GENETIC DETERMINATION OF YIELD RELATED TRAITS AND STRIPE RUST RESISTANCE IN WHEAT (*TRITICUM AESTIVUM* L.)

Talat Mahmood[1*] • Muhammad Niaz[1] • Ghulam Shabbir[1] • Zahid Akram[1] • Naeem Akhtar[2] • Shadab Shaukat[3]

AUTHOR'S AFFILIATION

[1]PMAS-Arid Agriculture University Rawalpindi, Pakistan
[2]College of Agriculture, University of Sargodha, Pakistan
[3]Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan
Corresponding author's email: drtalat@uaar.edu.pk

ABSTRACT

Background The information of the magnitude and type of gene action provide an ease to the breeders to obviate undesirable genotypes from experiment and include only productive material to accomplish breeding objectives. This study was conducted to determine gene action and its components in the inheritance of important yield contributing traits and stripe rust disease.

Methodology Four wheat varieties viz. Punjab 85 and Faisalabad 85 (resistant for stripe rust) while Inqalab 91 and Bhawalpur 94 (susceptible for stripe rust) were crossed in a full diallel fashion to study genetic parameters for the inheritance of traits i.e. flag leaf area, plant height, number of tillers plant^{-1}, 1000-grain weight, harvest index, chlorophyll content, yellow rust disease scoring and grain yield.

Results The genotypes studied had significant differences among themselves for different growth and yield traits. Regression line indicated over dominance type of gene action responsible for all traits under study.

Conclusion It was concluded that the degree of dominance was most favorable to improve resistance with yield and its traits. Traits showing dominance gene action could be utilized for the further improvement of wheat breeding lines having high yield and stripe resistance.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is an important cereal crop cultivated universally, and is the heart of diet for millions of people (Nazeer et al. 2010; Ahmad et al. 2018). In Pakistan during the year 2018-19, area under wheat crop was 8,740 thousand hectares and production 25,195 thousand tons with an average yield of 2883 kg per hectare. Wheat accounts for 8.9% value added in agriculture and 1.6% of GDP. It has been found that area under wheat cultivation was decreased by 0.6% while production increased by 0.5% as compare to the year 2017-18 (Anonymous 2019). Wheat is cultivated on about 40% of the country's total cultivated area (GOP 2019). The crop also accounts for an estimated 37% of both protein intakes and food energy (Hussain et al. 2012). Such factors manifest the role of wheat in Pakistan's economy and agriculture sector. About 20% of diet calories of the world are provided by wheat grain. It contains 70% carbohydrates, 12% proteins, 22% crude fibers, 2% fat, 12% moisture and 1.8% minerals (Ahmad et al. 2007)

Average yield of wheat in Pakistan is far below than its potential which demands that breeders should develop different techniques to enhance the per-unit-productivity of this most important and widely used cereal crop. Perception about genetic mechanism concerned in the manifestation of yield controlling traits is useful in developing superior genotypes. The components of variation i.e. additive, non-additive and epistasis are necessary for plant improvement (Ajmal et al. 2011).

Several biotic and abiotic stresses can limit the production of wheat in Pakistan (Ahmad et al. 2018). Among these, yellow rust (*Puccinia striiformis*) also called stripe rust is the most common rust that occurs in temperate areas. The stripe rust infection results in stunted growth and weaker plants, leading to yield losses as high as 50%, due to damaged tillers and shriveled grains (Shahin et al. 2020). Significant wheat yield losses have been reported in Pakistan, particularly in KPK province and northern districts of the Punjab i.e., Rawalpindi, Chakwal, Attock, Sialkot and Jhelum due to yellow rust. Hussain et al. (2011) reported that yellow rust may reduce wheat yield as much as 84%, and there is dire need to control this disease.

It is necessary for breeders to concentrate on development of productive wheat varieties with resistance against diseases through crossing of good parents which have the high degree of general combining ability (El-Basyoni et al. 2019).

Plant breeders and pathologists are making continuous efforts to evolve disease resistant as well as high yielding varieties in order to deal with the pressure generated by continuous changing rust races through the strategies like durable resistance (Babar et al. 2010; Kandil et al. 2016). In the present research, gene action study was made to evaluate the pattern of inheritance and extant of combining ability in different parents and their possible crosses to utilize in future research for developing wheat varieties resistant to yellow rust.

MATERIALS AND METHODS

The research study was carried out in the experimental area of the Department of Plant Breeding & Genetics, PMAS-Arid Agriculture University Rawalpindi, Pakistan to investigate the gene action of yield contributing traits and inheritance pattern of stripe rust disease on yield and yield contributing traits. The research material comprised of four spring wheat varieties of diverse genetic background screened from existing germplasm maintained by the department viz., Punjab-85 and Faislabad-85 (resistant for yellow rust), Inqalab-91 and Bhawalpur-94 (susceptible for yellow rust). These varieties were crossed in a full diallel fashion. The F_1, (twelve hybrids) and their parents (four) were sown in the field area of the Department of Plant Breeding and Genetics, PMAS-Arid Agriculture University Rawalpindi, Pakistan in three replications using the Randomized Complete Block Design (RCBD). Each replication was consisting of a single row of 1 m length having distance of 30 centimeters between rows, while 7.5 cm between plants. Morocco wheat variety was used as spreader of yellow rust inoculum and was planted along the borders as well as after every five entries of each replication. Data for yellow rust was recorded when maximum disease was observed in Morocco. The yellow rust severity was recorded as percent of infection on each genotype using modified Cobb's scale (Table 1) as described by Peterson et al. (1948). Five guarded plants of each genotype from each replication were selected at random and data recorded for the traits including flag leaf area, plant height, number of tillers plant^{-1}, 1000-grain weight, harvest index (%), chlorophyll content, yellow rust disease scoring and grain yield.

