



GENETIC ANALYSIS OF DRY MATTER PARTITIONING IN WHEAT (*TRITICUM AESTIVUM* L.) UNDER DROUGHT CONDITIONS

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ABSTRACT

Seventy five diversified wheat germplasm accessions were screened under glass-house and field conditions in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during 2012-13 to assess the variability and genetic potential for drought tolerance. Selected seven genotypes SNI/PBW65 / 3 / KAUZ*2 / TRAP // KAUZ, TURACO / PRINIA, WEAVER // VEE/PJN / 3 / MILAN, KARIEGA, PF70402 / ALD'S' // PAT72 / 160 // ALD'S' / 3 / PEW'S', CONDOR'S' / ANA75 // CONDOR'S' / MUS'S' and PB96 / V87094 // MH97 were crossed in all possible combinations to study the inheritance pattern of dry matter partitioning traits under normal and drought conditions. The genetic material comprising F₁ crosses alongwith parents were evaluated under field conditions with three replications following completely randomized block design under both water regimes. Data regarding biological yield per plant, grain yield per plant and harvest index showed highly significant genotypic differences under normal i.e. 70.75**, 16.11** and 23.05** and under drought conditions i.e. 104.56**, 14.04** and 18.74**, respectively. The scaling test revealed partial adequacy for biological yield per plant and harvest index under both water regimes whereas it was partially adequate (as Wr+Vr values were non-significant) for grain yield per plant under normal and fully adequate under drought conditions. The values of additive component (D) were found significantly higher for biological yield per plant (53.42 and 60.03), grain yield per plant (6.68 and 7.07) and harvest index (6.85 and 8.05) under normal and drought, respectively indicating additive type of gene action with partial dominance as values of degree of dominance were found less than one (0.31-0.82) under both water regimes. Moderately high estimates of heritability were recorded ranging from 62-74 percent under both conditions. As the grain yield was found under control of additive genetic effects, hence early generation selection through pedigree or modified pedigree method was suggested to identify elite genotypes.

KEYWORDS: *Triticum aestivum*; wheat; genotypes; dry-matter partitioning; drought tolerance; gene action; yield traits; Pakistan.

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INTRODUCTION

Sustainable food production is major challenge to the scientists and policy makers to meet the future demands in view of global climate change and increasing population. Wheat (*Triticum aestivum* L.) is foremost among cereals and indeed among all crops, as direct and indirect source of food for human beings. It has been pointed out that global wheat requirement is predicted to enhance by about 1.6 percent per year while it will be 2 percent annually in developing countries like Pakistan (37). Consequently, the world average wheat yield enhancement is need of the day. The rate of genetic yield improvement is too low

to achieve desired results (39). Most of the land resources of the world are arid and semi-arid and limited water availability is one of the major causes affecting wheat productivity and sustainability (9). The problem of drought is acute in the developing world where 37 percent of wheat growing areas are semi-arid with low moisture as a limiting factor for high yield (35). In Pakistan, the irrigated area under wheat crop is 7 million hectares having mean productivity of 2500-2800 kg per hectare while rainfed area is 1.4 million hectares yielding only 500-1300 kg per hectare (26). The crop success in rainfed area depends upon the rainfall and its distribution.

As a result of global warming, temperature is continuously rising and water is depleting thus resulting in limiting agricultural productivity. In Pakistan, about one fourth of total cultivated area is drought affected and one third of the total wheat area depends on the erratic and unevenly distributed rainfall (44). The issue of shortage of water is aggravated with the passage of time. According to reports, there is a great difference between water availability and requirements in Pakistan. The demand for water is increasing @ 3 percent annually while the supply is decreasing one percent annually. Water availability has been decreased upto 70 percent since 1951 till 2008 (3, 6, 31). As a consequence, the growth rate of agriculture is also decreasing due to water shortages. Both drought and heat are becoming the major future threats in reducing wheat production in Pakistan.

