

## GENETIC STUDIES OF BIOMASS PARTITIONING IN WHEAT UNDER WATER STRESS CONDITIONS

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### ABSTRACT

Seven diverse wheat genotypes were selected and crossed in all possible combinations to study the inheritance pattern of dry matter partitioning traits under normal and drought conditions. The F<sub>1</sub> hybrids along with their parental accessions were evaluated under field conditions with three replications following completely randomized block design under both water regimes. Data regarding biological yield plant<sup>-1</sup>, grain yield plant<sup>-1</sup> and harvest index were recorded. Significant genotypic differences were observed among genotypes for the traits under study. The scaling test revealed partial adequacy of the data for all the traits under both water regimes except grain yield plant<sup>-1</sup> under drought condition where it was found fully adequate. All the traits exhibited additive type of gene action with partial dominance under both regimes. Moderately high estimates of heritability were recorded. Early generation selection through pedigree or modified pedigree method was suggested for the traits controlled by additive gene action.

**Key words:** Wheat, grain and biological yields, harvest index, gene action, drought.

### INTRODUCTION

Sustainable food production to meet the future demands in the scenario of global climate change and increasing population is the major challenge to the scientists and policy makers. 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% per year while it will be 2% annually in developing countries like Pakistan (Rosegrant *et al.*, 1997). 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 (Sayre *et al.*, 1997). 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 (Boyer, 1982). The problem of drought is acute in the developing world where 37% of wheat growing areas are semi-arid with low moisture as a limiting factor for high yield (Rajaram, 2001). In Pakistan, the irrigated area under wheat crop is seven million hectares having mean productivity 2500-2800 kg ha<sup>-1</sup> while rainfed area is 1.4 million hectares yielding only 500-1300 kg ha<sup>-1</sup> (Kisana, 2007). The crop success in rainfed area depends upon the rainfall and its distribution. Uncertain rainfalls and frequent crop failures during dry periods discourage input use. The dry land wheat yields, therefore, depress the already low overall national average (2.8 tons ha<sup>-1</sup>).

As a result of global warming, temperature is continuously rising and water is depleting. 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. 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 requirement in Pakistan. The demand for water is increasing at the rate of 3% while the supply is decreasing at the rate of 1% annually. Water availability has been decreased up to 70% since 1951 till 2008 (Ahmed *et al.*, 2009; Mustafa, 2011; Ali *et al.*, 2013). 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 (Rabbani *et al.*, 2003). Wheat plant possesses great genotypic variability for yield and yield components in response to water stress severity (Dencic *et al.*, 2000). 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 (Chowdhary, 1990). It has also been found that grain yield significantly correlated with biological yield and harvest index under water stress conditions (Desalgn *et al.* 2000; Satish and Thakur, 2004).

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 for the development drought tolerant wheat varieties. 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 with the objective to find out new genetic combinations for drought tolerance through diallel mating design and the inheritance pattern of dry matter partitioning in wheat.

## MATERIALS AND METHODS

The research work presented was carried out at the University of Agriculture, Faisalabad, Pakistan situated between longitude 73°-74° East, latitude 30°-31° North, with an elevation of 184 meters above sea level. Soil pH and EC of the field was 7.5 and about 4.8 dSm<sup>-1</sup>, respectively. Seven wheat genotypes were selected and sown during the crop season 2012-13 for hybridization in all possible combinations in a complete diallel fashion. The selected parents have been detailed in Table 1. At maturity, all the spikes were harvested separately on the basis of various crosses. F<sub>0</sub> from all the crosses were threshed manually keeping seed of each cross separately. The sowing of 42 F<sub>1</sub> hybrids along with seven parents was done in the field following randomized complete block design 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 plant<sup>-1</sup> were recorded. Harvest index percentage was calculated for each of the genotype using the formula given as under;

$$\text{Harvest index (\%)} = \frac{\text{Grain yield plant}^{-1}}{\text{Biological yield plant}^{-1}} \times 100$$

Analysis of variance technique according to Steel *et al.* (1997) was applied to data to reveal significant differences among genotypes under study for both the water regimes. For further analysis to calculate genetic components of variation, the statistical procedures given by Hayman (1954a, b) and Jinks (1954) and by Mather and Jinks (1982) were applied.

