

Original Research Article

Graphical architecture of some production traits in F₂ wheat populations

ABSTRACT

Inheritance study for earliness and yield related traits in 8 x 8 F₂ half diallel progenies was carried out at The University of Agriculture, Peshawar-Pakistan during 2006-07. The experiment was planted in randomized complete block (RCB) design having four replications. Highly significant differences were observed among parental genotypes and their F₂ populations for all traits revealing greater genetic variability and thus allowing for further analysis. Mean values for days to heading, plant height, spike length, grains per spike and biological yield ranged from 108.5 - 116.5 days, 76.2 – 126.9 cm, 10.2 – 12.6 cm, 45.75 – 66.47 and 3583 – 8500 kg/ha, respectively. Parental genotypes Iqbal-2000, Ghaznavi-98 and Takbeer appeared to have appreciable mean values for majority of the traits while Takbeer x Ghaznavi-98, Iqbal-2000 x Ghaznavi-98 and Takbeer x Iqbal-2000 performed better than the rest among F₂ populations. According to genetic analysis, Vr/Wr graphs indicated over-dominance type of gene action for all traits among parental genotypes and their F₂ populations. Traits like days to heading, plant height and spike length were controlled by recessive genes while grains per spike and biological yield were under dominant gene control. Distribution of array points along the regression line indicated that wheat cultivars Takbeer and the landrace Khattakwal possessed maximum dominant and recessive genes, respectively for plant height. However, cultivar Iqbal-2000, Ghaznavi-98, Margalla-99 and Tatar-96 possessed maximum dominant genes for days to heading, spike length, grains per spike and biological yield, respectively.

Keywords: Diallel analysis, additive and non-additive gene action, over-dominance, inheritance, *Triticum aestivum* L.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important cereals not only in Pakistan but in most parts of the world. It is a major staple food item that fulfills nutritional requirement of our population in the form of protein and carbohydrates. Wheat occupies more acreage than

any other crop in Pakistan as it is grown under irrigated as well as rainfed conditions all over the country. Wheat produced in the country fulfills most part of our requirement but still the additional demands are met through imports at the cost of huge foreign investment. To overcome the nutritional demands of this ever increasing population, improvement in wheat production is still a major concern for wheat breeders in Pakistan.

Hayman's genetic analysis is a useful tool which has been widely used by plant breeders for constructing their desirable plant type using available genetic resources (Hayman 1954a, b). It provides useful information regarding nature of gene action and inheritance pattern of a particular trait that directs the plant breeders to practice selection in earlier generations or delay till advanced generations. Earlier studies revealed the importance of additive as well as non-additive gene action for inheritance of various earliness and yield associated traits among different wheat populations (Kutlu and Olgun, 2015). Additive type of gene action with partial dominance for spikelets per spike was reported by Ivanovska *et al* (2000) while Sangwan and Chaudhary (1999) identified non-additive gene action for grain yield and related traits in wheat. Similarly Singh *et al* (2002) reflected additive gene control for grains per spike, number of tillers per plant and grain yield in wheat. However, Navabi *et al* (2004) reported transgressive segregation among all the F₂ wheat populations and F₅ single seed-descent lines in wheat. Moreover, Jadoon *et al* (2012), Rabbani *et al* (2009) and Akram *et al* (2008) reported significance of both additive and non-additive gene action in inheritance of various yield related traits and delay in selection for improvement of these traits. Therefore, in light of past review, the present study was thus designed to investigate the inheritance mechanism involved in earliness and other yield related traits among eight parental genotypes and their F₂ wheat populations.

MATERIALS AND METHODS

Breeding material and procedure

The experimental material consisted of eight wheat cultivars/lines and their 28 F₂ progenies (direct crosses) obtained after selfing from a full 8×8 diallel F₁ crosses. The experiment was planted in randomized complete block (RCB) design having four replicates during 2006-07 at The University of Agriculture, Peshawar - Pakistan. Each experimental unit consisted of a four row plot of five meter length with a row to row spacing of 30 cm. The

nitrogen (N) and Phosphorus (P) were applied @ 120:60 NP kg ha⁻¹, respectively in form of Urea and DAP fertilizers. Half dose of nitrogen and full dose of phosphorus were applied at the time of seed bed preparation while the remaining half dose of nitrogen (urea) was applied at the time of first irrigation. Recommended cultural practices including land preparation, fertilizers, irrigation and weed control were applied same and time to time as and when required uniformly to all the entries to have less environmental effects.