Drought drastically affects plant growth and development and thus reduces crop productivity (33). Wheat plant possesses great genotypic variability for yield and yield components in response to water stress severity (12). The stability of genotypes regarding yield and yield related traits is highly desirable both as cultivar and as source parents for drought tolerance breeding programme. Pre-anthesis biomass production and harvest index are important attributes to enhance yield especially under stress environments. Significant differences among varieties for grain yield, biological yield and harvest index under water stress condition have been observed (10). It has also been found that grain yield significantly correlated with biological yield and harvest index under water stress conditions (13, 38).

Table 1. Parents selected for crossing.

Codes	Genotype	Source	Remarks
G ₁	SNI/PBW65/3/KAUZ*2/TRAP//KAUZ	CIMMYT	Sensitive
G ₂	TURACO/PRINIA	CIMMYT	Tolerant
G ₃	WEAVER//VEE/PJN/3/MILAN	CIMMYT	Tolerant
G ₄	KARIEGA	CIMMYT	Tolerant
G ₅	PF70402/ALD'S//PAT72/160// ALD'S'/3/PEW'S'	CIMMYT	Tolerant
G ₆	CONDOR'S//ANA75//CONDOR'S'/ MUS'S'	CIMMYT	Tolerant
G ₇	PB96/V87094//MH97	PAKISTAN	Sensitive

Exploring the genetic diversity, having sound knowledge of genetic mechanism of yield and related traits and the skill to combine better parents is the key to launch an effective breeding programme. Various biometrical procedures help plant breeders to ascertain information required for successful breeding programme. Hayman's graphical approach is a useful statistical technique, which provides information in early generations on genetic mechanisms involved in character expression; also suitable particularly for self-pollinated crops like wheat.

The present study was designed to find out the inheritance pattern of dry matter partitioning traits in wheat under normal and drought conditions.

MATERIALS AND METHODS

This study was carried out in the field area of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan during the year 2012-13. The area is situated in the North East Punjab (Pakistan) between longitude 73°-74° East, latitude 30°-31° North, with an elevation of 184 meters above sea level. Soil pH and EC of field was 7.5 and about 4.8 dS/m, respectively. Diversified wheat germplasm comprising 75 accessions belonging to national and international sources were collected from Wheat Research Institute, AARI, Faisalabad-Pakistan to explore the genetic variability present in the wheat germplasm for drought tolerance. As a consequence of assessment phases, five tolerant and two sensitive wheat genotypes (Table 1) were identified and sown for hybridization in all possible combinations in a complete diallel fashion.

At maturity, all spikes were harvested separately on the basis of various crosses. F_0 from all crosses were threshed manually keeping seed of each cross separately. The sowing of F_1 hybrids (42 genotypes) alongwith the parents (7 genotypes) was done in the field following RCBD replicated thrice in two sets. Each genotype was sown in two rows of 3 m length keeping the distances of 15 and 30 cm among plants and rows, respectively. After germination, only one seedling per hole was maintained. At the beginning and end of each replication, non-experimental lines were raised to minimize the border effects. All the standard agronomic and plant protection practices were adopted uniformly except irrigation. One set was normally irrigated while no irrigation was applied to the other set after germination. At maturity, ten plants were tagged at random for each parent and cross and for each replication under normal and drought conditions and data regarding biological yield and grain yield per plant were recorded. Harvest index percentage was calculated for each genotype using the formula given Here.

$$\text{Harvest index (\%)} = \frac{\text{Grain yield/plant}}{\text{Biological yield/plant}} \times 100$$

Analysis of variance technique according to Steel *et al.* (42) was applied to data to reveal significant differences among genotypes under study for both water regimes. For further analysis to calculate genetic components of variation, the statistical procedures given by Hayman (19, 20), Jinks (24) and Mather and Jinks (29) were applied.

