14}$	92.36	144.17	93.77	5.86	21.95	34.21	84.00	2.59	15.79	26.38
	$P_{11} \times P_{15}$	100.84	155.10	78.14	5.35	22.51	33.58	91.13	2.72	15.17	24.96
	$P_{12} \times P_{13}$	94.36	157.00	85.95	6.95	24.46	36.51	80.46	2.53	16.29	31.27
	$P_{12} \times P_{14}$	95.16	153.21	70.32	4.91	21.72	36.45	93.14	2.69	14.25	28.21
	$P_{12} \times P_{15}$	99.61	157.06	81.71	5.44	21.16	33.08	94.78	2.92	18.65	27.39
	$P_{13} \times P_{14}$	107.56	172.20	126.43	6.50	20.60	36.29	85.22	2.58	16.38	33.50
	$P_{13} \times P_{15}$	108.76	174.10	121.85	6.25	21.84	36.92	77.21	2.61	15.92	32.82
	$P_{14} \times P_{15}$	112.62	169.81	124.08	6.18	20.07	39.38	91.54	2.89	18.26	30.64
$LSD_{0.05}$		4.00	13.98	15.56	0.31	1.52	0.34	14.33	0.68	7.74	4.62

Genetic action:

Significant genotypic difference is the base requirement for half diallel analysis in Hyman's approach. Mean squares due to genotypes were highly significant for all traits recorded at the two generations and under the two sites shown in Table (3). Variances (V_r) and covariances (W_r) were estimated and the uniformity of W_r, V_r were detected for all the studied cases, in both the generations by insignificant t^2 values indicating the validity of assumptions made by Hayman (1954a) as clearly shown in Table (3). The components of variations D, H_1, H_2, F, h^2 and E as expected values using least square technique were calculated and given in the two Tables (6 and 7). The environmental effects indicated by (E) values reached the significant level in all traits except plant height revealing their sensitivity to the environmental changes.

The estimated values of additive component (D) for most traits except maturity date, plant height, no. of spikelets/spike and straw yield/plant in the two generations and under the two sites, suggesting the possibility of improving such traits by selection in the following generations under similar environmental conditions. Presence of dominance effects were substantiated by significant estimates of H_1 for all traits recorded in both generations and under the two sites. Moreover, H_1 values were higher than D estimates in all cases regardless its sign. Also, H_2 estimated values which represent dominance variance adjusted for asymmetric gene distribution were highly significant for all cases and were higher than those of D in most cases. H_2 values were smaller than those of $H1$ in all the studied traits except for plant height, no. of grains/spike, grain yield/main spike and grain yield/ plant indicating unequal proportion of positive and negative alleles for each trait in the parental genotypes. This would indicate the importance of non-additive genetic variance in the inheritance of these traits. Hence, it could be concluded that the selection procedures would be effective when additive, dominance and epistatic effects are involved in the genetic control of such traits especially, when they acted at the same direction. The relative frequency of dominant to recessive alleles in parental genotypes (gene symmetry) as indicated by (F) values which showed unequal gene frequencies was positive and significant in heading date, maturity date, no. of spikes/plant and 1000-kernel weight under generations in the two sites (Tables 6 and 7), suggesting that the dominant alleles were more frequent than the recessive ones.

These finding confirmed by the ratio of KD /KR that was more than unity in heading and maturity date, no. of spikes/ plant, no. of spikelets/spike, 1000 kernel weight, grain yield/plant and straw yield/plant in the two generations and under both sites indicating that dominant alleles have increasing effects in inheritance the mentioned traits (Mather and Jinks, 1982). The overall dominance effects of heterozygous loci (h^2) were found to be positive and highly significant for all the recorded traits except for plant height. This means that the dominance effects were mainly attributed to heterozygous phase in all crosses.

$(H_1/D)^{0.5}$ derivative values which measure the average degree of dominance overall loci were greater than unity for all the investigated traits indicating that these traits controlled mainly by over dominance genetic effects. $H_2/4H_1$ value was used to estimate the average frequency of negative (v) versus positive (u) alleles in the parental genotypes. This ratio theoretically equals 0.25 when the distribution of positive equal negative genes among the genetic make up of parents. As shown in the two Tables (6 and 7), this ratio seemed to be smaller than 0.25 for all the studied traits except for no. of spikelets/spike in the two generations and under the two sites revealing that positive and negative alleles were not equally distributed in the parental genotypes. Present results were also supported by Subhani and Chowdhry (2000); Ahmed *et al*. (2015); Kandil *et al*. (2016); Kumar *et al*. (2016); Ljubičić *et al*. (2017) and Nagar *et al*. (2020).

The the estimates of ratio for number of gene groups controlling the traits to exhibit dominance h^2/H_2 was calculated to determine the number of effective gene groups that control the character and exhibit dominance. Data showed that, more than unity for most traits in both F_1 and F_2 generations, there was involvement of more than one major gene groups in inheritance of these traits, about four and three effective gene groups controlled grain yield/main spike, grain yield/plant and straw yield/plant in the two generations and under Izraa and kardan conditions. Very low h^2/H_2 ratios were obtained for heading and maturity dates and no. of spikelets/spike in F_1 and F_2 under the two sites suggesting that among the genes governing each of these traits, one or more of high dominance effect led to disportionate h^2/H_2 fraction as previously stated by Crumpacker and Allard (1962) especially when such gene groups distributed independently. The prediction for measurement of completely dominant and recessive parents (r^2) exhibited the highest values in $F_1$and F_2 (0.841 and 0.886 respectively) under Izraa as well as (0.848 and 0.894) under kafrdan for grain yield/plant (Tables 6 and 7). Rabbani *et al.* (2009), EL-Hosary and Nour El Deen (2015); Kandil *et al*. (2016) and El-Gammaal and Yahya (2018) studied the genetic parameters in bread wheat diallel crosses under drought stress conditions and obtained results more or less in harmony with these findings.