Data Collection

Ten plants from parental cultivars/lines and thirty from F₂ generations were selected at random to collect data on days to heading, plant height, spike length, grains per spike and biological yield. Days to heading were recorded as number of days taken from germination to 50% spike emergence while plant height was recorded from ground level to tip of spike excluding awns. Spike length was measured from base of 1st spikelet to tip of last spikelet, excluding awns. Grains per spike were recorded as an average of produce of thirty spikes obtained after manual threshing. Biological yield was taken by harvesting the selected plants from each sub-plot/replication; sun dried and plants weighed in parental genotypes and F₂ populations.

Statistical analysis:

After compilation, data for all the traits were analyzed using statistical package 'SAS 6.12' following Steel *et al* 1997 to see whether significant differences existed among the genotypes for further analysis. Traits showing significant differences were further subjected to "t²" and "regression analysis" for adequacy of additive-dominance model and Hayman (1954 a, b) diallel analysis to study nature of gene action controlling these traits using computer software 'Dial-98' for half diallel F₂ wheat populations following procedures outlined by Morley-Jones (1965).

RESULTS AND DISCUSSION

Highly significant differences observed among parental genotypes and their F₂ populations for all the traits displayed greater genetic variability and thus allowing for further analysis (Table 1). Mean performance revealed that genotypes Tatara-96 and Ghaznavi-98 exhibited appreciable mean value for days to heading, Ghaznavi-98 for plant height while cultivars Iqbal-2000, Inqalab-91 and Margalla-99 for spike length among parents. However, the

landrace Khattakwal with maximum mean values for plant height and biological yield produced minimum grains per spike (Table 2). Similarly Iqbal-2000 x Ghaznavi-98 with minimum plant height (79.20 cm) and early flowering (109 days) performed better than other populations for most of the traits among the F_2 populations. Data showing significant differences were then subjected to two scaling tests i.e. “ t^2 ” and “regression analysis” for adequacy of additive-dominance model. The model is considered fully adequate if data for a particular trait fulfills the conditions of both tests, partially adequate if the conditions of one of these tests are fulfilled and inadequate if data fails to satisfy the condition of both tests. Hayman’s genetic analyses are performed only when this model is either fully adequate or partially adequate. In present study data regarding grains per spike and biological yield showed full adequacy of the model whereas days to heading, plant height and spike length showed partial adequacy of additive-dominance model (Table 3). Detail description of genetic analysis for each trait is as under

Days to heading

According to Hayman’s genetic analysis, V_r - W_r graph reflected involvement of over-dominance for days to heading as the regression line cuts the V_r -axis below the origin (Fig. 1a). Cultivars Iqbal-2000, Wafaq-2001 and Tatar-96 possessed maximum dominant genes being closest to the origin while Margalla-99 being farthest from origin, possessed maximum recessive genes for days to heading. Genotypes Khattakwal and Margalla-99 showed maximum influence of environment for earliness as they were away from the regression line. Moreover, non-significant deviation of regression line from unit slope confirmed the absence of non-allelic interactions for days to heading. Positive correlation ($r = 0.49$) of $V_r + W_r$ values with parental values reflected the importance of recessive gene for controlling days to heading (Fig. 1b). These results confirmed the earlier findings of Ivanovska *et al* (2000), Mishra *et al* (1994b) and Singh *et al* (2003) who reported over-dominance to be responsible for yield related traits in bread wheat population.

Plant height (cm)

V_r - W_r graph revealed that over-dominance was mainly responsible for controlling plant height as the regression line cuts the V_r -axis below origin (Fig. 2a). Earlier researcher (Ivanovska *et al* 2000, Mishra *et al* 1994b and Singh *et al* 2003) also reported over dominance for quantitative traits in F_2 wheat populations. However, Ali and Khan (1998), Joshi *et al* (2004),

Singh *et al* (2002) and Zwart *et al* (2004) reported additive genetic effects for most of the traits. Considerable variation existed among wheat genotypes for plant height as indicated by the distribution of parents along regression line inside the limiting parabola. Wheat cultivars Takbeer, Wafaq-2001, Ghaznavi-98 and Iqbal-2000, being closer to origin, possessed maximum number of dominant genes while Khattakwal possessed maximum recessive genes for plant height. Margalla-99 and Inqalab-91 being in the middle of regression line possessed equal number of dominant and recessive alleles. When V_r+W_r values were plotted against the parental values, positive correlation ($r = 0.74$) reflected involvement of recessive genes for plant height (Fig. 1b). Moreover, the position of parental genotypes along the regression line and non-significant deviation of regression line from unit slope confirmed the influence of environmental conditions on plant height and absence of non-allelic interactions for inheritance of this trait.