RESULTS AND DISCUSSION

Highly significant differences ($P \leq 0.01$) were observed for total plant biomass, grain yield and harvest index as evident from mean squares from the analysis of variance for the indicated traits (Table 2). It is clear from data that sufficient genetic variability is present for the mentioned traits which is a pre-requisite for launching any breeding programme and for further genetic studies. Presence of significant variability permitted for further genetic analysis (19, 20, 24).

Table 2. Mean squares of various plant traits in a 7×7 diallel cross under normal and drought.

Traits (Normal)	Replications (df = 2)	Genotypes (df = 49)	Error (df = 96)
Biological yield	6.24	70.75**	24.72
Grain yield	0.213	16.11**	5.40
Harvest index	17.02	23.05**	13.06
Traits (Drought)			
Biological yield	26.05	104.56**	17.26
Grain yield	6.07	14.04**	3.27
Harvest index	6.40	18.74**	7.2

**Significant at $P \leq 0.01$

Validity of additive-dominance genetic model

The validity of additive-dominance model was tested by analysis of variance of $W_r + V_r$ and $W_r - V_r$ and joint regression test for the traits under study under normal and drought conditions (Table 3). The value of 'b' for all the traits i.e. biological yield per plant, grain yield per plant and harvest index deviated significantly from zero but not from unity under both water regimes. The unit slope of regression lines for the plant characters studied, justified the assumptions as required for model fitness (29). It also indicated the presence of intra allelic gene

interaction as well as independent distribution of genes among parents for the indicated traits alongwith action independency of genes (17).

The simple genetic model was fully adequate for grain yield per plant under drought as the values of mean squares displayed significant ($P \leq 0.05$) differences between the arrays ($W_r + V_r$) and non-significant differences within arrays ($W_r - V_r$) for grain yield under drought. It also pointed out the presence of dominance and absence of epistasis. The data were found partially adequate for grain yield under normal while for total plant biomass and harvest index under both the water regimes

as a result of non-significant ($P > 0.05$) differences between the arrays ($W_r + V_r$). Fully or partially

adequate data were further processed to find out the genetic components of variation.

Table 3. Scaling tests for adequacy of additive-dominance model for various traits under normal and drought

Traits (Normal)	Regression slope	Mean squares	Remarks	Joint regression(b)	Traits (Normal)	Regression slope
	b_0	b_1	W_r+V_r	$W_r - V_r$		
Biological yield	6.82*	0.42 ^{NS}	1108.3 ^{NS}	58.98 ^{NS}	Partially adequate	$b = 0.9416 \pm 0.1380$
Grain yield	3.08*	0.63 ^{NS}	42.90 ^{NS}	2.31 ^{NS}	Partially adequate	$b = 0.8296 \pm 0.2689$
Harvest index	3.28*	-0.36 ^{NS}	93.81 ^{NS}	21.76 ^{NS}	Partially adequate	$b = 0.9247 \pm 0.1176$
Traits (Drought)						
Biological yield	3.19*	0.30 ^{NS}	1577.75 ^{NS}	193.95 ^{NS}	Partially adequate	$b = 0.9130 \pm 0.2866$
Grain yield	5.04*	1.14 ^{NS}	39.44*	1.82 ^{NS}	Fully adequate	$b = 0.8152 \pm 0.1618$
Harvest index	6.07*	0.35 ^{NS}	23.44 ^{NS}	3.22 ^{NS}	Partially adequate	$b = 0.9448 \pm 0.1556$

*Significant at $P \leq 0.05$; NS=Non-significant, Where, b_0 : coefficient of regression deviating from zero, b_1 : coefficient of regression deviating from unity, b: regression coefficient, Mean squares are from analysis of variance of values ($W_r + V_r$ between arrays) and ($W_r - V_r$ within arrays)