Heritability in broad sense [$h^2_{b.s.}$] ranged from 81% for no. of grains/spike in F_1 under Izraa conditions to 97% in F_1 under kafrdan for all the studied traits. While, the ratio of additive genetic portion to the phenotypic variance computed as narrow sense heritability [$h^2_{n.s.}$] was relatively moderate for heading date, maturity date, 1000-kernel weight grain yield/plant and straw yield/plant in the two generations and under the to sites ranged from 30% to 52% or whereas low (Tables 7 and 8). These results confirm that additive gene effects play a major role in the genetic variation of these traits under the targeted conditions and that selection in early segregating generations could be effective for isolating good new recombinants suitable to the targeted environments. Therefore, the pedigree selection method program for improving such traits might be promising. Similar conclusions were previously obtained by Esmail (2002); Memon *et al*. (2007); Kumber (2011); EL-Hosary and Nour El Deen (2015); Kandil *et al*. (2016); Fellahi *et al*. (2017) and Al-Timimi *et al*. (2020).

Table 6. Estimates of genetic parameters and some of its derived ratios in F_1 diallel cross analysis for all traits recorded in bread wheat under Izraa and kafrdaan conditios.

Characters	Heading date (days)		Maturity date (days)		Plant height (cm)		No. of spikes/plant		No. of spikelets / spike	
Genetic Parameters	Izraa	Kafrdan	Izraa	Kafrdan	Izraa	Kafrdan	Izraa	Kafrdan	Izraa	Kafrdan
E	10.80**	10.04**	13.05**	13.97*	0.95	1.24	1.78**	2.31**	0.68**	0.88**
D	1.98**	2.57**	0.07	0.09	-0.15	-0.20	4.71**	6.12**	-0.07	-0.09
H_1	7.67**	8.82**	6.79**	7.81**	5.79**	6.66**	9.36**	10.76**	3.96**	4.55**
H_2	6.98**	8.03**	6.50**	7.48**	6.55**	7.53**	6.70**	7.71**	2.32**	2.97**
h^2	9.46**	10.88**	13.69**	15.74**	0.56	0.64	1.16**	1.33***	2.76**	3.17**
F	2.29**	2.38**	2.56**	1.71**	-0.17	-0.22	4.70**	6.11**	-0.04	-0.05
$D-H_1$	-8.24	-10.71	-8.42	-10.95	-7.32	-9.52	-8.51	-11.06	-4.98	-6.47
$(H_1/D)^{0.5}$	2.68	3.08	13.19	15.17	9.00	10.35	1.92	2.21	9.00	10.35
$H_2/4H_1$	0.18	0.21	0.19	0.22	0.23	0.21	0.14	0.16	0.28	0.26
K_D/K_R	1.12	1.29	1.68	1.78	0.90	0.84	3.72	4.28	9.00	10.35
h^2/H_2	0.90	0.69	0.87	0.94	1.05	1.42	1.11	1.45	0.43	0.69
$H_{n.s.\%}$	47	49	34	35	18	19	21	22	20	21
$H_{b.s.\%}$	96	97	84	85	93	94	88	89	92	93
r^2	0.689	0.780	0.798	0.712	0.697	0.782	0.483	0.341	0.386	0.377

Characters	1000 kernel weight (g)		No. of grains/ spike		Grain yield/main spike (g)		Grain yield/ plant (g)		Straw yield/ plant (g)	
Genetic Parameters	Izraa	Kafrdan	Izraa	Kafrdan	Izraa	Kafrdan	Izraa	Kafrdan	Izraa	Kafrdan
E	1.78**	2.31**	3.83**	4.98**	2.81**	3.65**	1.21**	1.57**	1.32**	1.72**
D	0.93**	1.21**	1.43**	2.56**	2.92**	1.20**	1.15**	1.20**	0.58	0.75
H_1	7.21**	8.29**	6.70**	7.71**	6.55**	7.53**	4.63**	5.32**	8.04**	9.25**
H_2	6.97**	8.02**	7.36**	8.46**	7.37**	8.48**	6.11**	6.73**	7.96**	9.15**
h^2	30.05**	34.56**	14.25**	16.39**	33.79**	38.86**	10.39**	11.95**	25.99**	29.89**
F	0.85**	1.11**	-0.29	-0.38	-0.19	-0.25	-0.03	-0.04	0.16	0.21
$D-H_1$	-8.36	-10.87	-8.07	-10.49	-7.55	-9.82	-5.87	-7.63	-9.65	-12.55
$(H_1/D)^{0.5}$	3.79	4.36	5.37	6.18	3.63	4.17	9.00	10.35	5.08	5.84
$H_2/4H_1$	0.20	0.23	0.21	0.23	0.23	0.24	0.17	0.20	0.20	0.23
K_D/K_R	1.73	1.99	0.75	0.86	0.87	1.00	9.00	10.35	1.12	1.29
h^2/H_2	2.88	2.69	1.29	1.69	3.26	3.69	3.69	3.25	3.18	3.69
h^2 (n.s)%	30	32	25	26	23	27	49	52	33	34
h^2 (b.s)%	89	90	81	82	85	86	90	91	93	94
r^2	0.382	0.589	0.598	0.473	0.582	0.683	0.841	0.886	0.677	0.707

*** and **: Denote significance at $P \leq 0.05$ and 0.01 probability levels, respectively.**

Table 7. Estimates of genetic parameters and some of its derived ratios in F_2 diallel cross analysis for all traits recorded in bread wheat under Izraa and kafrdaan conditios