Spike length (cm)

Genetic analysis for spike length revealed that distribution of parental cultivars along the regression line confirmed sufficient amount of variation for spike length. The regression line cut the V_r -axis below the origin indicating that over-dominance played important role in the inheritance of spike length (Fig. 3a). Position of array points along the regression line showed that cultivars Ghaznavi-98 and Tatara-96 possessed maximum number of dominant genes while genotypes Margalla-99 and Inqalab-91 possessed maximum recessive genes for spike length. However, cultivars Khattakwal and Iqbal-2000 being in the centre of regression line possessed equal number of dominant and recessive genes. Ivanovska *et al* (2000), Mishra *et al* (1994b) and Singh *et al* (2003) also reported similar results in their studies. However, contrary to present findings Khan and Ali (1998) and Singh *et al* (2002) reported additive type of gene action for yield related traits in different wheat populations. Similar type of contradictions in other past studies were reported by Abdel-Sabour *et al* (1996) and Khan *et al* (2009) which could be attributed to residual heterozygosity among the parents. Positive correlation ($r = 0.868$) of $V_r + W_r$ with parental genotypes reflected recessive gene control for spike length (Fig. 3b). Moreover, non-significant deviation of regression line depicted absence of non-allelic interaction for spike length.

Grain spike⁻¹

Hayman's genetic architecture revealed that V_r - W_r graph reflected that over dominance gene action was mainly responsible for grains per spike as regression line intercepted

the Vr-axis well below the origin (Fig. 4a). Majority of wheat cultivars were found in cluster near origin which indicated an excess of dominant genes for grains per spike. However, the landrace Khattakwal being farthest from origin exhibited excess of recessive genes for said trait. When $V_r + W_r$ values were plotted against the parental values, negative correlation ($r = -0.96$) was observed which reflected dominant genes control for managing grains per spike (Fig. 4b). Similar results were reported by Khan and Ali (1998) and Sangwan and Choudhry (1999) in their studies for tillers plant⁻¹, grains spike⁻¹ and grain yield. Moreover, absence of non-allelic interactions was evident from significant deviation of regression line from unit slope.

Biological yield (kg ha⁻¹)

Like other parameters, the biological yield in parental genotypes and their F₂ populations was under the control of over-dominance as the regression line cuts Vr-axis below the origin (Fig.5a). cultivar Tatara-96 being closer to origin possessed maximum dominant genes while genotypes Inqalab-91 and Margalla-99 being farthest from origin, possessed large number of recessive genes for biological yield. Moreover, cultivars Tatara-96, Ghazavi-98, Inqalab-91 and Margalla-99 were closer to regression line than Iqbal-2000, Khattakwal, Wafaq-2001 and Takbeer and thus least affected by the environment. Negative correlation ($r = -0.39$) among parental genotypes and $V_r + W_r$ values suggested that inheritance of said trait was controlled by dominant genes (Fig. 5b). Over-dominance type of gene action for biological yield and grain yield was also reported by earlier researchers like Asif *et al* (2000), Biranvand *et al* (2013) and Pall and Kumar (2009). However, Salehi *et al* (2014) observed that average degree of dominance was less than unity and therefore, suggested partial dominance effects for this trait in wheat genotypes.

CONCLUSION

Over-dominance played a major role in inheritance of studied traits among F₂ wheat populations indicating selection in earlier generations would be least effective for improvement. Wheat cultivars Takbeer, Wafaq-2001, Ghaznavi-98 and Iqbal-2000 possessed maximum dominant genes for plant height while Iqbal-2000, Wafaq-2001 and Tatara-96 for days to heading. Similarly Tatara-96 and Ghaznavi-98 exhibited maximum dominant genes for spike

length, Margalla-99 for grains spike⁻¹ while Iqbal-2000, Ghaznavi-98, Tatara-96 and Wafaq-2001 for biological yield.

