

Genetic Component and Wr-Vr Graph Analysis in Bread Wheat (*Triticum aestivum* L.) Genotypes

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ABSTRACT

This study was performed to investigate gene actions for some important traits using half diallel mating design in wheat at research farm of Lovely Professional University. Seven wheat genotypes viz., MP 1203, LOK 1, HD 2932, MP 3173, HI 1544, MP 4010 and GW 273 were crossed in all possible combinations except reverse during 2017-18 cropping season. The resultant F₁ hybrids were planted following a randomized complete block design using three replications in the subsequent wheat growing season of 2018-19. Genetic component analysis found that additive effect was non-significant but dominance effect (H₁) was significant and greater in magnitude indicating dominance gene action for protein content and grain yield/plant. All traits under study showed that the value of regression coefficient slope deviated significantly from zero but not from unity, which indicated absence of non-allelic interaction. Regression line intercepted Wr axis below the origin, which indicated the presence of over dominance for days to 50% heading, days to maturity, number of productive tillers/plant, ear length, ear weight, number of ears/plant, biological yield/plant, harvest index and grain yield/plant. The value of mean degree of dominance was greater than one, indicating availability of over dominance for all traits except plant height and number of spikelets/ear.

Key words : Genetic component, Wr-Vr graph, wheat

INTRODUCTION

Wheat (*Triticum aestivum* L.) is a highly self-pollinated crop belonging to Poaceae family. *T. aestivum* is hexaploid (2n = 6x = 42) having basic chromosome number (x) 7. It is major staple food in India and provides 20% of total food calories to global level (Msundi *et al.*, 2021). For the wheat improvement programmes, the knowledge of gene action controlling the desired traits to be improved helps to develop an effective breeding program. Analysis of quantitative variation to estimate additive, dominance and additive x additive epistasis in most of self-pollinated crops is proposed (Kamara *et al.*, 2021). Half diallel crossing pattern among the genotypes is to determine the nature and magnitude of genotypes. Gene action not only helps breeder in selecting desirable parental genotypes and their crosses

but also gives an opportunity to select most effective technique among the hybrid populations for separation of superior genotypes in a symmetric way. However, it remains unutilized in the wheat crop. The future scope of hybrid technology in wheat depends on the male sterility systems, floral biology, level of combining ability, heterosis and its exploitation at commercial level that may be useful in breaking yield barriers and enhancing the productivity in the major wheat belt of the country (Gunasekaran *et al.*, 2020).

MATERIALS AND MEHTODS

The experimental trial consisted of seven bread wheat varieties (MP-1203, LOK-1, HD-2932, MP-3173, HI-1544, MP-4010 and GW-273) and their possible 21 hybrids made by half diallel design. These were grown in RBD with

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one standard check variety (HD-3987) in three replications at Research Farm, Lovely Professional University during *rabi* season 2018-19. Five plants were randomly taken from each entry in each of three replications and tagged for observations. The observations were recorded on whole plot basis for morphological traits.

RESULTS AND DISCUSSION

Genetic component analysis was observed on diallel crosses and its parents using yield and yield attributing traits. Results have been given in Tables 1 and 2. This approach was applied to know the allelic content of the parent used

in the diallel with respect to morphological and quality traits. In addition, this analysis also furnished information regarding the presence or absence of epistasis.

Genetic component analysis found that additive effect was non-significant but dominance effect (H_1) was significant and greater in magnitude which indicated dominance gene action for ear length, ear weight, number of grains/ear, 1000-grain weight, harvest index, canopy temperature, protein content and grain yield/plant. And H_2 genetic variance was significant which indicated symmetrically distribution of alleles in plant height, number of spikelets/ear and number of ears/plant. But in some traits,

Table 1. Proportion of genetic components of variation for F_1 generation of wheat