Characters	Heading date (days)		Maturity date (days)		Plant height (cm.)		No. of spikes/plant		No. of spikelets / spike	
Genetic Parameters	Izraa	Kafrdan	Izraa	Kafrdan	Izraa	Kafrdan	Izraa	Kafrdan	Izraa	Kafrdan
E	10.92**	11.29**	12.57**	13.60**	0.85	1.19	2.23**	3.12**	0.51**	0.71**
D	2.50**	3.25**	0.13	0.17	-0.12	-0.16	4.84**	6.29**	-0.02	-0.03
H_1	10.02**	12.53**	6.35**	7.94**	5.52**	6.90**	9.20**	11.50**	4.30**	5.38**
H_2	9.11**	11.84**	6.39**	8.31**	6.33**	8.23**	6.75**	8.78**	4.62**	6.01**
h^2	9.41**	10.82**	17.13**	19.70**	0.26	0.30	3.99**	4.59**	2.27**	2.61**
F	0.42	0.57	-0.11	-0.15	-0.15	-0.20	4.72	6.37	-0.01	-0.01
$D\text{-}H_1$	-10.82	-14.07	-7.83	-10.18	-6.96	-9.05	-8.22	-10.69	-5.38	-6.99
$(H_1/D)^{0.5}$	2.73	3.14	9.69	11.14	9.00	10.35	1.88	2.16	9.00	10.35
$H_2/4H_1$	0.18	0.23	0.20	0.23	0.23	0.24	0.15	0.19	0.26	0.28
K_D/K_R	1.15	1.38	0.81	0.97	9.00	10.80	3.72	4.46	9.00	10.80
h^2/H_2	0.79	0.84	0.93	0.75	1.03	1.04	1.40	1.82	0.33	0.40
$H_{n.s.\ \%}$	45	46	30	31	16	17	18	19	22	23
$H_{b.s.\ \%}$	92	95	85	86	93	94	85	86	94	95
r^2	0.644	0.642	0.670	0.569	0.553	0.345	0.522	0.368	0.417	0.407
Characters	**1000 kernel weight (g.)**		**No. of grains/ spike**		**Grain yield/main spike (g.)**		**Grain yield/ plant (g.)**		**Straw yield/ plant (g.)**	
Genetic Parameters	**Izraa**	**Kafrdan**	**Izraa**	**Kafrdan**	**Izraa**	**Kafrdan**	**Izraa**	**Kafrdan**	**Izraa**	**Kafrdan**
E	1.30**	1.82**	3.62**	5.07**	2.47**	3.46**	1.28**	1.79**	1.57**	2.20**
D	1.68**	1.93**	2.50**	1.65**	2.90**	1.17**	1.14**	2.08**	0.62	0.81
H_1	5.85**	7.31**	7.74**	9.68**	7.76**	9.70**	5.35**	6.69**	9.22**	11.53**
H_2	5.51**	7.16**	8.39**	10.91**	8.82**	11.47**	7.05**	8.57**	9.34**	12.14**
h^2	11.35**	13.05**	16.63**	19.12**	31.33**	36.03**	9.42**	10.83**	30.4**	34.96**
F	0.47	0.63	-0.03	-0.04	-0.04	-0.05	-0.05	-0.07	0.04	0.05
$D\text{-}H_1$	-6.84	-8.89	-9.32	-12.12	-9.08	-11.80	-6.77	-8.80	-11.08	-14.40
$(H_1/D)^{0.5}$	4.00	4.60	5.35	6.15	4.00	4.60	9.00	11.21	5.25	6.04
$H_2/4H_1$	0.19	0.24	0.21	0.23	0.23	0.24	0.19	0.22	0.20	0.23
K_D/K_R	1.47	1.76	0.97	1.16	0.98	1.18	9.00	10.80	1.02	1.22
h^2/H_2	1.38	1.68	1.32	1.61	2.37	2.89	3.24	4.01	3.17	32.98
$H_{n.s.\ \%}$	31	32	23	24	22	23	44	52	32	33
$H_{b.s.\ \%}$	91	92	83	84	88	89	93	94	85	87
r^2	0.593	0.607	0.622	0.587	0.790	0.697	0.848	0.894	0.688	0.728

* and **: Denote significance at $P \leq 0.05$ and 0.01 probability levels, respectively.

Graphical analysis:

Mather and Jinks (1982) concluded that Hayman's (1954 a and b) analysis is the most useful for determining significance of principal genetic components. This procedure suggests that the diallel set of data could be graphically analyzed. The graph of W_r on V_r prospectively provides information on three points 1) it supplies a test of adequacy of the model in the absence of non-allelic interaction and with independent distribution of the genes among the parents. W_r is related to V_r by a straight regression line of unit slope. 2) a measure of the average level of dominance is provided by the departure from the origin of the point where the regression line cuts the W_r axis and 3) the relative order of the points along the regression line indicates the distribution of dominant and recessive genes among the parent arrays. Fig's. (1 to 7) illustrate variance (V_r) and covariance (W_r) graphs for all traits recorded under the two water treatments in two seasons.