The data recorded for all these traits were subjected to analysis of variation according to Steel et al. (1997). Variation of genetic components was calculated according to the procedure set by Hayman (1954) and Mather and Jinks (1971).

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) indicated significant differences among the genotypes for growth and yield traits studied (Table 2). Different traits were studied individually for genetic determination. The essential role of both additive and non-additive gene action were found in some definite studied traits.

Flag leaf area
The analysis of variance of diallel data for flag leaf area indicated significant differences for items a, b, and b_2 (Table 3). The significant 'a' and 'b' items indicated the role of additive and dominance effects of genes in the inheritance of flag leaf area. The significant value of b_2 indicated unbalanced distribution of genes between parents. Non-significant value of b_1 and b_3 indicated that there was no involvement of specific dominant gene in the genetic control of flag leaf area. The significant value of 'c' indicated the presence of maternal effects and non-significant of 'd' indicated the absence of reciprocals effects. The positive and significant value of D, H_1 and H_2 (Table 3) showed the presence of additive and dominance gene effects in governing flag leaf area. The value of D was smaller than H_1 and H_2 showing that dominance effects were more important in the expression of flag leaf area than those genes having additive effects. The H_1 was greater than H_2 implied that rate of gene distribution in the parents was unbalanced at the additive loci in the parents. The F value was positive indicating existence of more dominant genes than recessive genes. Higher value of H_1 than D also indicated higher degree of dominant genes. The significant 'E' indicated the involvement of environmental effects in the expression of this trait. The value of average degree of dominance $(H_1/D)^{0.5}$ exceeded from unity indicating the presence of over dominance. The regression line cut off the Wr-axis below the origin also showed the involvement of over dominance type of gene action. The Vr-Wr graphical expression (Figure 1) indicated that the varieties Punjab-85, Faisalabad-85 and Inqlab-91 owed maximum dominant genes while Bhawalpur-94 had maximum recessive genes responsible for flag leaf area. Comparable results were revealed by Ajmal et al. (2011); Ahmed et al. (2015)

Plant height
The analysis of variance of diallel data for plant height indicated significant differences for all items (Table 3). The significant 'a' and 'b' items indicated the role of additive and dominance effects of genes in the inheritance of plant height. The presence of directional dominance effect and asymmetrical distribution of genes among parents was indicated by significant values of b_1 and b_2. The item b_3 was also significant showing involvement of specific

Table 1 Mean squares of formal analysis of variances for the indicated traits in 4x4 diallel crosses of wheat

SOV		DF	Flag leaf area	Plant height	Tillers plant^{-1}	1000-grain weight	Harvest index	Disease score	Grain yield
a,		3	3.11*	92.02**	10.54**	57.71**	30.06**	408.81**	1278464**
b,		6	6.57**	136.01**	6.23**	8.99**	40.52**	472.4**	281699.4**
	b_1	1	3.06NS	470.28**	2.74NS	9.08**	0.24NS	2260.21**	950539.4**
	b_2	3	11.92**	70.90**	0.52NS	11**	74.09**	98.39NS	225821.8**
	b_3	2	0.31NS	66.54**	16.55**	5.94**	10.31**	139.51NS	31095.93**
C		3	5.64**	125.59**	5.76*	23.56**	46.7**	4.92NS	2187744**
D		3	1.68NS	167.24**	8.88**	0.37NS	12.78**	848.98**	65859.25**
Rep		2	5.24**	0.05NS	16.66**	1.18NS	0.72NS	12420.38**	3008NS
Error		30	0.92	4.43	1.49	0.47	1.99	70.77	1971.93
Total		47							

**=highly significant, *= significant, NS = non-significant, SOV: Source of variance, DF: Degree of freedom

Table 2 Mean squares, mean and CV% for the indicated traits in 4x4 diallel cross of wheat genotypes

SOV	DF	Flag leaf area	Plant height	Tillers plant^{-1}	1000-grain weight	Harvest index	Disease score	Grain yield
Replications	2	5.87 NS	20.18NS	16.41NS	0.85 NS	0.91 NS	2.24 NS	2953 NS
Genotypes	15	4.72**	30.57**	7.48**	28.67**	33.85**	876.31**	819121**
Error	30	0.98	41.28	1.53	1.59	1.91	29.23	1972
Mean		22.54	85.44	8.95	42.49	40.77	21.16	5947.3
CV (%)		4.41	7.52	13.85	2.97	3.4	5.54	0.75

**=highly significant, *= significant, NS = non-significant, SOV: Source of variance, DF: Degree of freedom

Table 3 Estimation of genetic component of variation for the indicated traits in 4x4 diallel cross of wheat genotypes