## RESULTS AND DISCUSSION

**Genetic Analysis:** Highly significant (P = 0.01) differences 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 (Steel *et al.*, 1997). It is clear from the table 2 that sufficient genetic variability is present for the mentioned traits which has been a pre-requisite for launching any breeding program and for further genetic studies (Singh and Chaudhary, 1999). Existence of significant differences among wheat genotypes for the above mentioned traits has been reported by Inamullah *et al.*, (2006), Golparvar (2014) and Ahmad *et al.*, (2016). Presence of significant variability permitted for further genetic analysis (Hayman, 1954a, b; Jinks, 1954.)

**Tests for validity of Additive-Dominance Genetic Model:** The two scaling tests, joint regression analysis and analysis of variance of (W<sub>r</sub> + V<sub>r</sub>) and (W<sub>r</sub> – V<sub>r</sub>) were performed to test the validity for additive-dominance genetic model for indicated plant traits of wheat under normal and drought (Table 3). The value of 'b' for all the traits deviated significantly from zero but not from unity under both water regimes. The unit slope of regression lines for all the plant characters studied, justified the assumptions as required for model fitness (Mather and Jinks, 1982). It also indicated the presence of intra-allelic gene interaction as well as independent distribution of genes among parents for the indicated traits along with action independency of genes (Irshad *et al.*, 2014).

According to the second scaling test to find out the adequacy of data, the values of mean squares displayed significant (P 0.05) differences between the arrays (W<sub>r</sub> + V<sub>r</sub>) and non-significant differences within the arrays (W<sub>r</sub> – V<sub>r</sub>) for grain yield plant<sup>-1</sup> under drought conditions. It can be concluded that the simple genetic model was fully adequate for grain yield plant<sup>-1</sup> under drought and it also pointed out the presence of dominance and absence of epistasis. Irshad *et al.*, (2014) reported has also reported fully adequacy of data for grain yield under stress environment. 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<sub>r</sub> + V<sub>r</sub>) indicating the presence of dominance and non-allelic gene interactions (Shakeel *et al.*, 2011; Farooq *et al.*, 2015). Fully or partially adequate data were further processed to find out the genetic components of variation.

**Estimation of Genetic Components of Variation:** The estimation of genetic components of variation for biological yield plant<sup>-1</sup> (Table 4) revealed that the additive component 'D' was positive, significant and reasonably higher than dominance components 'H' pointing out the predominance of additive genetic effects

for controlling the trait under both water regimes (Golparvar, 2014; Irshad *et al.*, 2014). The values of 'H<sub>1</sub>' were found higher than 'H<sub>2</sub>' 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 component  $H_2 / 4H_1 = 0.25$  indicates the symmetrical proportion of negative and positive dominant genes among parents (Farshadfar *et al.*, 2011). 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  $4DH_1 + F / 4DH_1 - F > 1$ . The values of dominance effects 'h<sup>2</sup>' 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 nature of inheritance for biological yield under both moisture conditions.

For grain yield plant<sup>-1</sup>, the additive component was found positive and significant while non-additive 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 plant<sup>-1</sup> under both conditions. The almost equal values of 'H<sub>1</sub>' were noted with 'H<sub>2</sub>' under both conditions indicating even distribution of genes among parents, supported by the values (0.24 and 0.24) of  $H_2 / 4H_1$  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  $4DH_1 + F / 4DH_1 - F$  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  $4DH_1 + F / 4DH_1 - F$  which was greater than one. The values of 'h<sup>2</sup>' were found negative and non-significant under both environments indicating no major role of heterozygous loci for the trait under study. The partial dominance mode of inheritance for grain yield was observed as it was evident from the values of degree of dominance less than one (0.40 and 0.58) under both water regimes.