The values of regression coefficient (b) of parent-offspring covariance (W_r) on parental array variance (V_r) are illustrated in Figs. (1-10). Values were significantly differed from zero indicating real relationship between Wr and Vr for all traits under study. The slope of regression line “b” deviated significantly from unity for maturity date in the two generations and under the two sites indicating the presence of additive and dominance without any complications by the epistatic effects.
For heading date , plant height , no. of spikes/plant ,1000 kernel weight, no. of grais/spike ,grain yield/main spike and straw yield/plant in both generations and under the two sites, the regression lines intercept W_r below the origin suggesting the major role of over-dominance and confirmed again $(H_1/D)^{0.5}$ derived ratios. Regarding for the other cases, partial dominance had an important role in controlling number of spikelets/spike and grain yield/plant in F_1 and F_2 generations and under the two sites the regression line intercept W_r axe above the origin. The scattered parental array points along the regression line for all studied cases indicate the presence of different genetic systems (types of alleles) among parents for each trait. The present results were also supported by for one and/or moe traits in bread wheat, Chowdhry et al. (2002); Farshadfar *et al*. (2013); EL-Hosary and Nour El Deen (2015); Kumar et al. (2016); Fellahi *et al*. (2017); Kumar *et al*. (2017); Ljubičić *et al.* (2017); Al-Timimi *et al*. (2020) and Nagar *et al.* (2020).
The relative position of array points and Wr/Vr graph clearly showed the fact that, significantly negative r(Vr+Wr),Yr values means that parents containing most dominant alleles have the lowest Vr+Wr estimates and “r” will be positive if the case is reverse. The relative order of parental points along regression line designated one and/or of the following parents; (P6, P7, P13, P14 and P15) at the upper end and so it possessed more recessive genes contributed to the lowest estimate and “r” will be positive if the case is reverse of contained the highest frequency of recessive alleles for heading date, maturity date, plant height, 1000 kernel weight, grain yield/main spike and grain yield/plant. Such recessiveness genes resulting a negative effect (low parental measurement “Yr^{-}”) in grain yield and its components under treatments (Figs 1, 2, 3, 6, 8 and 9). As well as (P1) for number of spikes/plant (Fig. 4), (P12) for number of sikelets/spike (Fig. 5), (P3, P5 and P8) for number of grains/spike (Fig. 7) and (P1, P11 and P12) for straw yield/plant (Fig. 10) in the two generations and under the two sites.
While, the parents that were closer to the origin possessed maximum dominant genes (P10 and P11) for heading date, maturity date, plant height and number of spikes/plant; (P1 and P4) for number or spikelets/spike, 1000 kernel weight, number of grains/spike and grain yield/main spike and (P5) for both traits grain and straw yield. Therefore, these genotypes contain more of dominant genes in both F_1 and F_2 generations under the two sites, the present findings were also supported by the earlier results of various researchers (Farshadfar *et al*. 2013; Kumar *et al.* 2016; Kumar *et al*. 2017 and Al-Timimi *et al.* 2020).
However, both dominant and recessive alleles were approximately of equal portion in the genetic makeup of P2, P5, P9, P10 and P12 which had a moderate Yr values (Figs 1-10). It could be concluded that the parental genotypes exhibited high level of genetic diversity, thus considered valuable to be included in crosses for developing new high yielding recombinants of bread wheat suitable for similar stress conditions. These findings confirm more or less those previously obtained by EL-Hosary and Nour El Deen (2015); Fellahi *et al*. (2017); Ljubičić *et al*. (2017) and Al-Timimi et al. (2020). While, the graphical representation of Wr-Vr graphs (Fig. 1, 3, 4, 6, 7, 8 and 10) supported the results and indicated the over dominance type of gene action, as the regression line cuts Wr-axis just below the origin for heading date, plant height, number of spikes/plant, 1000 kernel weight, number of grains/spike, grain yield/main spike and straw yield/plant in both F_1 and F_2 generations and under two sites.
In conclusion, biparental mating and/or diallel selective mating would be useful to exploit both additive and non-additive gene effects. Diallel selective mating system is a good technique, which delays quick fixation of gene complexes, and permits break down of linkage, general fostering of recombination and concentration of favorable gene complexes into central gene pool by a series of multiple crosses. Additive and nonadditive gene effects were involved in the expression of all traits. Meanwhile, the parental genotypes (P1, P4, P5, P10 and

P11) contains more of dominant genes in both F_1 and F_2 generations under the two sites for grain yield and its components, The six crosses P6×P13, P7×P13, P8×P10, P9×P15, P10×P12 and P11×P15 in F_1 and the three crosses P8×P10, P9×P11 and P10×P12 in F2 under Izraa conditions recorded the heighest values, as well as the five crosses P6×P13, P6×P15, P11×P15,P12×P15 and P14×P15 in F_1 and the three crosses P8×P14, P9×P15, P12×P15 and P14×P15 in F_2 under kafrdan conditions expressed the highest values for grain yield and its components could be an excellent candidate for improving grain yield in both F_1 and F_2 generations. Average value of the allelic frequency products suggested unequal distribution of dominant and recessive alleles for most of traits under study. Dominance effects acted in the direction of increasing value for yield and its components and clearly showed that selection in early generation may not be useful. Therefore, selection of superior plants should be delayed through later generations and suggested that present findings could be effective to improve these traits and useful in formulating future breeding programme to develop early maturing and high yielding bread wheat genotypes. Information in this regard would help ACSAD breeders to make better selection of desirable parents to develop an efficient breeding program to improve wheat genotypes with high production capacity under arid, semi arid and sub humid regions.

Recommendation

It is highly recommended to use the superior crosses in bread wheat breeding programs to ensure the trasngressive segregants genotypes in the following generations. Selection superior genotypes having greater and highly heritable grain yield under arid, semi arid and sub humid regions possessed favorable genes and could be characterized as the most tolerant under rainfed conditions. These new early maturing and improved genotypes considerd to be used as parents in future breeding programms or distributed to the targeted farmers.

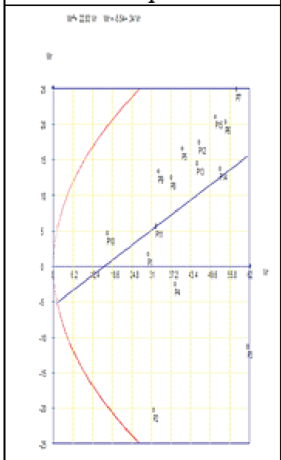
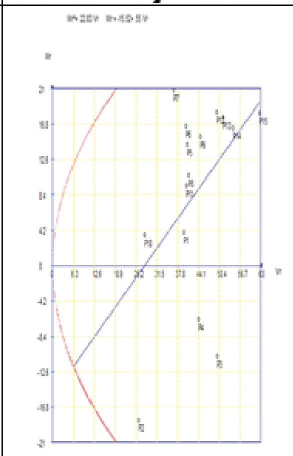
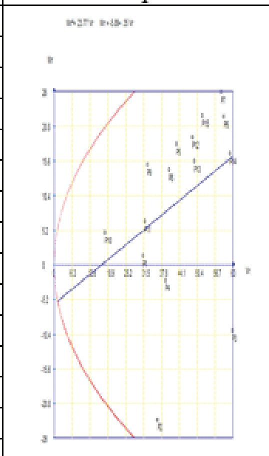
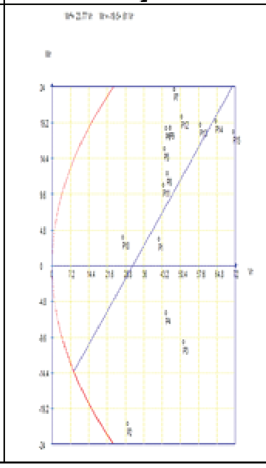
Izraa				Kafrdan			
F_1	F_2	p	$\bar{Y}_r$	F_1	F_2	p	$\bar{Y}_r$
		P_1	93.31			P_1	96.10
		P_2	99.12			P_2	97.49
		P_3	95.58			P_3	98.82
		P_4	99.91			P_4	101.90
		P_5	103.45			P_5	105.52
		P_6	100.69			P_6	102.71
		P_7	104.23			P_7	106.32
		P_8	102.66			P_8	104.71
		P_9	102.27			P_9	104.31
		P_{10}	103.84			P_{10}	105.92
		P_{11}	107.77			P_{11}	109.93
		P_{12}	104.23			P_{12}	106.32
		P_{13}	102.27			P_{13}	104.31
		P_{14}	104.63			P_{14}	106.72
		P_{15}	88.50			P_{15}	90.27

Fig .1. Wr, Vr graphs for heading date in the two generations and under both sites.