Parameter	Flag leaf area	Plant height	Tillers plant^{-1}	1000-grain weight	Harvest index	Disease score	Grain yield
D	2.96*	22.78*	22.78*	6.95*	26.37*	35.34	146462.40*
H1	5.60*	98.86*	98.86*	7.44*	37.70*	230.35	216017.20*
H2	3.80*	87.95*	87.95*	5.70*	25.77*	239.2	181344.40*
F	4.43*	19.16*	19.16*	-0.83*	33.71*	-16.39	-38072.84*
h^2	0.56NS	116.61*	116.61*	2.16*	-0.37	538.54*	222938.00*
E	0.30*	1.44*	1.44*	0.15*	0.66*	40.38*	652.26*
$(H1/D)^{0.5}$	1.37*	2.08*	2.08*	1.03*	1.19*	2.55	1.21*
kd/(kd+kr)	0.77*	0.60*	0.60*	0.47*	0.76*	0.45*	0.44*
h^2/H_2	0.19NS	1.76*	1.76*	0.50*	-0.01	3.00*	1.63*
H	0.87NS	-10.74*	-10.74*	1.50*	-0.24	-23.77*	-472.61*
uv	0.17*	0.22*	0.22*	0.19*	0.17*	0.26*	1.63*

**=highly significant, *= significant, NS = non-significant, D: Additive variance, H1: Dominance variance 1, H2: Dominance variance 2, F: Product of add. by dom. Effects, h2: Square of difference P vs. All, E: Environmental variance, whole, (H1/D)0.5: Average degree of dominance, kd/(kd+kr): Proportion of dominant genes, h2/H2: Number of effective factors, H: Average direction of dominance, v: Balance of positive and negative alleles

dominant genes in genetic control of this character. The positive and significant value of D (Table 3) indicated existence of many differences between the parents used. The H_1 and H_2 were significant and H_1 was greater than H_2 implied that alleles with positive and negative effects were unequal at the additive loci in the parents. Positive value of F indicated the existence of more dominant genes as compared to recessive genes. The value of average degree of dominance exceeded from unity indicating presence of over dominance. The Vr/Wr graphical analysis (Figure 2) indicated that three varieties Punjab-85, Inqalab-91 and Bhawalpur-94 owed the maximum dominant genes. On the other hand, Faislabad-85

had maximum recessive genes responsible for plant height. The regression line cut off the Wr-axis below origin showed the involvement of over dominance gene action in plant height. Similar results were revealed by Naseem et al. (2015).

Number of tillers plant^{-1}

Number of tillers plant^{-1} showed significant values for all the items except b_1 and b_2 indicating prominence of additive, dominance, maternal and reciprocal effects (Table 3). The involvement of specific dominant gene was indicated by significant value of b_3. Non-significant value of b_1 and b_2 indicated absence of unidirectional dominance and

asymmetrical distribution of genes. H_1 was less than H_2 implied that alleles with positive and negative effects were unequal at the additive loci in the parents. The value of D was found less than H_1 and H_2 indicating that additive effects were not more important for number of tillers per plant (Table 3). Negative value of F indicated occurrence of more recessive genes than dominant genes. The value of average degree of dominance $(H1/D)^{0.5}$ exceeded from unity indicating existence of over dominance. Vr-Wr graph also indicated that over dominance type of gene action responsible for this trait (Figure 3). The Punjab-85 and Faislabad-85 possessed maximum number of dominant genes; in contrast Bhawalpur-94 had maximum number of recessive genes. Similar results were revealed by Ahmad et al. (2007).

1000-grain weight

The diallel ANOVA for 1000-grain weight (g) indicated the significant differences for all items except'd' (Table 3). The significant 'a' and 'b' item indicated the role of additive and dominance effects of gene in inheritance for 1000-grain weight. The presence of directional dominance effect and asymmetrical distribution of genes among parents was indicated by significant values of b_1 and b_2. The item b_3 was also significant showing the involvement of specific dominant gene in genetic control of this character. The value of 'd' was non-significant indicated the absence of non-maternal effects. The positive and significant value of D (Table 4) indicated existence of many differences between the parents used. The H_1 and H_2 were significant and H_1 was greater than H_2 implied that alleles with positive and negative effects were unequal at the additive loci in the parents. Negative F value signified the important role of recessive genes. The value of average degree of dominance $(H1/D)^{0.5}$ greater than unity indicated presence of over dominance. The regression line of Vr-Wr graph (Figure 4) intercepted the Wr-axis below the origin showing the involvement of over dominance type of gene action for 1000-grain weight. Faisalabad-85 and Punjab-85 owed the maximum number of dominant genes while Inqalab-91 had highest number to control 1000-grain weight. Similar results were reported by Shabbir et al. (2011).

Harvest index

The significant 'a' and 'b' items for harvest index (Table 3) indicated the role of additive and dominance effects of gene contributed in the inheritance of harvest index. The absence of unidirectional dominance effect was indicated by the non-significant value of 'b_1' and irregular distribution of genes among parents was indicated by significant value b_2. The unit 'b_3' was also significant showing the involvement of specific dominant gene in the genetic control of this

character. The maternal and non-maternal effects were also present indicated by significance of 'c' and 'd'. The positive and significant value of D (Table 3) indicated existence of many differences between the parents used. The H_1 and H_2 were significant and H_1 was greater than H_2 implied that unequal gene distribution in parents. Positive value of F indicated the presence of dominant genes higher in number than recessive genes. The value of average degree of dominance was more than 1 indicating over dominance that was also confirmed by the graphical representation (Figure 5) as regression line cut off the Wr –axis below the point of origin indicated over dominance type of gene action. The Faisalabad-85 and Punjab-85 had maximum number of dominant genes; in contrast Bhawalpur-94 had maximum number of recessive genes. Similar results were revealed by Ahmed et al. (2015) and El-Orabey et al. (2019).