Parameters/Components	Days to 50% heading	Days to maturity	Plant height (cm)	No. of productive tillers/plant	No. of spikelets/ear	Ear length (cm)	Ear weight (g)	No. of ears/plant
D	3.23*	5.87*	26.14*	11.34*	3.39*	-0.13	-0.08	8.78*
F	-1.69	5.35	-31.86	14.08*	-1.43	-0.43	-0.17	13.11
H_1	8.21*	24.40*	-2.99	13.94*	-0.15	1.30*	0.47*	17.24*
H_2	7.00*	21.77*	-0.12	9.52*	0.16	1.33*	0.54*	12.46
h_2	0.20	10.75*	-3.26	1.60	-0.93	1.94*	0.62*	1.93
E	1.14*	2.05*	14.19*	3.21*	1.95*	0.35*	0.11*	3.57*
$\sqrt{(H_1/D)}$	1.60	2.04	0.34	1.11	0.21	3.17	2.46	1.40
$H_2/4H_1$	0.21	0.22	0.01	0.17	-0.26	0.26	0.29	0.18
$[\sqrt{4DH_1} + F/\sqrt{4DH_1}] - F$	0.72	1.58	-0.29	3.54	0.00	0.31	0.39	3.28
h_2/H_2	0.03	0.49	26.42	0.17	-5.84	1.46	1.16	0.16
h^2 (ns)	0.52	0.17	0.66	0.13	0.53	0.16	0.04	0.03

*Significant at $P=0.05$. NS-Not Significant.

Additive effect : D-Mean Fr over arrays, F-Dominance effect, H_1 -Component of genetic variance due to dominance effects corrected for the genes distributed, H_2 -Overall dominance effects of heterozygous loci, h_2 -Environmental component, E - $\sqrt{(H_1/D)}$: Mean degree of dominance, $H_2/4H_1$ -Proportion of gene with +ve and -ve effects, $[\sqrt{4DH_1} + F/\sqrt{4DH_1}] - F$ -Ratio of dominant and recessive genes and h_2/H_2 -Number of gene groups.

Table 2. Proportion of genetic components of variation for F_1 generation of wheat

Parameters/Components	No. of grains/ear	1000-grain weight (g)	Biological yield/plant	Harvest index (%)	Canopy temperature	Chlorophyll content	Protein content (%)	Grain yield/plant
D	35.30	-1.97	331.40*	0.91	0.37	3.35	0.07	20.37
F	-6.47	4.72	163.26	2.93	0.83	2.04	0.21	13.16
H_1	203.15*	114.54*	1351.38*	45.92*	3.37*	24.01	8.56*	142.49*
H_2	206.97*	107.30*	1292.70*	36.79*	2.59*	24.53*	7.09*	141.95*
h_2	142.38*	88.64*	587.93*	-1.98	5.16*	0.75	0.16	50.58*
E	15.69*	21.09*	179.40*	8.00*	0.28*	4.60*	0.26	29.94*
$\sqrt{(H_1/D)}$	2.40	7.64	2.02	7.10	3.01	2.68	10.99	2.65
$H_2/4H_1$	0.26	0.23	0.24	0.20	0.19	0.26	0.21	0.25
$[\sqrt{4DH_1} + F/\sqrt{4DH_1}] - F$	0.93	1.37	1.28	1.59	2.18	1.26	1.31	1.28
h_2/H_2	0.69	0.83	0.46	-0.05	2.00	0.03	0.02	0.36
h^2 (ns)	0.22	0.01	0.18	0.17	0.15	0.04	0.25	0.06

*Significant at $P=0.05$. NS-Not Significant.

Additive effect : D-Mean Fr over arrays, F-Dominance effect, H_1 -Components of genetic variance due to dominance effects corrected for the genes distributed, H_2 -Overall dominance effects of heterozygous loci, h_2 -Environmental component, E - $\sqrt{(H_1/D)}$ -Mean degree of dominance, $H_2/4H_1$ -Proportion of gene with +ve and -ve effects, $[\sqrt{4DH_1} + F/\sqrt{4DH_1}] - F$ -Ratio of dominant and recessive genes and h_2/H_2 -Number of genes group.

additive and dominance effect (D , H_1 and H_2) was significant, which explained that both types of gene actions i.e. additive and dominance were involved in the expression of the days to 50% heading, days to maturity, number of productive tillers/plant and biological yield/plant. Significant additive effect without significant of dominance effect was observed for plant height and number of spikelets/ear traits. Positive value of F_r indicated that the proportion of dominance allele was in excess than the recessive allele for all traits except days to 50% heading, ear length, ear weight, plant height, number of spikelets/ear and number of grains/ear. Environmental component (E) was positive and significant for all traits under study, suggesting environmental influence in the modification of these traits (Ahmad *et al.*, 2017).