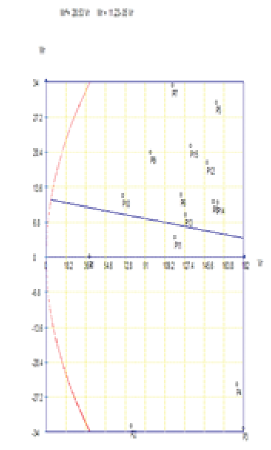
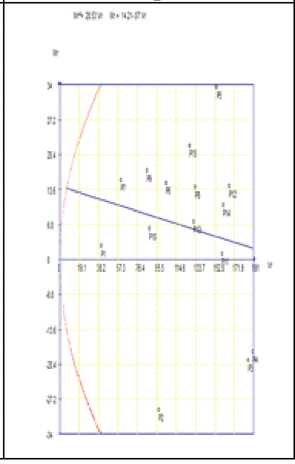
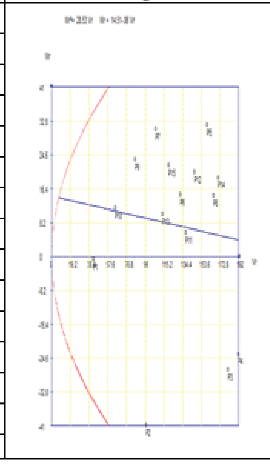
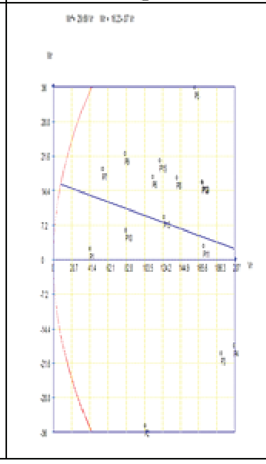
Izraa				Kafrdan			
F_1	F_2	p	$\bar{Y}_r$	F_1	F_2	p	$\bar{Y}_r$
		P_1	151.20			P_1	154.22
		P_2	158.76			P_2	161.94
		P_3	158.76			P_3	161.94
		P_4	163.38			P_4	166.65
		P_5	169.26			P_5	172.65
		P_6	166.32			P_6	169.65
		P_7	170.10			P_7	173.50
		P_8	166.32			P_8	169.65
		P_9	165.90			P_9	169.22
		P_{10}	167.58			P_{10}	170.93
		P_{11}	171.78			P_{11}	175.22
		P_{12}	168.00			P_{12}	171.36
		P_{13}	165.90			P_{13}	169.22
		P_{14}	168.42			P_{14}	171.79
		P_{15}	162.54			P_{15}	165.79

Fig .2. W_r, V_r graphs for maturity date in the two generations and under both sites.

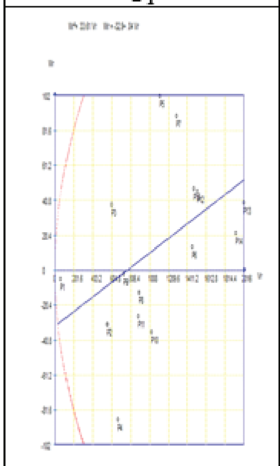
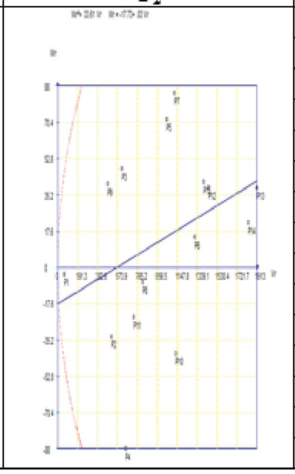
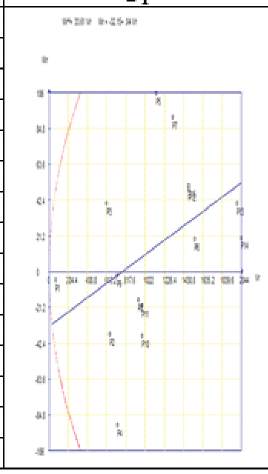
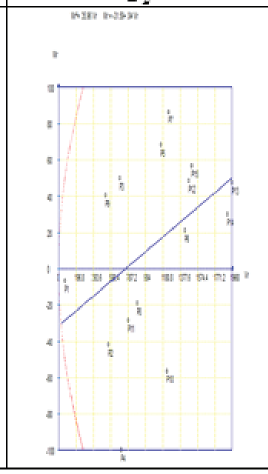
Izraa				Kafrdan			
F_1	F_2	p	$\bar{Y}_r$	F_1	F_2	p	$\bar{Y}_r$
		P_1	89.32			P_1	92.00
		P_2	97.37			P_2	100.29
		P_3	99.67			P_3	102.66
		P_4	95.07			P_4	97.92
		P_5	92.77			P_5	95.55
		P_6	99.28			P_6	101.27
		P_7	106.95			P_7	109.09
		P_8	108.87			P_8	111.04
		P_9	106.57			P_9	108.70
		P_{10}	103.50			P_{10}	105.57
		P_{11}	102.35			P_{11}	106.44
		P_{12}	103.88			P_{12}	108.04
		P_{13}	105.42			P_{13}	109.63
		P_{14}	107.72			P_{14}	112.03
		P_{15}	98.90			P_{15}	100.88

Fig .3 . W_r, V_r graphs for plant height in the two generations and under both sites.