Disease score

The significant 'a' and 'b' item for disease score (Table 3) indicated the role of additive and dominance properties of gene effect involved in the inheritance of disease (stripe rust). The presence of directional dominance effect was indicated by significant values of b_1. Non-significant value of b_3 indicated that there was no involvement of specific dominant gene in the genetic control of stripe rust disease. The 'c' was non-significant indicated deficiency of maternal effects. The significance of 'd' showed the presence of reciprocal differences other than 'c'. The positive value of D (Table 3) indicated existence of many differences between the parents used for yellow rust. H_1 was greater than H_2 implied that alleles with positive and negative effects were unequal at the additive loci in the parents. Negative value of F indicated that more recessive genes than dominant genes were existed. The value of average degree of dominance exceeds from unity indicating presence of over dominance. In graphical representation of yellow rust disease scoring (Figure 6), the regression line cut off the Wr–axis below the point origin indicated that over dominance type of gene action responsible for this trait. The Inqalab-91and Bhawalpur-94 had maximum number of dominant genes; in contrast, Punjab-85 had maximum number of recessive genes. Similar results were revealed by El-Basyoni et al. (2019).

Grain yield

The significant 'a' and 'b' item indicated the role of additive and dominance effects of genes contributed in the inheritance of grain yield (Table 3). The presence of directional dominance effect and asymmetrical distribution of genes among parents was indicated by significant values of b_1 and b_2. The item 'b_3' was also significant showing involvement of specific dominant gene in the genetic control of
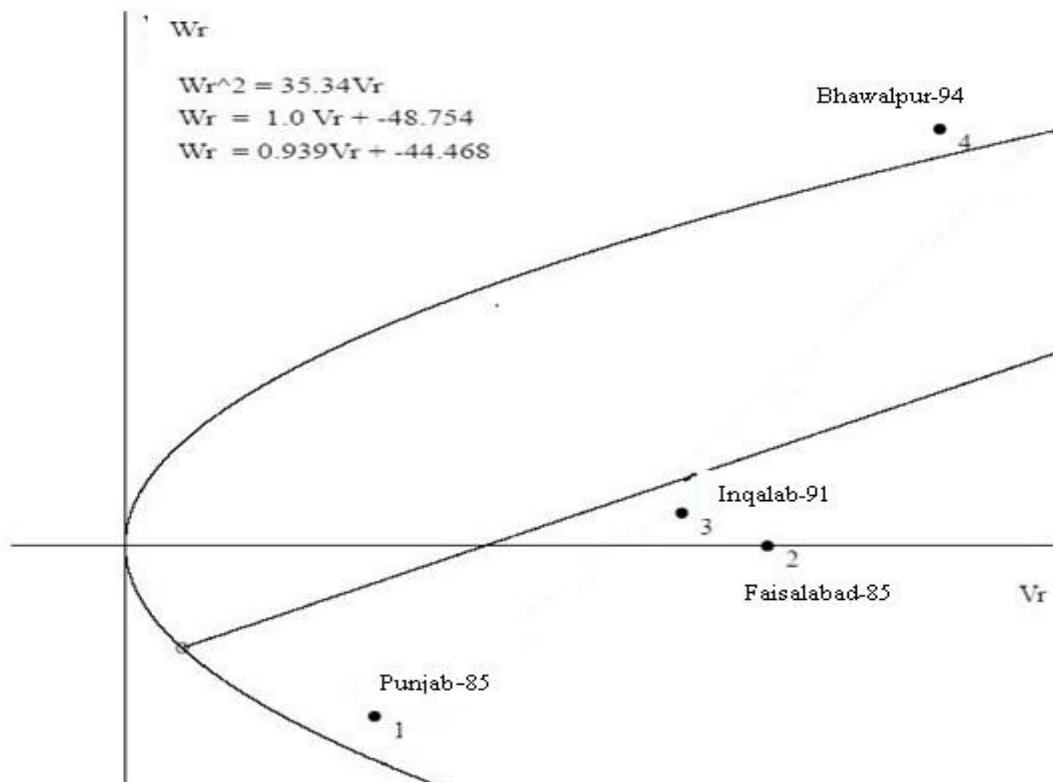
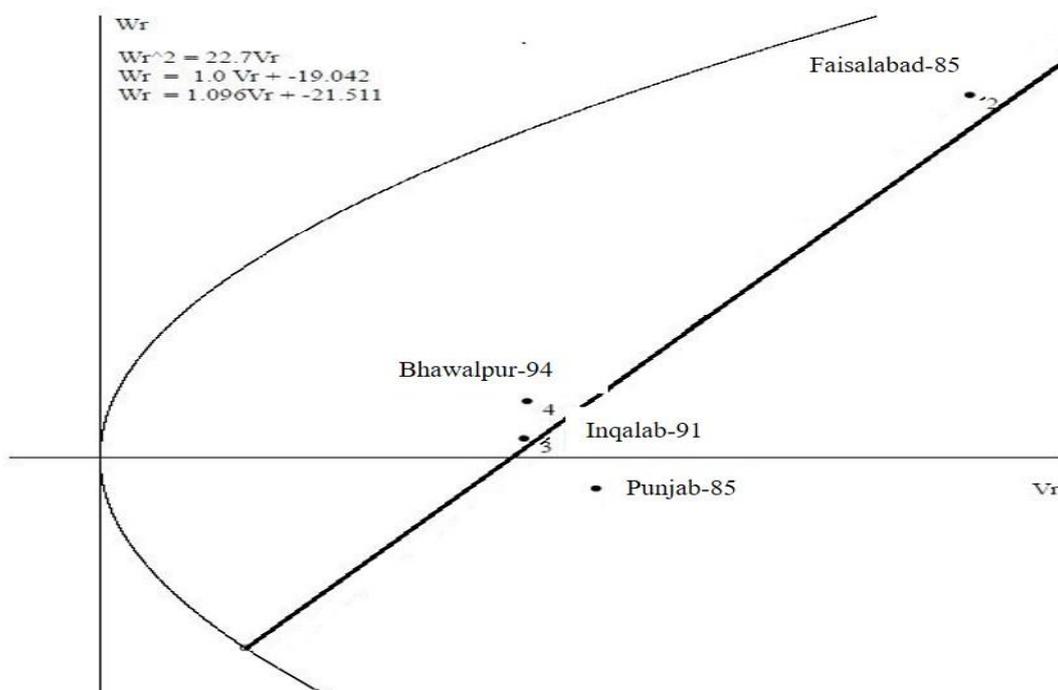**Figure 1** Wr/Vr graph for flag leaf area of wheat genotypes