Table 4. Components of genetic variation under both regimes

Components	Biological yield/plant		Grain yield/plant		Harvest index (%)	
	Normal	Drought	Normal	Drought	Normal	Drought
D	53.42 ± 2.2*	60.03 ± 5.18*	6.68 ± 0.69*	7.07 ± 0.67*	6.85 ± 1.29*	8.05 ± 0.21*
H_1	5.07 ± 5.17	22.39 ± 12.47*	1.08 ± 1.67	2.39 ± 1.62	1.12 ± 3.12	5.47 ± 0.50*
H_2	1.83 ± 4.56	19.32 ± 10.99	1.03 ± 1.47	2.29 ± 1.43	0.47 ± 2.75	3.76 ± 0.44*
F	25.11 ± 5.2*	20.29 ± 12.43	-0.18 ± 1.66	1.41 ± 1.61	1.09 ± 3.11	-2.63 ± 0.50*
(h^2)	-3.79 ± 3.06	-2.71 ± 7.38	-0.89 ± 0.99	-0.46 ± 0.96	-1.23 ± 1.84	-1.21 ± 0.30*
E	8.64 ± 0.83*	6.20 ± 1.83*	1.88 ± 0.25*	18 ± 0.24*	4.67 ± 0.46*	2.55 ± 0.07*
$\sqrt{H_1}/D$	0.31	0.61	0.40	0.58	0.77	0.82
$(\sqrt{4DH_1} + F) / \sqrt{4DH_1} - F$	7.43	1.77	0.93	1.41	1.49	0.67
$(H_2 / 4H_1)$	0.09	0.22	0.24	0.24	0.10	0.17
$h^2(n.s)$	0.63	0.66	0.62	0.62	0.64	0.74

D: additive variance, H_1 : Dominance variance, H_2 : Proportion of positive and negative genes in the parent, F: Relative frequency of dominant and recessive alleles in the parents, (h^2): Dominance effect (over all loci in heterozygous phase), E: Environmental Variance, $\sqrt{H_1}/D$: Mean degree of dominance, $(\sqrt{4DH_1} + F) / \sqrt{4DH_1} - F$: Proportion of dominant and recessive genes in the parents, $(H_2 / 4H_1)$: Proportion of genes with positive and negative effects in the parents, $h^2(n.s)$: Heritability narrow sense. (Note: The value of variance is significant (*) when the value exceeds 1.9996 after dividing with its standard error

Genetic analysis

Biological yield per plant: The estimation of genetic components of variation for biological yield revealed that additive (D) component was positive, significant and reasonably higher than non-additive (H) components pointing out the predominance of additive genetic effects for controlling the trait under both water regimes

(Table 4). The values of H_1 were found higher than H_2 indicating uneven distribution of genes among parents, supported by lower values (0.09 and 0.22) of $H_2 / 4H_1 < 0.25$ under both environments. The positive F value under both environments indicated the higher frequency of dominant genes than recessive ones, supported by the higher values (7.43 and 1.77) of $\sqrt{4DH_1} + F / \sqrt{4DH_1} - F$

– $F > 1$. The values of h^2 were found negative and non-significant under both environments indicating no major effect of heterozygous alleles for controlling the trait. The values of degree of dominance were found to be 0.31 and 0.61

(less than one) demonstrating partial dominance which was further supported by the interception of regression lines above the origin in graphs (Fig. 1 a-b) under normal and conditions.