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243

244 **Table 1. Mean squares for some quantitative traits among F₂ half diallel wheat populations**
245 **at Peshawar, Pakistan**

SOV	Df	Plant height	Days to heading	Spike length	Grains spike ⁻¹	Biological yield (kg ha ⁻¹)
Reps	3	101.54*	9.57*	1.36*	65.95*	2706997 ^{ns}
Genotypes	35	445.42*	11.69*	1.67*	79.11*	5232400*
Error	105	42.93	2.26	0.34	8.91	131417

246 * stands for significant F test (0.05) while ns indicates non-significant

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249 **Table 2: Mean performance of parent cultivars and F₂ generation for plant height,**
 250 **days to flowering, spike length, grains spike⁻¹ and biological yield**

S.No.	Genotypes	Plant Height (cm)	Days to Flowering	Spike Length (cm)	Grains Spike ⁻¹	Biological yield (kg/ha)
1	Tatara-96	93.65	112.25	10.83	53.00	4250
2	Wafaq-2001	95.38	113.50	11.15	55.50	4583
3	Takbeer	92.63	114.00	11.18	55.00	5625
4	Iqbal-2000	92.38	114.25	12.18	55.25	4459
5	Margalla-99	100.65	116.50	12.30	56.00	3583
6	Ghaznavi-98	83.23	112.00	10.88	55.00	5417
7	Khattakwal	126.9	114.00	11.10	45.75	6542
8	Inqalab-91	90.05	114.00	12.60	54.00	3750
9	Tat x waf	82.62	110.75	10.63	60.54	6417
10	Tat x Tak	85.71	111.25	11.25	62.22	5375
11	Tat x Iqb	85.13	113.00	11.08	65.15	5125
12	Tat x Mar	83.66	112.00	10.98	61.11	5834
13	Tat x G-98	109.45	112.50	11.23	60.29	6250
14	Tat x K-wal	84.74	113.50	11.18	62.32	5084
15	Tat x Inq	98.15	112.25	11.28	61.90	5642
16	Waf x Tak	87.99	112.25	11.83	63.21	6334
17	Waf x Iqb	82.67	110.50	10.68	63.36	5833
18	Waf x Mar	105.67	112.75	10.33	60.36	7625
19	Waf x G-98	85.76	112.50	11.38	62.25	5208
20	Waf x K-wal	83.67	109.75	10.75	60.00	6083
21	Waf x Inq	86.18	112.00	10.55	65.89	5959
22	Tak x Iqb	82.66	110.00	11.15	65.07	6083
23	Tak x Mar	87.34	111.75	11.03	63.89	6500
24	Tak x G-98	87.95	108.50	10.78	66.04	7042
25	Tak x K-wal	88.02	111.25	10.20	60.61	8354
26	Tak x inq	86.35	110.75	11.20	60.73	6333
27	Iqb x Mar	85.99	111.75	11.75	63.22	6417
28	Iqb x G-98	76.20	109.25	11.35	66.47	5125
29	Iqb x K-wal	96.91	111.00	11.65	63.68	6604
30	Iqb x Inq	81.14	110.00	10.68	60.04	5834
31	Mar x G-98	82.97	110.25	11.18	59.79	7125
32	Mar x K-wal	106.05	111.50	11.73	64.89	7750
33	Mar x Inq	88.44	109.25	11.48	59.07	6334
34	G-98 x K-wal	86.33	112.75	11.30	64.72	7167
35	G-98 x Inq	81.49	109.25	10.98	62.50	6625
36	K-wal x Inq	113.38	112.25	11.28	62.68	8500
Range		76.2-126.9	108.5-116.5	10.2-12.6	45.75-66.47	3583-8500
Mean		90.76	111.81	11.19	60.58	6046
CV(%)		7.22	1.34	5.23	4.93	19.30
LSD		9.19	2.11	0.82	4.19	1636

251 **Table 3: Scaling tests of additive-dominance model for yield and associated traits in 8x8 F₂ half diallel**
 252 **wheat populations during 2006-07**
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Parameters	t ²	Regression analysis (t value of b)		Conclusions
		b = 0	b = 1	
Days to heading	0.68 ^{ns}	1.11 ^{ns}	2.59*	Model was partially adequate
Plant height	0.01 ^{ns}	1.82 ^{ns}	1.12 ^{ns}	Model was partially adequate
Spike length	0.30 ^{ns}	1.55 ^{ns}	0.83 ^{ns}	Model was partially adequate
Grains spike ⁻¹	3.16 ^{ns}	6.72**	2.36 ^{ns}	Model was fully adequate
Biological yield	0.02 ^{ns}	2.45*	1.0 ^{ns}	Model was fully adequate