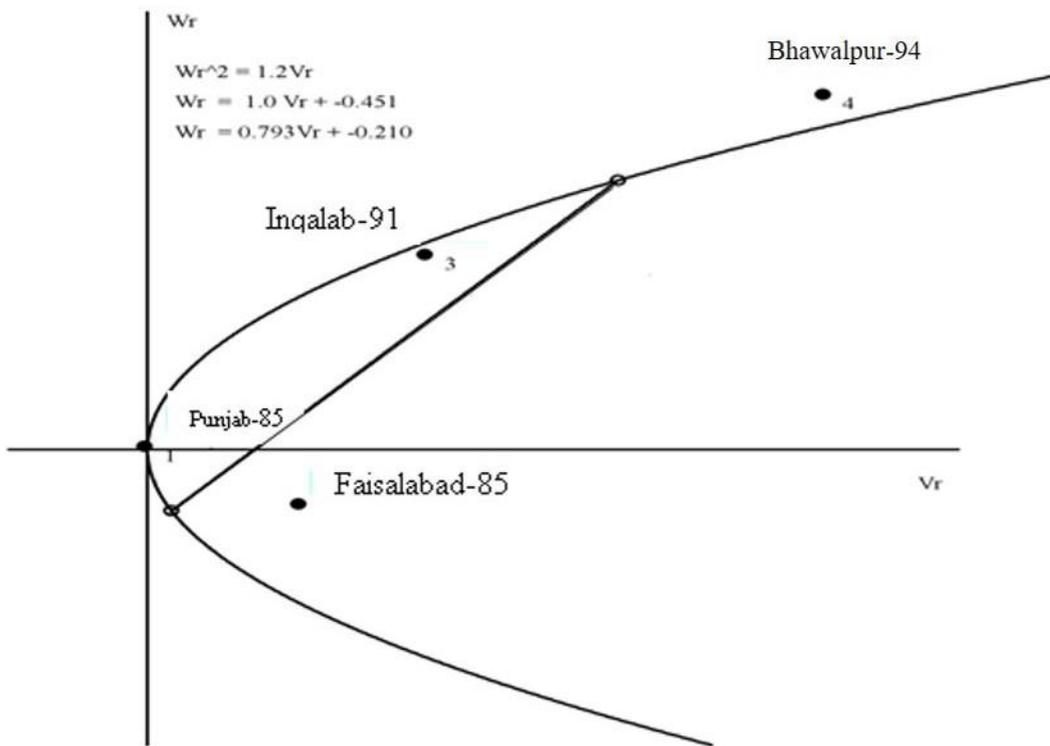**Figure 2** Wr/Vr graph for plant height of wheat genotypes