Table 4. Components of genetic variation under both regimes

Components	Biological yield/plant		Grain yield/plant		Harvest index (%)	
	Normal	Drought	Normal	Drought	Normal	Drought
D	53.42 ± 2.2*	60.03 ± 5.18*	6.68 ± 0.69*	7.07 ± 0.67*	6.85 ± 1.29*	8.05 ± 0.21*
H_1	5.07 ± 5.17	22.39 ± 12.47*	1.08 ± 1.67	2.39 ± 1.62	1.12 ± 3.12	5.47 ± 0.50*
H_2	1.83 ± 4.56	19.32 ± 10.99	1.03 ± 1.47	2.29 ± 1.43	0.47 ± 2.75	3.76 ± 0.44*
F	25.11 ± 5.2*	20.29 ± 12.43	-0.18 ± 1.66	1.41 ± 1.61	1.09 ± 3.11	-2.63 ± 0.50*
(h^2)	-3.79 ± 3.06	-2.71 ± 7.38	-0.89 ± 0.99	-0.46 ± 0.96	-1.23 ± 1.84	-1.21 ± 0.30*
E	8.64 ± 0.83*	6.20 ± 1.83*	1.88 ± 0.25*	18 ± 0.24*	4.67 ± 0.46*	2.55 ± 0.07*
$\sqrt{H_1}/D$	0.31	0.61	0.40	0.58	0.77	0.82
$(\sqrt{4DH_1} + F) / (\sqrt{4DH_1} - F)$	7.43	1.77	0.93	1.41	1.49	0.67
$(H_2 / 4H_1)$	0.09	0.22	0.24	0.24	0.10	0.17
$h^2(n.s)$	0.63	0.66	0.62	0.62	0.64	0.74

D: additive variance, H_1 : Dominance variance, H_2 : Proportion of positive and negative genes in the parent, F: Relative frequency of dominant and recessive alleles in the parents, h^2 : Dominance effect (over all loci in heterozygous phase), E: Environmental Variance, $\sqrt{H_1}/D$: Mean degree of dominance, $(\sqrt{4DH_1} + F) / (\sqrt{4DH_1} - F)$: Proportion of dominant and recessive genes in the parents, $(H_2 / 4H_1)$: Proportion of genes with positive and negative effects in the parents, $h^2(n.s)$: Heritability narrow sense. (Note: The value of variance is significant (*) when the value exceeds 1.9996 after dividing with its standard error

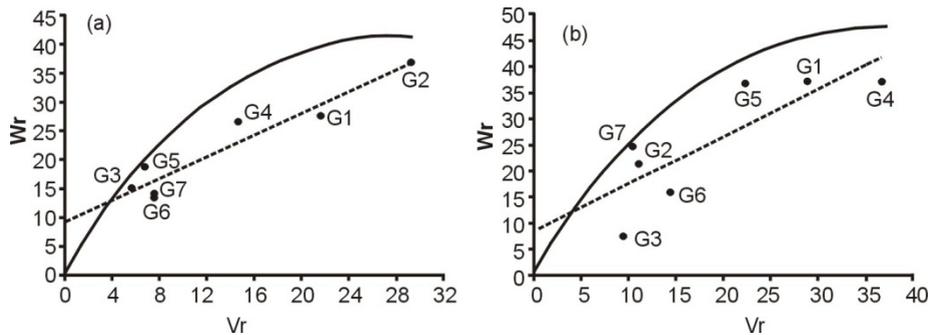


Fig. 1(a-b): Covariance/variance W_r/V_r graph for biological yield/plant under (a) normal and (b) drought conditions

The graphical illustration regarding distribution of array points over regression for biological yield showed that genotype G_3 was found nearest to the point of origin. Hence, it possessed the most number of dominant genes followed by G_6 under both conditions (Fig. 1a-b). Genotype G_2 was found away from the point of origin having abundant number of recessive genes followed by G_1 under normal while, G_4 got that position under drought followed by G_1 . The additive with partial dominance control of biological yield per plant in wheat has been reported by Farooq (16)

while over dominance was reported by Akhtar (5) under rainfed condition. The difference in results might be due to the different genetic material. Heritability is directly attributed to genetic improvement of the trait under consideration. The moderately high values of narrow sense heritability were observed for biological yield per plant under normal (63%) and drought (66%). High narrow sense heritability estimates show that the trait is under additive genetic control. Low values of heritability for biological yield were found by Subhani *et al.* (43) indicating the

dominance genetic effects controlling the trait.