The estimation of genetic components of variation for harvest index revealed that the additive component 'D' was positive and significant under both water regimes whereas, non-additive components 'H' were significant only in case of drought (Table 4). However, the 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<sub>1</sub>' were found higher than 'H<sub>2</sub>' 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  $4DH_1 + F / 4DH_1 - F > 1$ . The negative 'F' value under drought indicated the higher frequency of recessive genes, supported by the lower value (0.67) of  $4DH_1 + F / 4DH_1 - F < 1$ . The values of 'h<sup>2</sup>' 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 type of inheritance pattern for harvest index.

**Graphical Analysis:** The object of the graphical analysis was to evaluate the genetic relationship among parents and mode of inheritance of traits under question. The interception of regression line on the graph represents degree of dominance and the distribution of array points around regression line provided the frequency of dominant and recessive genes among parents (Singh and Chaudhary, 1999). The graphical representation of the traits under consideration is shown in the figures from 1-3(a-b) under both the water regimes. The additive with partial dominance genetic control was observed for all the traits under both the conditions as the regression lines intercept the W<sub>r</sub>-axis above the origin. The additive with partial dominance type of gene action for biological yield plant<sup>-1</sup> in wheat has been reported by Farooq (2010), Golparvar, (2014) and Irshad *et al.*, (2014), for grain yield under both irrigated and stress conditions in wheat was reported by Farooq (2008), Akhtar (2010), Farooq (2010) and for harvest index by Mishra *et al.*, (1996), Ullah (2004) and Inamullah *et al.*, (2006).

The graphical illustration regarding distribution of array points over regression for biological yield plant<sup>-1</sup> showed that genotype G<sub>3</sub> was found nearest to the point of origin. Hence, it possessed the most number of dominant genes followed by G<sub>6</sub> under both the conditions (Figure 1a-b). Genotype G<sub>2</sub> was found away from the point of origin having abundant number of recessive genes followed by G<sub>1</sub> under normal while, G<sub>4</sub> got that position under drought followed by G<sub>1</sub>. The graphical representation for grain yield plant<sup>-1</sup> under normal condition (Figure 2a) showed that being nearest to the origin, the genotype G<sub>5</sub> had the most number of dominant genes while, genotype G<sub>1</sub> displayed abundant number of recessive genes for the trait under consideration. Likewise, genotypes G<sub>2</sub> was found nearest to the origin having maximum number of dominant genes followed by genotype G<sub>5</sub> and genotype G<sub>4</sub> got maximum number of recessive genes being far away from the point of origin under drought (Figure 2b). Regarding the graphical representation of array points over regression line for harvest index, being nearest to the origin, genotype G<sub>7</sub> possessed the most number of dominant genes under both conditions while in case of abundant number of recessive genes, genotypes G<sub>4</sub> and G<sub>6</sub> got that position as they were

found away from the origin under normal and drought, respectively (Figure 3a-b).

**Table 1. Parental genotypes selected for crossing.**

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

**Heritability:** Heritability is the extent of transmissible variability from one generation to the next. It is equal to the ratio of genetic variance to total phenotypic variance for a plant trait. Heritability is the component of the genetic advancement of a trait through selection (Hanson, 1963). The moderately high values of narrow sense heritability were observed for biological yield plant<sup>-1</sup> (63

and 66%), for grain yield plant<sup>-1</sup> (62 and 62%) and for harvest index (64 and 74%) under normal and drought conditions, respectively. High narrow sense heritability values in wheat were also reported for biological yield by Golparvar, (2014), for grain yield by Farooq *et al.*, (2015) and Ahmad *et al.*, (2016) and for harvest index by Irshad *et al.*, (2014).