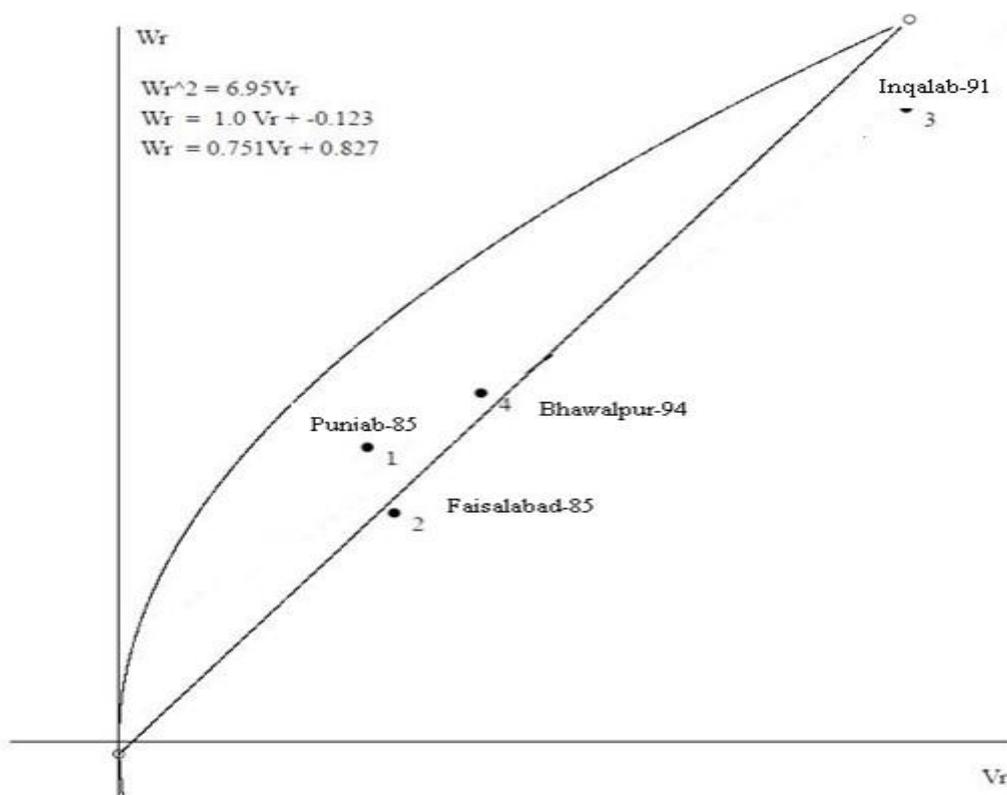**Figure 3** Wr/Vr graph for number of tillers plant^{-1} of wheat genotypes

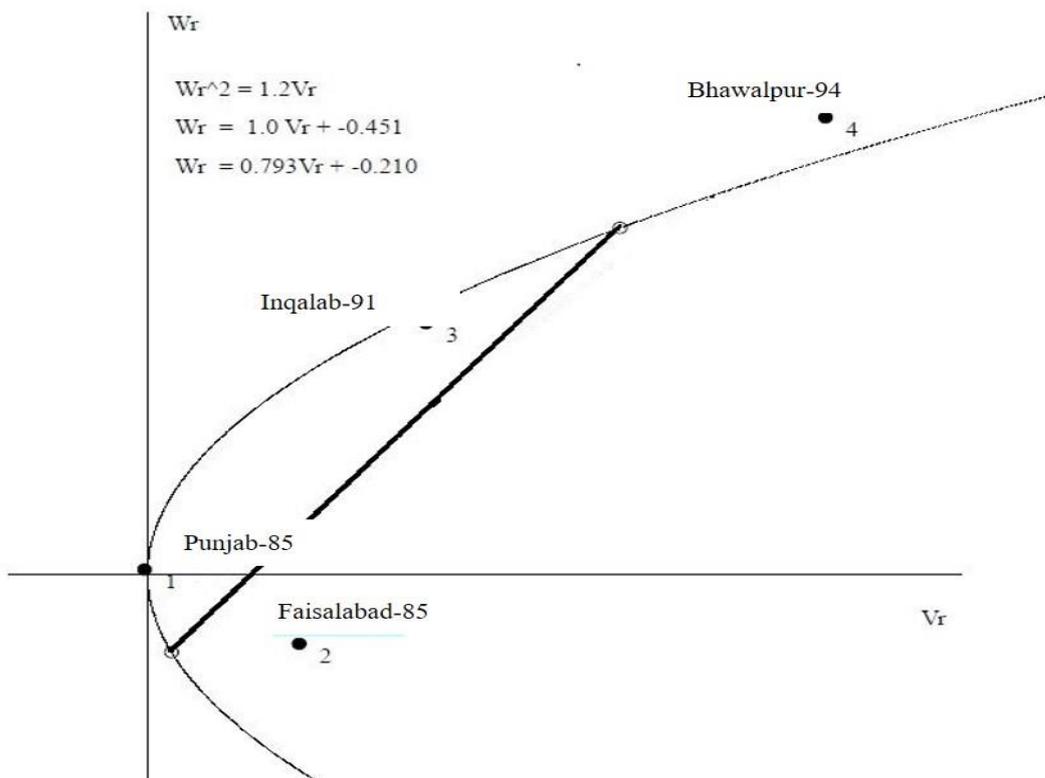**Figure 4** Wr/Vr graph for 1000-grain weight of wheat genotypes