The value of mean degree of dominance was greater than one, which indicated availability of over dominance for all traits except plant height and number of spikelets/ear. The value of $H_2/4H_1$ was less than 0.25 which indicated asymmetrical distribution of dominant and recessive alleles for all traits except grain yield/plant for these traits among the parents. The value of $[\sqrt{4DH_1} + F/\sqrt{4DH_1}] - F$ was more than one which indicated, excess of dominant genes present among the parents than recessive genes for all traits except number of days to 50% heading, ear length, ear weight, plant height, number of spikelets/ear and number of grains/ear (Table 3). Narrow sense

heritability being lower for all traits indicated that dominance variance was more than the additive variance. Similar findings were reported by Kutlu and Olhun (2015), Hosary and Deen (2015), Ahmad *et al.* (2016) and Omar *et al.* (2020).

The W_r , V_r graph and the regression coefficient of W_r and V_r along with their standard errors for each of 16 characters have been presented in Fig. 1 to 16. All traits under studies observed that the value of regression coefficient slope deviated significantly from zero but not from unity, which indicated absence of non-allelic interaction (Mansour and Moustafa, 2016; Afridi *et al.*, 2019).

Regression line intercepted W_r axis below the origin, which indicated the presence of over dominance for days to 50% heading, days to maturity, number of productive tillers/plant, ear length, ear weight, number of ears/plant, biological yield/plant, harvest index and grain yield/plant. Regression line intercepted W_r axis above the origin indicating the presence of partial dominance for plant height, number of spikelets/ear, number of grains/ear, canopy temperature, chlorophyll content and protein content. Regression line intercepted W_r axis on origin, which indicated the presence of complete dominance for 1000-grain weight. Similar findings were reported by Kumar *et al.* (2018). The value of mean degree of dominance was greater than one, which indicated availability of over dominance for all traits except plant height and number of spikelets/ear.

Table 3. Frequency of dominant and recessive genes among parents for various traits

S. No.	Characters	Parents with more dominant genes	Parents with more recessive genes	Parents with equal frequency of both genes
1.	Days to 50% heading	HI-1544	LOK-1	GW-273 & MP-1203
2.	Days to maturity	HD-2932	LOK-1	MP-3173
3.	Plant height (cm)	GW-273	HI-1544	MP-4010 & MP-1203
4.	No. of productive tillers/plant	MP-3173	MP-4010	LOK-1
5.	No. of spikelets/ear	MP-1203	MP-3173	LOK-1 & GW-273
6.	Ear length (cm)	MP-1203	HD-2932	GW-273 & MP-4010
7.	Ear weight (g)	LOK-1	GW-273	HD-2932
8.	No. of ears/plant	MP-3173	MP-4010	MP-1203
9.	N. of grains/ear	HD-2932	MP-3173	GW-273
10.	1000-grain weight (g)	HD-2932	HI-1544	MP-4010
11.	Biological yield/plant	HI-1544	HD-2932	MP-3173
12.	Harvest index (%)	MP-3173	MP-4010	GW-273
13.	Canopy temperature	LOK-1	MP-3173	HI-1544, HD-2932 & MP-1203
14.	Chlorophyll content	HI-1544	MP-1203	MP-4010
15.	Protein content (%)	MP-3173	HD-2932	MP-4010
16.	Grain yield/plant	GW-273	MP-4010 & HD-2932	HI-1544 & MP-3173

Wr-Vr Graphs

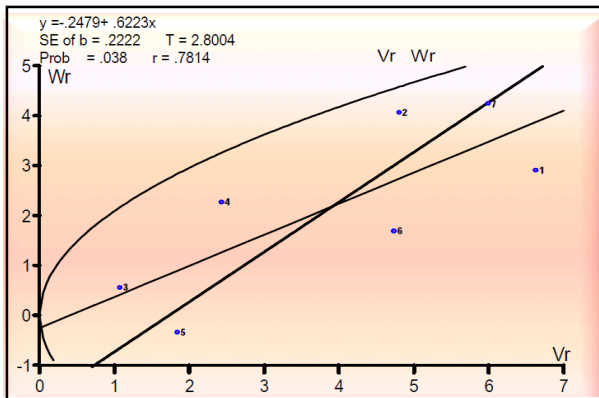


Fig. 1. Days to 50% heading.