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

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 0.01

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

Traits (Normal)	Regression slope		Mean squares		Remarks	Joint regression(b)
	b <sub>0</sub>	b <sub>1</sub>	Wr + Vr	Wr - Vr		
Biological yield	6.82*	0.42 <sup>NS</sup>	1108.3 <sup>NS</sup>	58.98 <sup>NS</sup>	Partially adequate	b = 0.9416±0.1380
Grain Yield	3.08*	0.63 <sup>NS</sup>	42.90 <sup>NS</sup>	2.31 <sup>NS</sup>	Partially adequate	b = 0.8296±0.2689
Harvest Index	3.28*	-0.36 <sup>NS</sup>	93.81 <sup>NS</sup>	21.76 <sup>NS</sup>	Partially adequate	b = 0.9247±0.1176
Traits (Drought)						
Biological yield	3.19*	0.30 <sup>NS</sup>	1577.75 <sup>NS</sup>	193.95 <sup>NS</sup>	Partially adequate	b = 0.9130±0.2866
Grain Yield	5.04*	1.14 <sup>NS</sup>	39.44*	1.82 <sup>NS</sup>	Fully adequate	b = 0.8152±0.1618
Harvest Index	6.07*	0.35 <sup>NS</sup>	23.44 <sup>NS</sup>	3.22 <sup>NS</sup>	Partially adequate	b = 0.9448±0.1556

\*=Significant at P 0.05; NS=Non-significant.

Where, b<sub>0</sub>: coefficient of regression deviating from zero, b<sub>1</sub>: coefficient of regression deviating from unity, b: regression coefficient, Mean squares are from analysis of variance of values (Wr + Vr between arrays) and (Wr-Vr within arrays)

**Table 4. Components of genetic variation under normal and drought conditions.**

Components	Biological Yield plant <sup>-1</sup>		Grain Yield plant <sup>-1</sup>		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 <sub>1</sub>	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 <sub>2</sub>	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 <sup>2</sup> )	-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*
H <sub>1</sub> /D	0.31	0.61	0.40	0.58	0.77	0.82
( 4DH <sub>1</sub> + F/ 4DH <sub>1</sub> - F)	7.43	1.77	0.93	1.41	1.49	0.67
(H <sub>2</sub> / 4H <sub>1</sub> )	0.09	0.22	0.24	0.24	0.10	0.17
h <sup>2</sup> (n.s)	0.63	0.66	0.62	0.62	0.64	0.74

D: additive variance, H<sub>1</sub>: Dominance variance, H<sub>2</sub>: Proportion of positive and negative genes in the parent, F: Relative frequency of dominant and recessive alleles in the parents, h<sup>2</sup>: Dominance effect (over all loci in heterozygous phase), E: Environmental Variance, H<sub>1</sub>/D: Mean degree of dominance, ( 4DH<sub>1</sub> + F / 4DH<sub>1</sub> - F): Proportion of dominant and recessive genes in the parents, (H<sub>2</sub> / 4H<sub>1</sub>): Proportion of genes with positive and negative effects in the parents, h<sup>2</sup>(n.s): Heritability narrow sense. (Note: The value of variance is significant (\*) when the value exceeds 1.9996 after dividing with its standard error