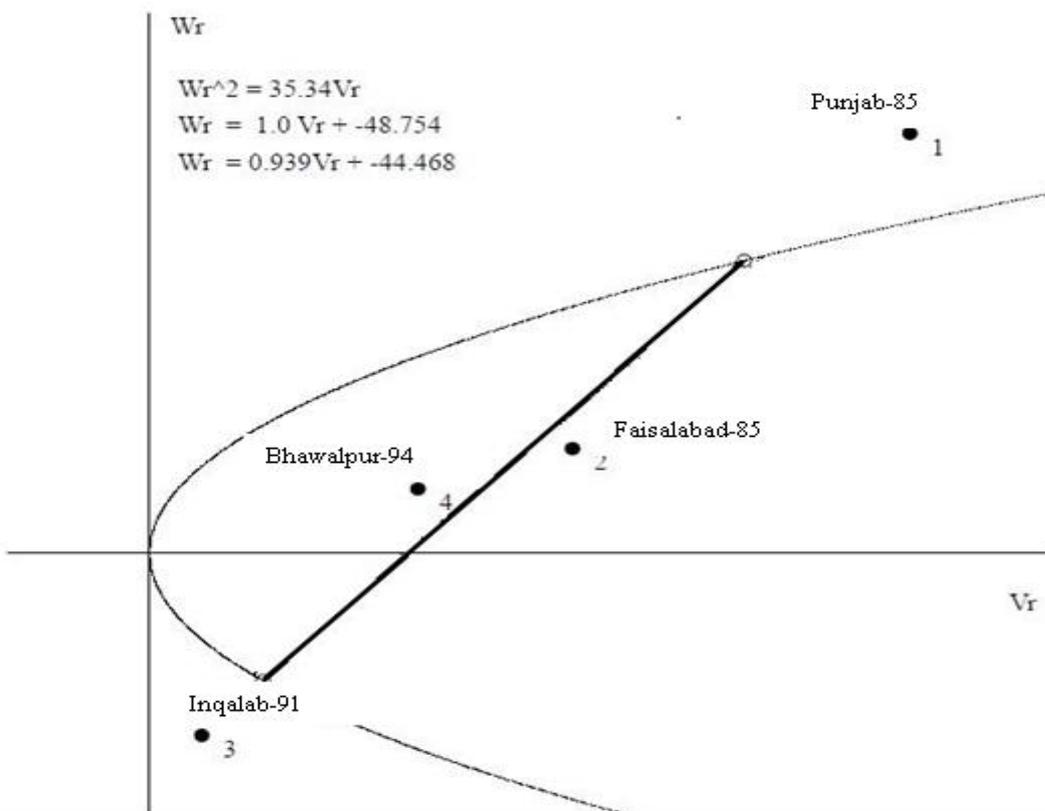**Figure 5** Wr/Vr graph for harvest index of wheat genotypes

Figure 6 Wr/Vr graph for disease scoring (stripe rust) in wheat genotypes
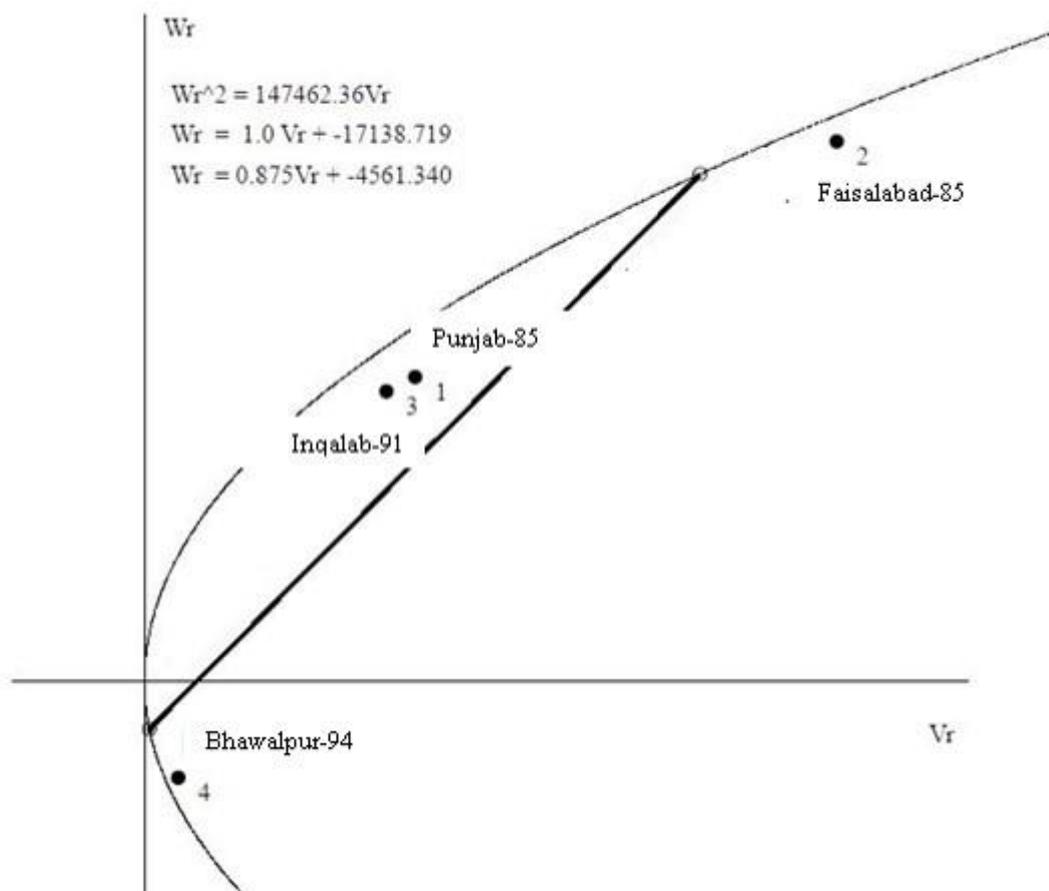
Figure 7 Wr/Vr graph for grain yield of wheat genotypes

this character. The 'c' and 'd' items were significant exhibited maternal and non-maternal effects were also present. The positive and significant value of D (Table 4) indicated existence of many differences between the parents used. The H_1 and H_2 were significant and H_1 was greater than H_2 indicated that alleles with positive and negative effects were unequal at the additive loci in the parents. The presence of more recessive genes indicated by negative sign of "F". The average value degree of dominance $(H1/D)^{0.5}$ exceeded from unity indicating the presence of over dominance that was also confirmed by Vr-Wr graph (Figure 7) as regression line cut off the Wr-axis below the point of origin showed the involvement of over dominance type of gene action for grain yield. The variety Bhawalpur-94 owed maximum number of dominant genes while Faisalabad-85 had maximum number of recessive genes responsible for grain yield.