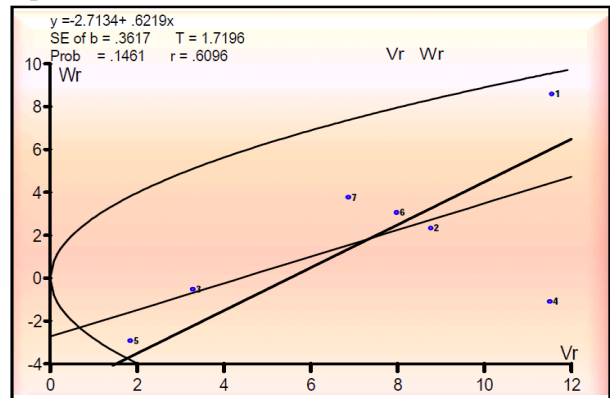


Fig. 2. Days to maturity.

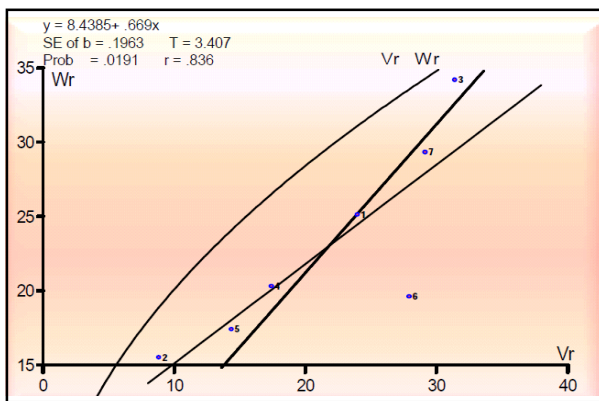


Fig. 3. Plant height (cm).

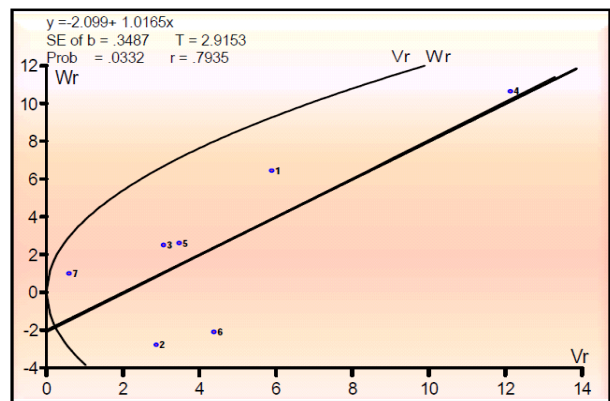


Fig. 4. Number of productive tillers/plant.

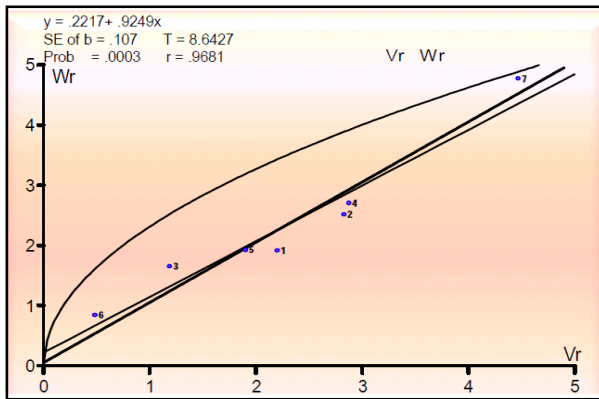


Fig. 5. Number of spikelets/ear.

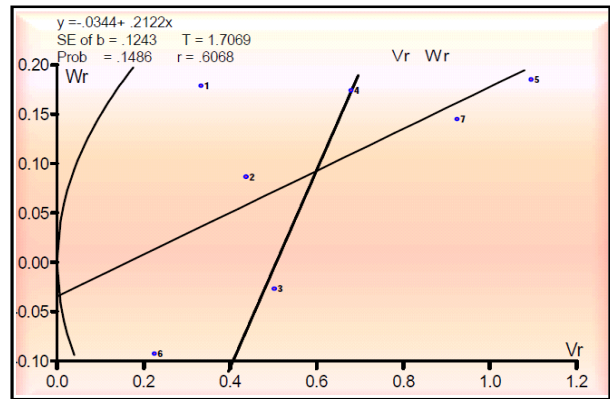


Fig. 6. Ear length (cm).