Grain yield per plant: The additive (D) component was found positive and significant while non-additive (H) components were positive but non-significant under both water regimes (Table 4). However, the values of D were found reasonably high pointing out the predominance of additive genetic effects for grain yield per plant under both conditions. The almost equal values of H_1 were noted with H_2 under both conditions indicating even distribution of genes, supported by the values of $H_2 / 4H_1$ (0.24 and 0.24) which were almost equal to 0.25. The negative F value under normal pointed out higher frequency of recessive genes, supported by the lower value (0.93) of $\sqrt{4DH_1 + F} / \sqrt{4DH_1 - F}$ which was less than one. The positive but non-significant (F) value under drought indicated the more frequency of

dominant genes than recessive ones, supported by the higher value (1.41) of $\sqrt{4DH_1 + F} / \sqrt{4DH_1 - F}$ which was greater than one. The values of h^2 were found negative and non-significant under both environments indicating no major role of heterozygous loci for the trait under study. The degree of dominance was found less than one (0.40 and 0.58) demonstrating partial dominance and it was further illustrated by the interception of regression lines over the origin in the figures for grain yield per plant (Fig. 2a-b) under normal and drought conditions. The moderately high values of heritability (h^2) were observed for grain yield per plant under normal (62%) and drought (62%). Earlier researchers (7, 18) reported that grain yield per plant is a multigenic trait having low heritability and is greatly influenced by the environment.

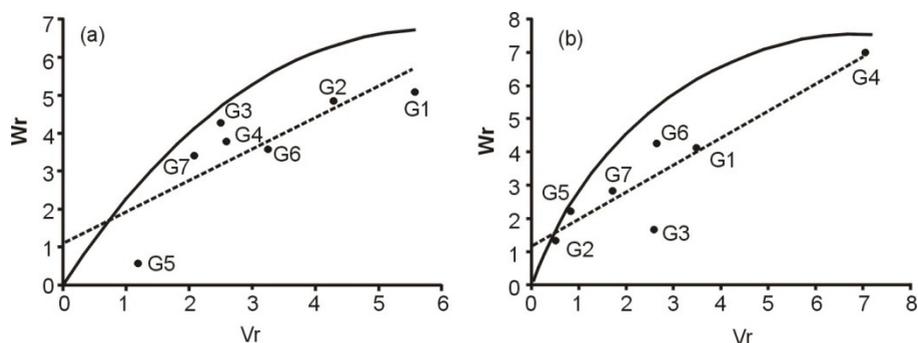


Fig. 2(a-b): Covariance/variance W_r/V_r graph for grain yield/plant under (a) normal and (b) drought conditions.

Thus, selection of wheat varieties on the basis of grain yield is difficult and needs to be delayed. But some of the researchers reported moderate (23) and high heritability estimates for grain yield per plant (2, 36) in wheat. The graphical representation of array points over regression line under normal condition (Fig. 2a) showed that being nearest to the origin, the genotype G_5 had the most number of dominant genes while, genotype G_1 displayed abundant number of recessive genes for the trait under consideration. Likewise, genotype G_2 was found nearest to the origin having maximum number of dominant genes followed by genotypes

G_5 and G_4 got maximum number of recessive genes being far away from the point of origin under drought (Fig. 2b). Additive control of grain yield under both irrigated and stress conditions has also been reported by Farooq (15, 16) and Akhtar (5) in wheat and Damborsky *et al.* (11), Mani *et al.* (28), Betran *et al.* (8) and Afarinesh *et al.* (1). In maize, contrastingly, non-additive type of genetic effects were found for this trait by Farooq *et al.* (14), Mahpara *et al.* (27) and Akbar *et al.* (4) in wheat and Rahim *et al.* (34) in maize. Over-dominance type of gene action was reported by Khan *et al.* (25), Inamullah *et al.* (22), and Hussain

et al. (21) in wheat while, Yousaf (45) in maize. The deviation regarding genetic control of grain yield by various researchers might be due to different genetic material having different genes controlling the trait, variation in allelic and non-allelic and environmental interactions with genes.