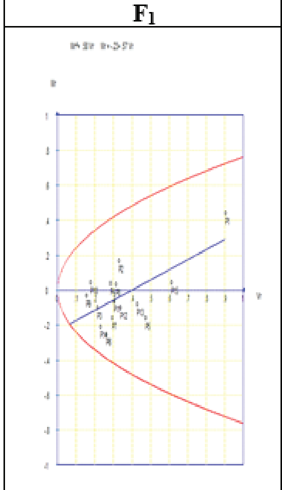
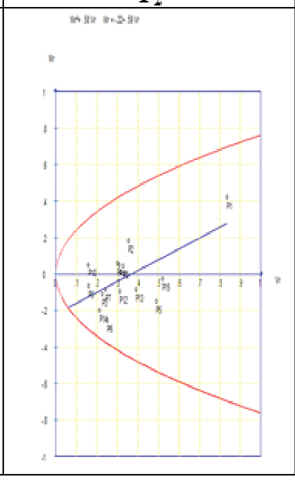
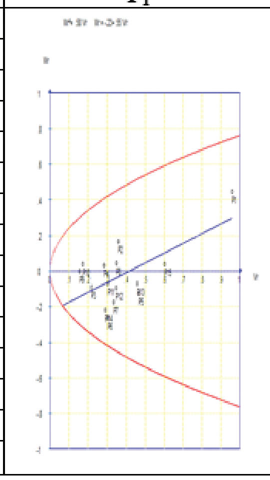
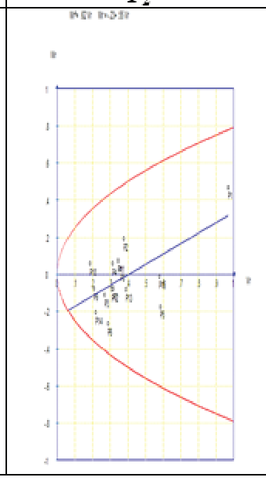
Izraa				Kafrdan			
F_1	F_2	p	$\bar{Y}_r$	F_1	F_2	p	$\bar{Y}_r$
		P_1	5.15			P_1	5.31
		P_2	6.06			P_2	6.87
		P_3	5.45			P_3	6.24
		P_4	6.06			P_4	6.87
		P_5	7.27			P_5	6.55
		P_6	5.45			P_6	5.25
		P_7	6.06			P_7	5.25
		P_8	4.85			P_8	6.80
		P_9	4.85			P_9	5.87
		P_{10}	5.15			P_{10}	4.95
		P_{11}	6.97			P_{11}	6.93
		P_{12}	4.38			P_{12}	5.67
		P_{13}	4.58			P_{13}	4.73
		P_{14}	5.00			P_{14}	5.67
		P_{15}	3.73			P_{15}	4.95

Fig .4 . W_r, V_r graphs for no. of spikes/plant in the two generations and under both sites.

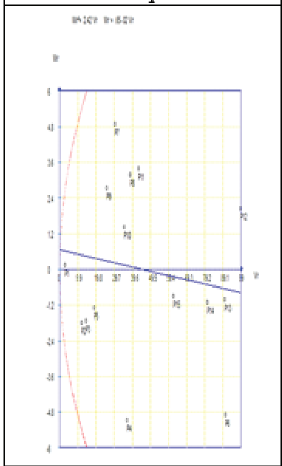
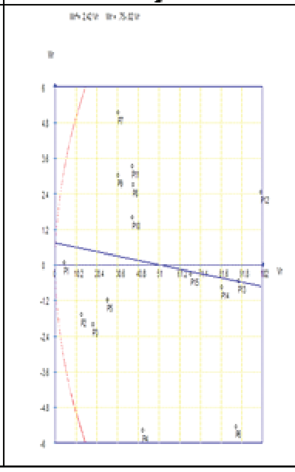
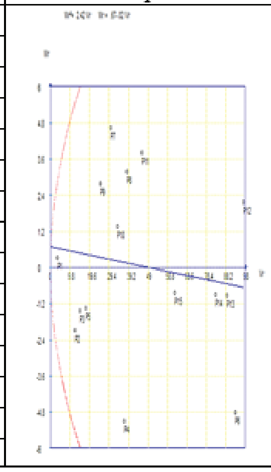
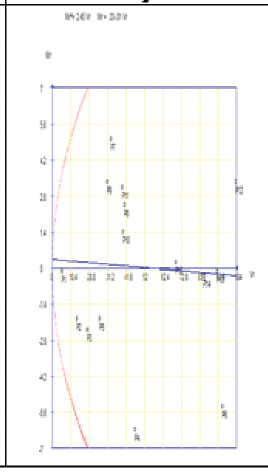
Izraa				Kafrdan			
F_1	F_2	p	$\bar{Y_r}$	F_1	F_2	p	$\bar{Y_r}$
		P_1	23.38			P_1	24.08
		P_2	28.75			P_2	30.19
		P_3	27.22			P_3	28.58
		P_4	28.75			P_4	30.19
		P_5	27.98			P_5	29.38
		P_6	24.92			P_6	26.16
		P_7	25.68			P_7	26.97
		P_8	25.68			P_8	26.20
		P_9	27.22			P_9	27.76
		P_{10}	25.68			P_{10}	26.20
		P_{11}	25.68			P_{11}	26.45
		P_{12}	24.92			P_{12}	25.66
		P_{13}	25.68			P_{13}	26.45
		P_{14}	27.22			P_{14}	28.03
		P_{15}	23.38			P_{15}	24.32

Fig .5. Wr, Vr graphs for number of spikelets/spike in the two generations and under both sites.