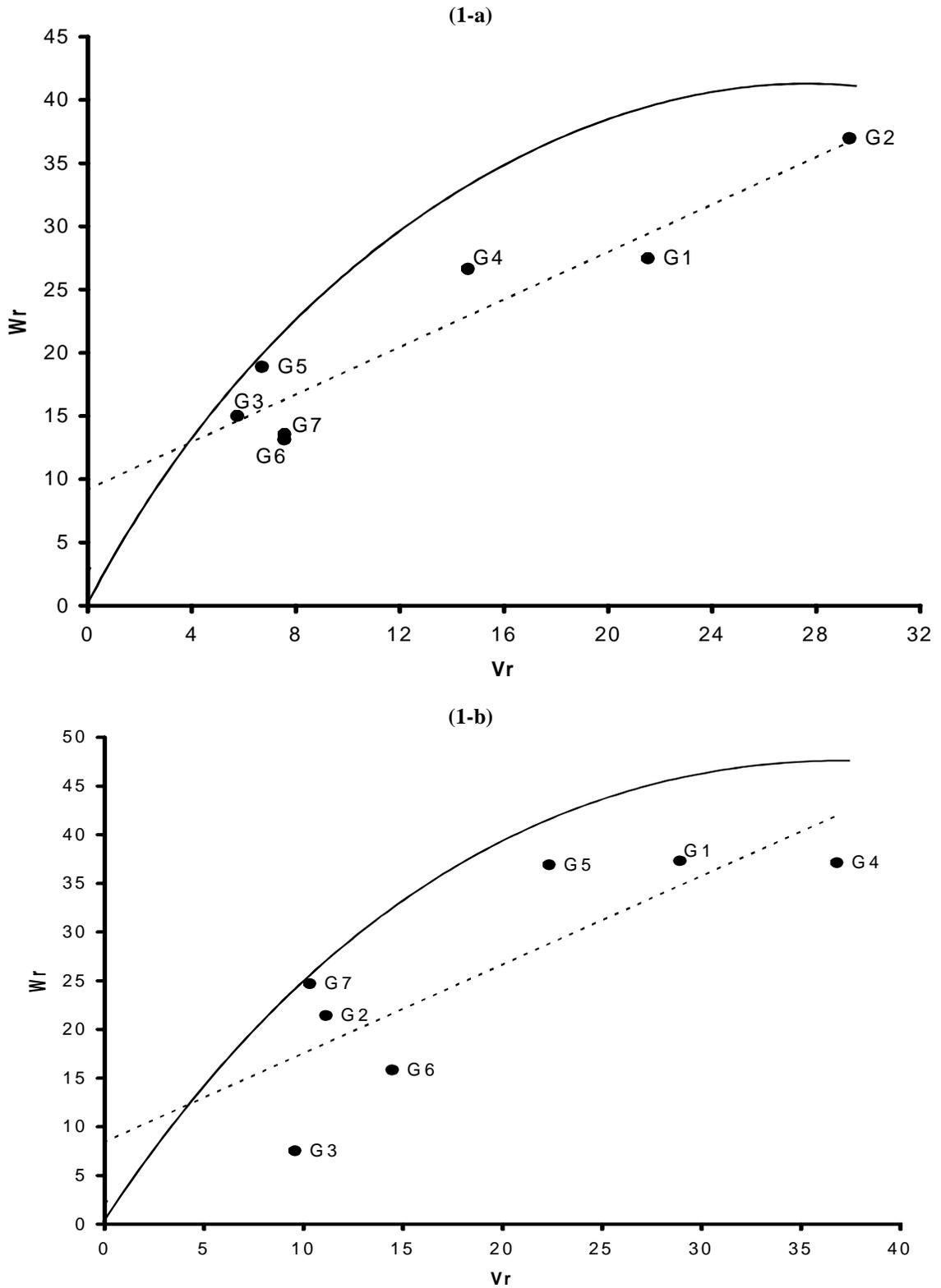


Fig. 1(a-b):  $Wr/Vr$  graph for biological yield  $\text{plant}^{-1}$  under (a) normal and (b) drought conditions.