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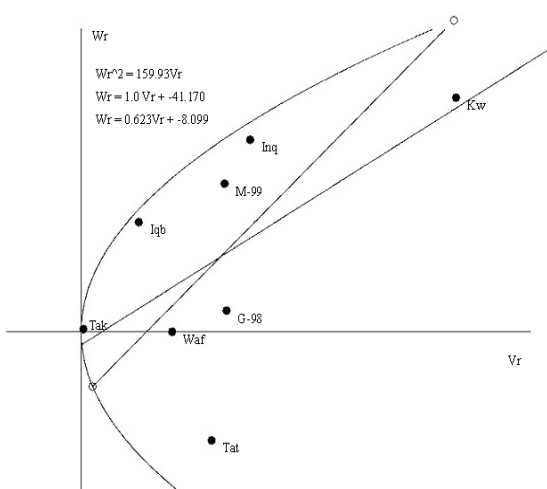


Fig. 1(A).

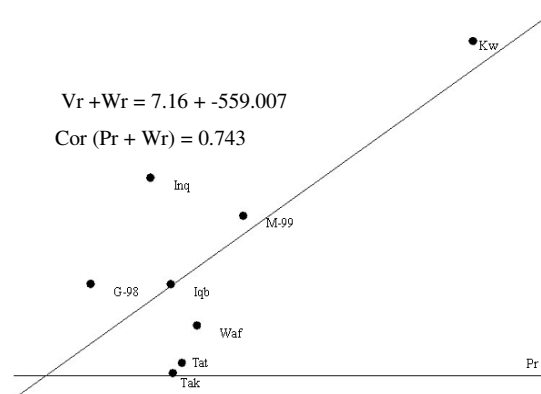


Fig. 1(B).

Fig. 1(a & b). Wr-Vr & Wr+Vr/P graphs for plant height among F₂ wheat populations at Peshawar

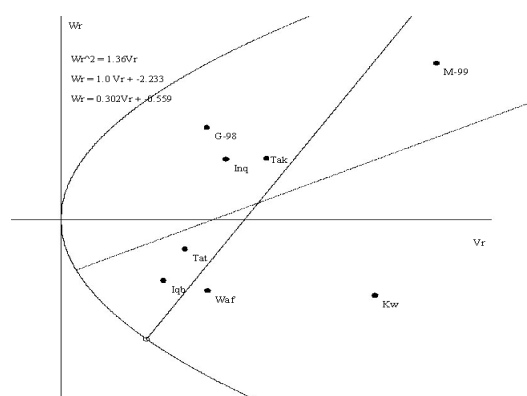


Fig. 2(A).

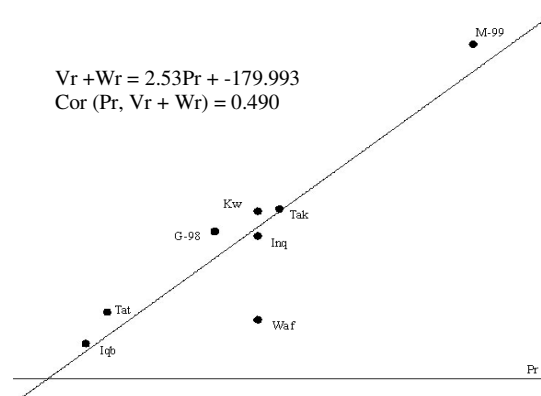


Fig. 2(B).

Fig. 2(a & b). Wr-Vr & Wr+Vr/P graphs for days to heading among F₂ wheat populations at Peshawar

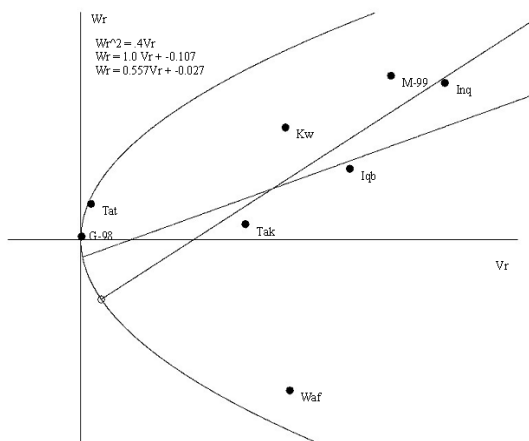


Fig. 3(A).