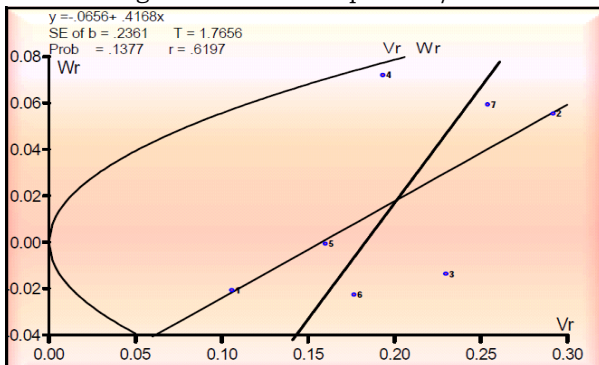


Fig. 7. Ear weight (g).

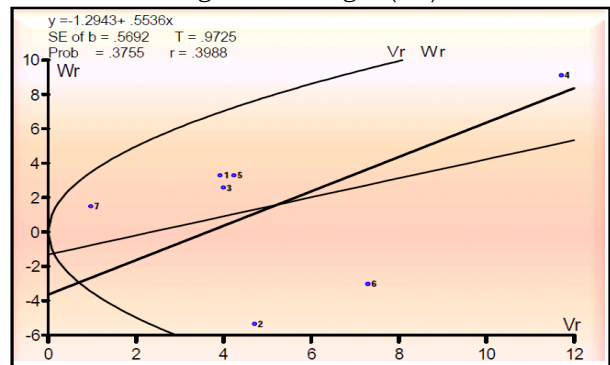


Fig. 8. Number of ears/plant.

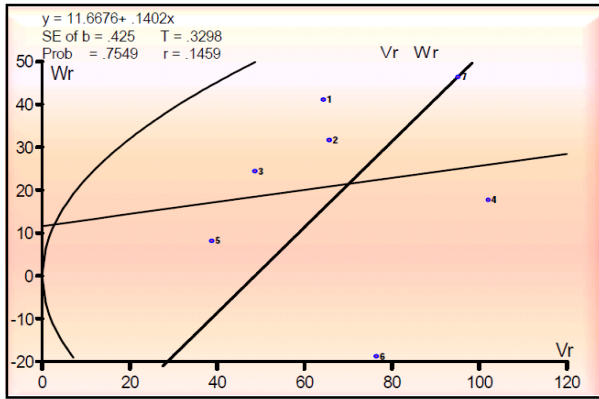


Fig. 9. Number of grains/ear.

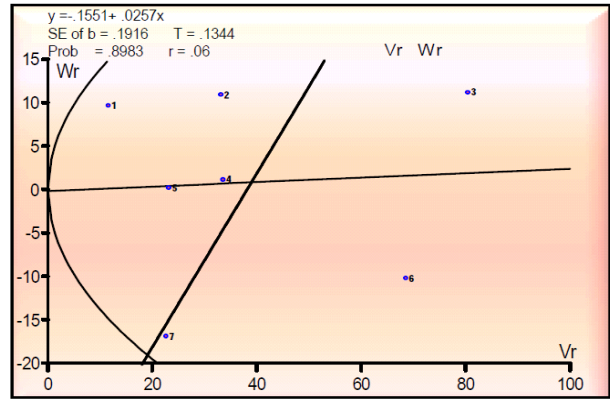


Fig. 10. 1000-grain weight (g).

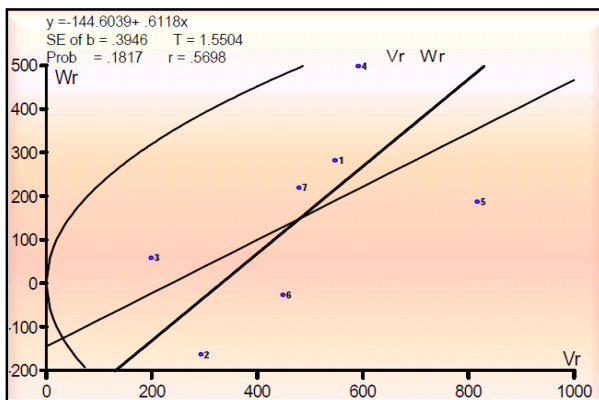


Fig. 11: Biological yield/plant (g).