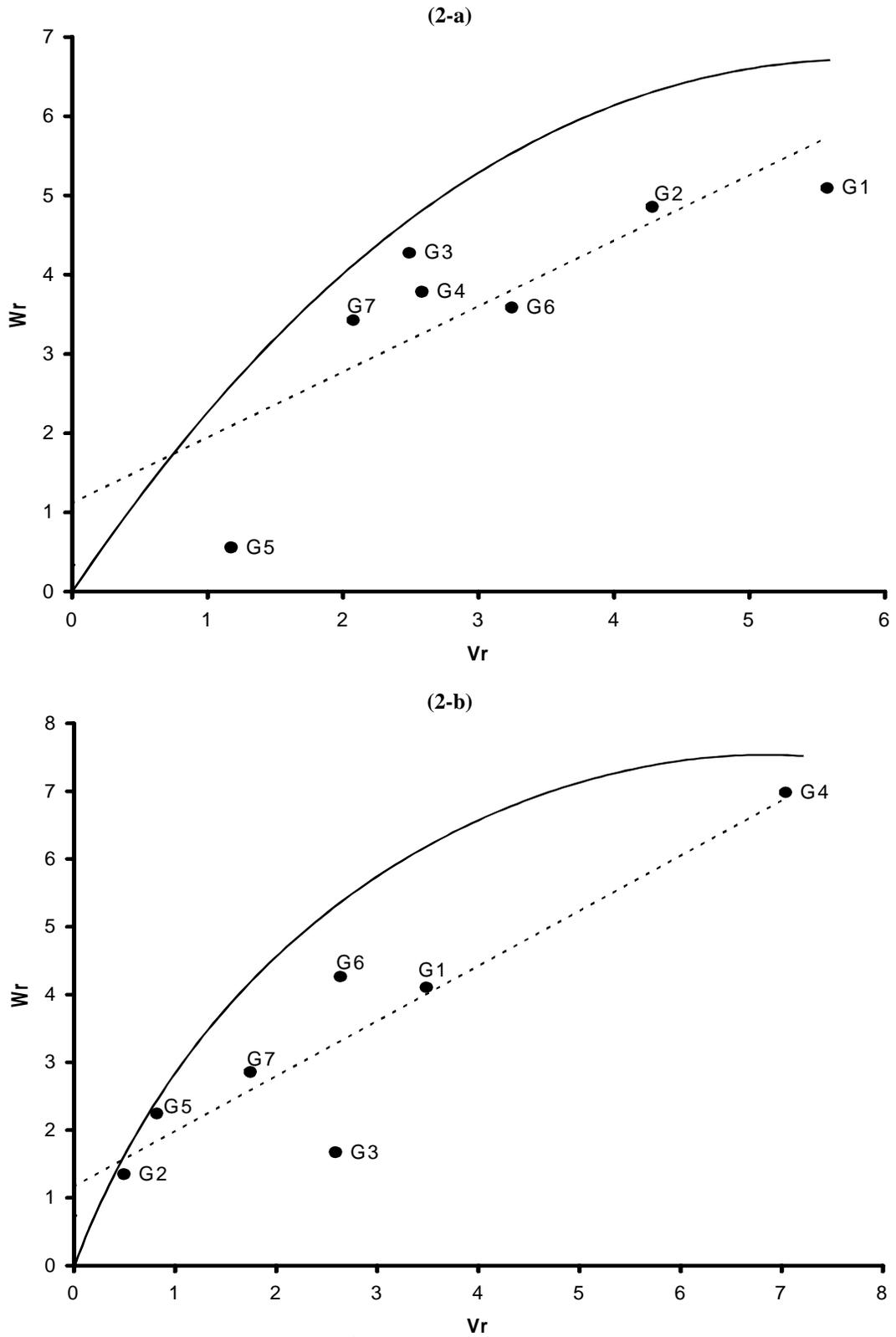


Fig. 2(a-b):  $W_r/V_r$  graph for grain yield  $\text{plant}^{-1}$  under (a) normal and (b) drought conditions.