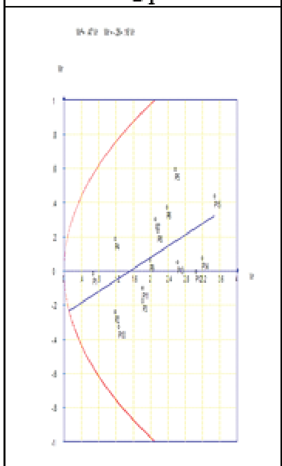
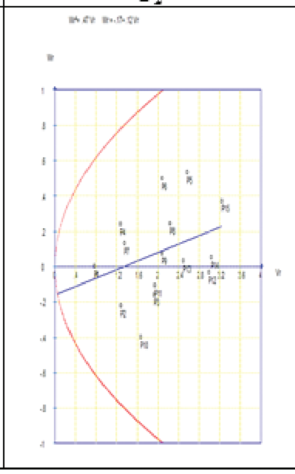
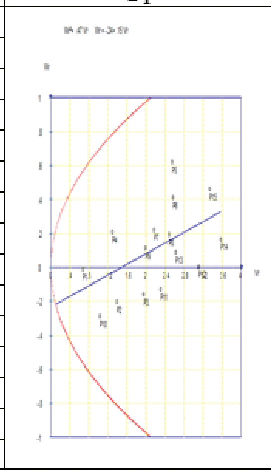
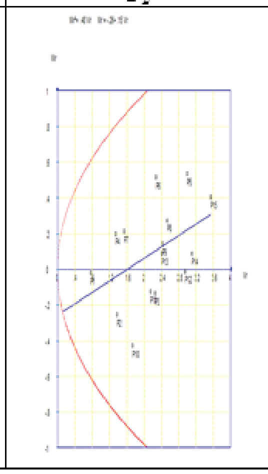
Izraa				Kafrdan			
F_1	F_2	p	$\bar{Y_r}$	F_1	F_2	p	$\bar{Y_r}$
		P_1	30.61			P_1	30.32
		P_2	29.03			P_2	29.14
		P_3	28.42			P_3	29.84
		P_4	29.95			P_4	29.23
		P_5	28.80			P_5	31.10
		P_6	30.14			P_6	27.87
		P_7	31.00			P_7	30.24
		P_8	30.61			P_8	30.43
		P_9	29.44			P_9	29.70
		P_{10}	28.29			P_{10}	28.88
		P_{11}	28.97			P_{11}	29.56
		P_{12}	28.39			P_{12}	31.14
		P_{13}	30.19			P_{13}	29.95
		P_{14}	27.33			P_{14}	31.34
		P_{15}	29.65			P_{15}	31.63

Fig .6. Wr, Vr graphs for 1000 kernel weight in the two generations and under both sites.

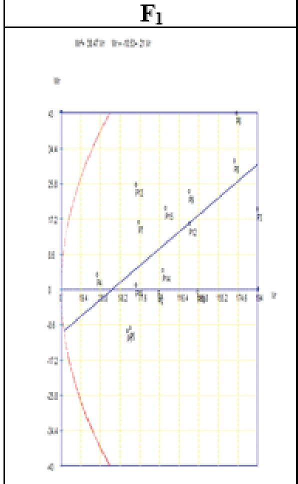
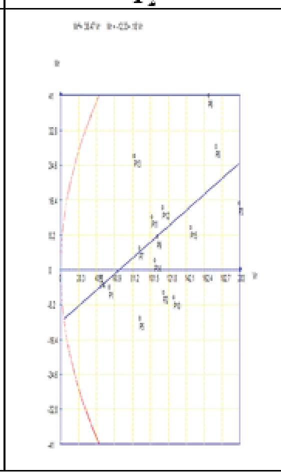
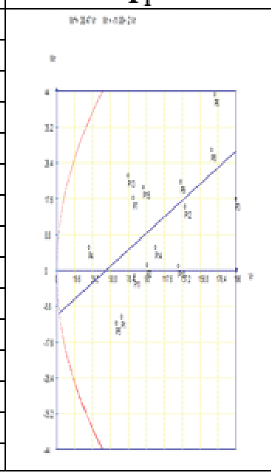
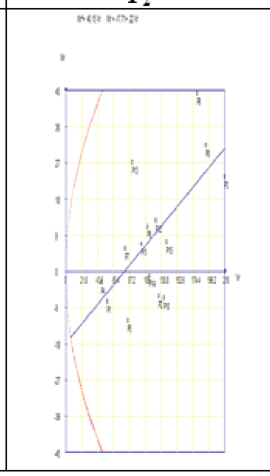
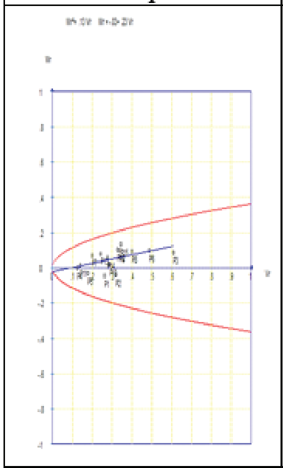
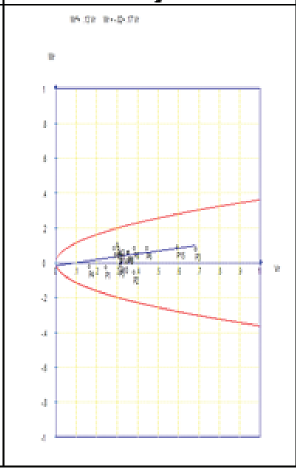
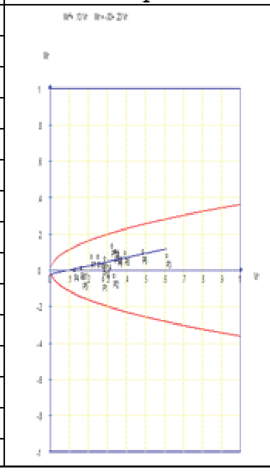
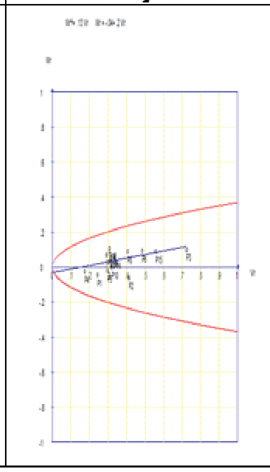
Izraa				Kafrdan			
F_1	F_2	p	$\bar{Y_r}$	F_1	F_2	p	$\bar{Y_r}$
		P_1	74.19			P_1	75.68
		P_2	67.26			P_2	70.90
		P_3	64.76			P_3	69.45
		P_4	64.44			P_4	68.13
		P_5	64.44			P_5	66.13
		P_6	74.81			P_6	72.59
		P_7	68.21			P_7	69.18
		P_8	63.49			P_8	65.60
		P_9	69.78			P_9	70.70
		P_{10}	74.19			P_{10}	71.98
		P_{11}	70.36			P_{11}	74.37
		P_{12}	65.07			P_{12}	68.73
		P_{13}	69.47			P_{13}	70.74
		P_{14}	78.58			P_{14}	72.10
		P_{15}	68.84			P_{15}	70.64