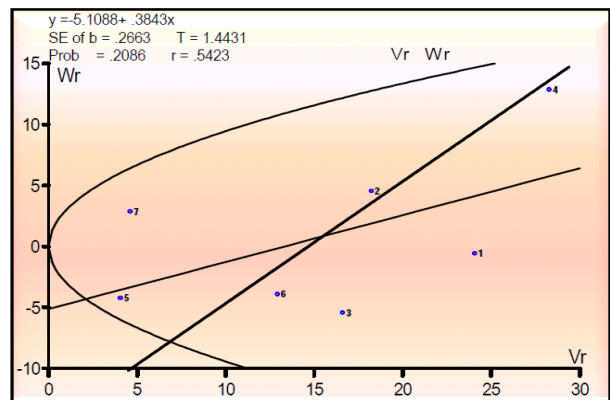


Fig. 12. Harvest index (%).

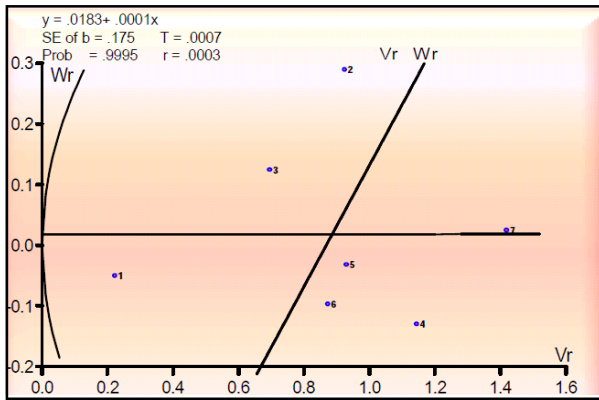


Fig. 13. Canopy temperature.

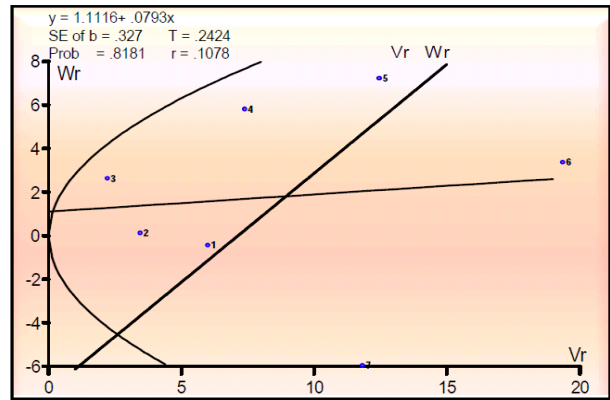


Fig. 14. Chlorophyll content.

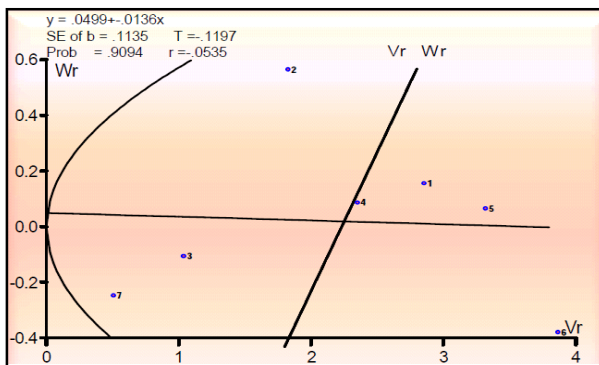


Fig. 15. Protein content (%).

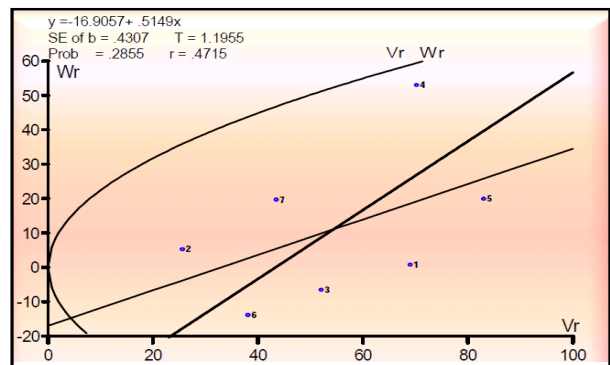


Fig. 16. Grain yield/plant.

A population with preponderance of additive genetic variance would support the improvement of characters through selection in segregating generation. If components of non-additive effect were important, hybridization would be more effective and breeding methods like bi-parental mating and selection breeding can be suggested.

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