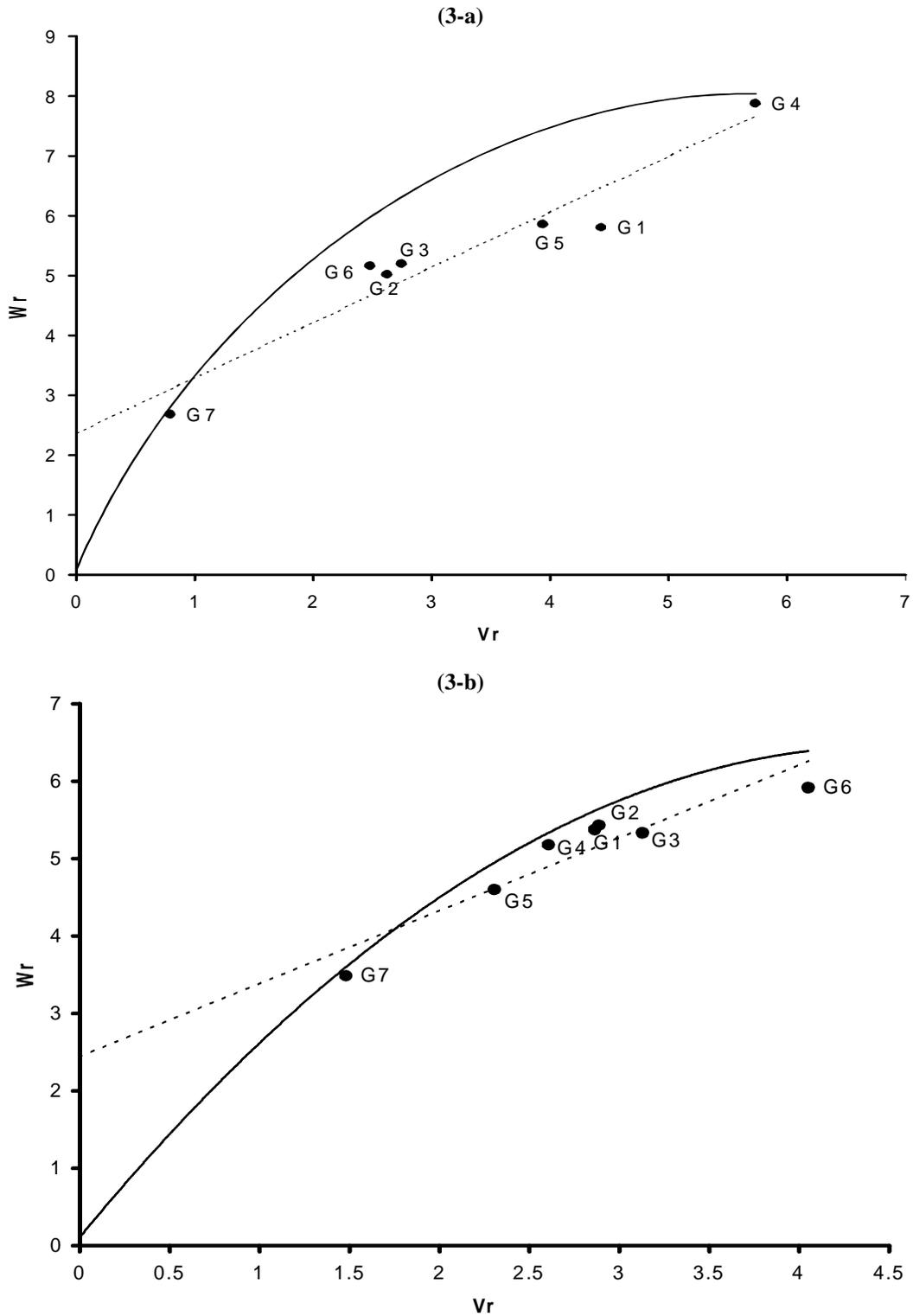


Fig. 3(a-b).  $W_r/V_r$  graph for harvest index under (a) normal and (b) drought conditions.

**Conclusion:** Results revealed greater amount of genetic variability in wheat genetic material studied indicating better chances for improvement for water stress tolerance following selection in later generations. All the traits

studied were found to be under control of additive genetic effects along with partial dominance and moderately high narrow sense heritability estimates revealed greater chances of genetic improvement for these traits. Selection

in early segregating generations can be practiced to improve these traits through pedigree or modified pedigree method of selection. These results will be supportive for future breeding programs aiming to develop drought tolerant genotypes.

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