Harvest index: The estimation of genetic components of variation for harvest index revealed that the additive (D) component was positive and significant under both water regimes whereas, non-additive (H) components were significant only in case of drought (Table 4). However, values of D were reasonably higher than H pointing out the predominance of additive genetic effects for harvest index under both conditions. The values of H_1 were found higher than H_2 indicating uneven distribution of genes, supported by lower values (0.10 and 0.17) of $H_2 / 4H_1 < 0.25$ under both environments. The frequency of dominant genes was found to be higher than the recessive genes under normal as the value of F was positive, also supported by the

higher value (1.49) of $\sqrt{4DH_1 + F} / \sqrt{4DH_1 - F} > 1$. The negative F value under drought indicated the higher frequency of recessive genes, supported by the lower value (0.67) of $\sqrt{4DH_1 + F} / \sqrt{4DH_1 - F} < 1$. The values of h^2 were found negative pointing out no importance of heterozygous loci for harvest index under both environments. The values of degree of dominance were found to be 0.77 and 0.82 (less than one) demonstrating partial dominance and it was further explained by the interception of regression lines in the graphs (Fig. 3a-b) under normal and drought, respectively. Regarding the graphical representation of array point over regression line, being nearest to the origin, genotype G_7 possessed the most number of dominant genes under both conditions while in case of abundant number of recessive genes, genotypes G_4 and G_6 got that position as they were found away from the origin under normal and drought, respectively (Fig. 3a-b).

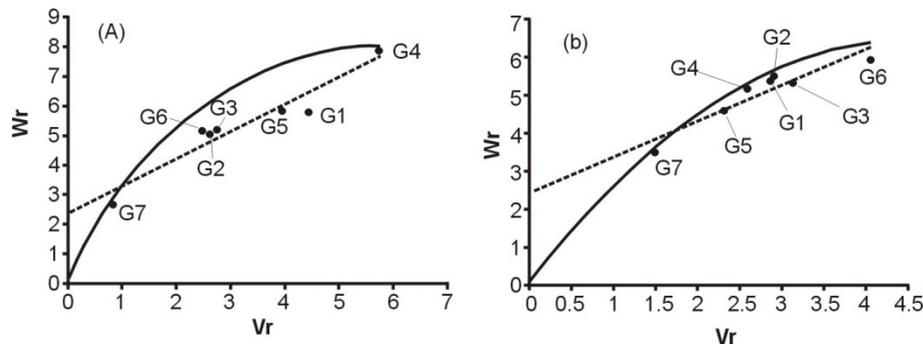


Fig. 3(a-b): Covariance/variance W_r/V_r graph for harvest index under (a) normal and (b) drought conditions

The moderately high values of heritability $_{(n.s)}$ were observed for harvest index under normal (64%) and drought (74%). Higher values of heritability were also found by Jatoi *et al.* (23) under both water regimes. The traits having high values of heritability showed better response to selection hence better chances of improvement. The additive with partial dominance control of harvest index in wheat has been reported by Srivastava

and Nema (41), Yildirim *et al.* (46), Mishra *et al.* (30), Ullah (32) and Farooq (16) while over dominance was reported by Singh and Singh (40) and Akhtar (5). The genetic information obtained would be helpful in improving harvest index under water stress conditions and high heritability values for harvest index will help in finding elite genotypes through early selection in the segregating generations.

CONCLUSION

The presence of ample amount of genetic variability in wheat genetic material after crossing provide more chances of improvement in the latter generations. The presence of additive genetic effects alongwith moderately high narrow sense heritability estimates revealed greater chances of genetic improvement for these traits through selection in early segregating generations. These results will be supportive for future breeding programmes aiming to develop drought tolerant genotypes.

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