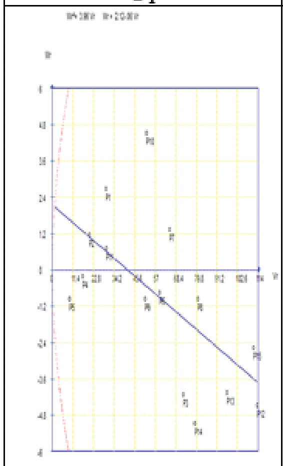
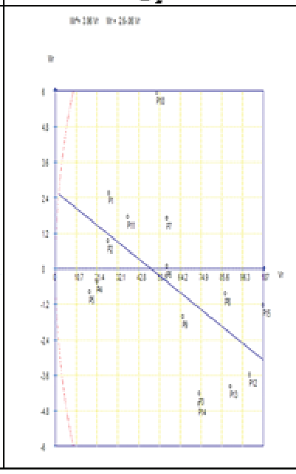
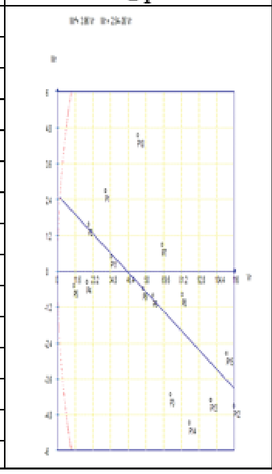
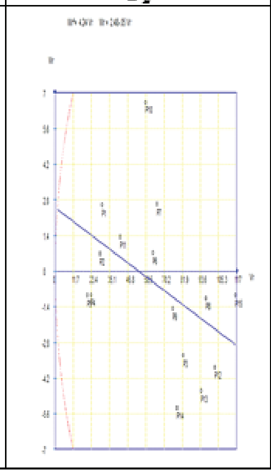
Fig .7. Wr, Vr graphs for no. of grains/spike in the two generations and under both sites.

	Izraa			Kafdran		
F1	F2	p	$\bar{Y}_r$	F1	F2	p

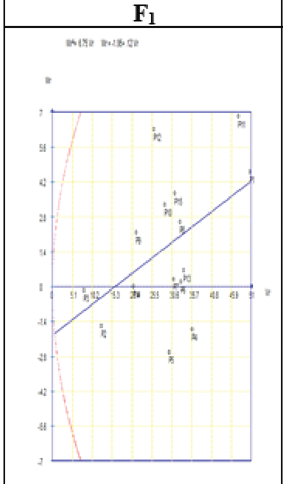
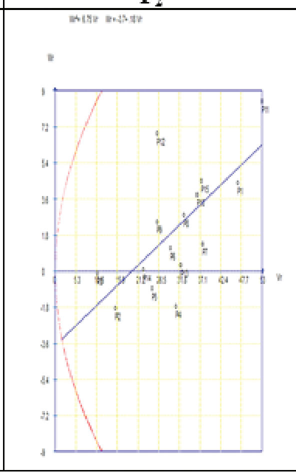
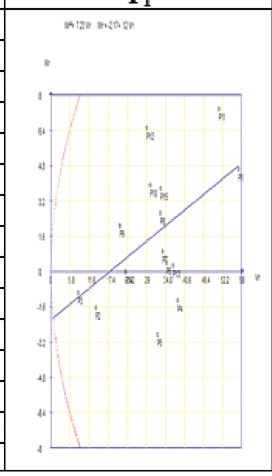
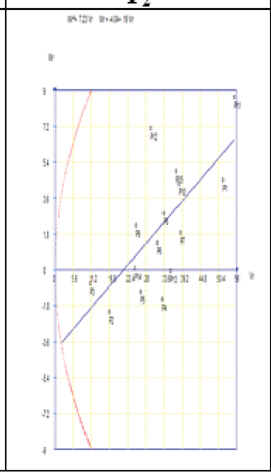
p	Izraa $\bar{Y}_r$	p	Kafdran $\bar{Y}_r$
P1	2.36	P1	2.43
P2	2.05	P2	2.11
P3	2.02	P3	2.08
P4	1.97	P4	2.03
P5	2.11	P5	2.17
P6	2.19	P6	2.24
P7	2.18	P7	2.22
P8	2.05	P8	2.09
P9	2.30	P9	2.34
P10	2.32	P10	2.37
P11	1.99	P11	2.07
P12	2.23	P12	2.32
P13	2.45	P13	2.54
P14	2.23	P14	2.32
P15	2.60	P15	2.65

Fig .8. Wr, Vr graphs for grain yield/main spike in the two generations and under both sites.

p	Izraa $\bar{Y}_r$	p	Kafdran $\bar{Y}_r$
P1	12.08	P1	12.81
P2	13.59	P2	14.41
P3	12.16	P3	12.90
P4	13.13	P4	13.93
P5	13.26	P5	14.06
P6	11.27	P6	11.73
P7	11.21	P7	11.67
P8	13.63	P8	14.18
P9	13.27	P9	13.80
P10	11.31	P10	11.77
P11	13.22	P11	14.30
P12	12.13	P12	13.11
P13	11.12	P13	12.03
P14	12.18	P14	13.17
P15	12.62	P15	13.13

Fig .9. Wr, Vr graphs for grain yield/plant in the two generations and under both sites.

p	Izraa $\bar{Y}_r$	p	Kafdran $\bar{Y}_r$
P1	34.80	P1	35.84
P2	40.27	P2	42.29
P3	35.50	P3	37.28
P4	33.59	P4	35.27
P5	42.08	P5	44.19
P6	37.96	P6	39.86
P7	36.86	P7	38.70
P8	31.44	P8	32.06
P9	33.29	P9	33.96
P10	32.54	P10	33.19
P11	39.77	P11	40.96
P12	19.74	P12	20.33
P13	24.36	P13	25.09
P14	28.82	P14	29.69
P15	18.53	P15	19.27

Fig .10. Wr, Vr graphs for straw yield/plant in the two generations and under both sites.

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