CONCLUSION

Regression line indicated over dominance type of gene action responsible for all traits like flag leaf area, plant height, number of tillers plant^{-1}, 1000-grain weight, harvest index, disease score (Stripe rust), grain yield. It was concluded that the degree of dominance was most favorable to improve resistance with yield and its traits. Traits showing dominance gene action can be utilized for improvement of further wheat breeding lines having high yield and stripe resistance.

REFERENCES

Ahmad T, M Tahir, MA Saleem, MA Zafar (2018) Response of soil application of boron to improve the growth, yield and quality of wheat (Triticum aestivum L.). *Journal of Environment & Agriculture*, **3(2):** 313–318.

Ahmad F, F Mohammad, M Bashir, HS Khan (2007) Inheritance of important traits in bread wheat over different planting dates using diallel analysis. *Sarhad Journal of Agriculture*, **23(4):** 955–963.

Ahmed HGM., SS Muhammad, K Adeel, F Anmol, S Saira, H Mariam, Z Siddra, B Mubra (2015) Genetic mechanisms of yield related morphological markers response to increase grain yield in different environment of hexaploid wheat. *Journal of Biodiversity and Environmental Sciences*, **6:** 158–164.

Ajmal S, I Khaliq, A Rehman (2011) Genetic analysis for yield and some yield traits in bread

wheat (*Triticum aestivum* L.). *Journal of Agricultural Research*, **49(4):** 447–454.

Anonymous (2019) Pakistan Economic Survey. Finance Division, Government of Pakistan.

Babar M, AF Mashhadi, A Mehvish, AN Zahra, R Waheed, A Hasnain, Sajid-ur-Rahman, N Hussain, M Ali, I Khaliq, A Aziz (2010) Identification of rust resistance genes Lr10 and Sr9a in Pakistani wheat germplasm using PCR based molecular markers. *African Journal of Biotechnology*, **9(8):** 1144–1150.

El-Basyoni IS, WM El-Orabey, S Morsy, PS Baenziger, Z Al-Ajlouni, I Dowikat (2019) Evaluation of a global spring wheat panel for stripe rust: Resistance loci validation and novel resources identification. *PLoS ONE*, **14(11):** https://doi.org/10.1371/journal.pone.0222755

El-Orabey WM, IS El-basyoni, SM El-Moghazy, MA Ashmawy (2019) Effective and ineffective of some resistance genes to wheat leaf, stem and yellow rust diseases in Egypt. *Journal of Plant Production*, **10 (4):** 361371.

GOP (2019) Economic survey of Pakistan. Ministry of Finance, Islamabad, Pakistan.

Hayman BI (1954) The theory and analysis of diallel crosses. *Genetics*, **39:** 789–809.

Hussain M, N Ahmad, F Muhammad, A Rehman, M Hussain MA Khan, M Hussain, S Ajmal (2011) Wheat breeding for high yield potential and durable resistance against yellow rust. *Pakistan Journal of. Phytopathology*, **23(1):** 56–61.

Hussain T, W Nazeer, M Tauseef, J Farooq, M Naeem, S Freed, M Iqbal, A Hameed, MA Sadiq, HM Nasrullah (2012) Inheritance of some spike related polygenic traits in spring wheat (*Triticum aestivum* L). *African Journal of Agricultural Research*, **7(9):** 1381–1387.

Kandil, AA, AE Sharief, SM Hasnaa, Gomma (2016) Estimates of gene action for yield and its components in bread wheat *Triticum aestivum* L. *International Journal of Agricultural Research*, **8(1):** 34–40.

Mather K, JL Jinks (1971) Biometrical Genetics. Chapman and Hall, London.

Naseem Z, S Masood, SNI Annum, MK Bashir, R Anum, A Qurban, A Arfan, K Naila, HK Nazar (2015) Critical study of gene action and combining ability for varietal development in wheat. *Life Science Journal*, **12:** 104–108.

Nazeer W, Z Ali, A Ali, T Hussain (2010) Genetic behaviour for some polygenic yield contributing traits in wheat (*Triticum aestivum* L.). *Journal of Agricultural Research*, **48 (3):** 167–176.

Peterson RF, AB Campbell, AE Hannah (1948) A diagrammatic scale for estimating rust intensity on leaves and stems of cereals. *Canadian Journal of Research Section C-Botanical Sciences*, **26:** 496–500.

Shabbir G, NH Ahmad, Z Akram, MI Tabassum (2011) Genetic behaviour and analysis of some yield traits in wheat (*Triticumaestivum* L.) genotypes. *Journal of Agricultural Research*, **49(1):** 1–9.

Shahin A, M Ashmawy, W El-Orabey, S Esmail (2020) Yield losses in wheat caused by stripe rust (*Puccinia striiformis*) in Egypt. *American Journal of Life Sciences*, **8(5):** 127–134.

Steel RGD, JH Torrie, DA Dickey (1997) Principles and Procedures of Statistics. A Biometrical Approach. 2nd Ed. McGraw HillBook Co., Inc., New York, USA, P 663.