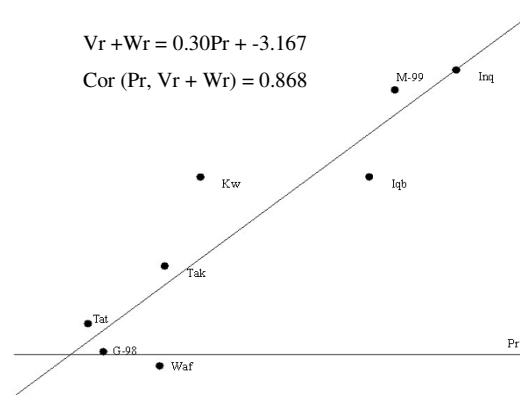


Fig. 3(B).

Fig. 3(a & b). Wr-Vr & Wr+Vr/P graphs for spike length among F₂ wheat populations at Peshawar

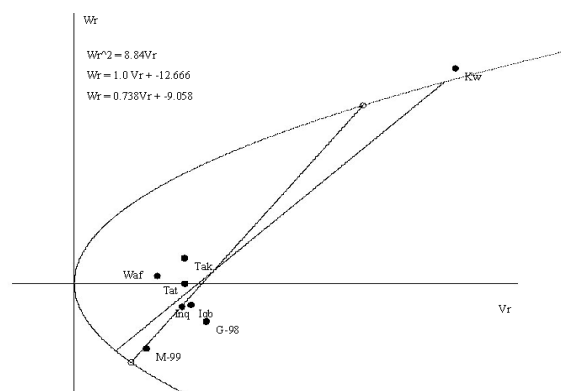


Fig. 4(A).

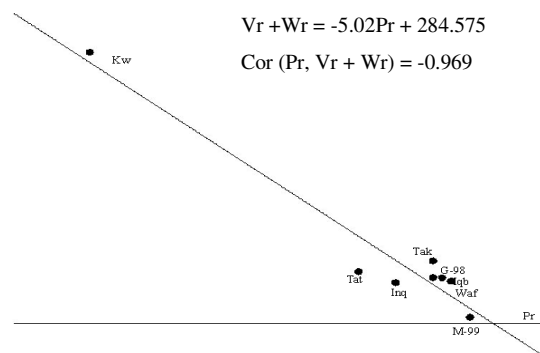


Fig. 4(B).

Fig. 4(a & b). Wr-Vr & Wr+Vr/P graphs for grains spike⁻¹ among F₂ wheat populations at Peshawar

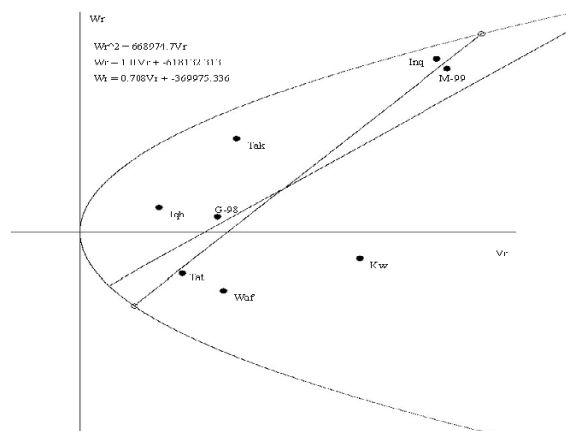


Fig. 5(A).

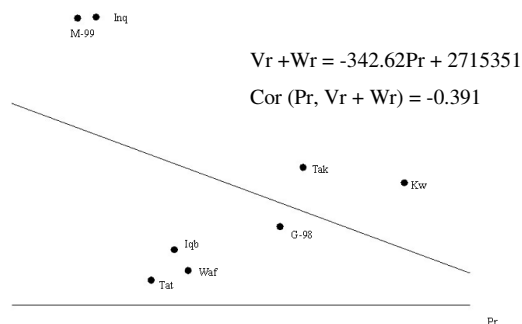


Fig. 5(B).

Fig. 5(a & b). Wr-Vr & Wr+Vr/P graphs for biological yield among F₂ wheat populations at Peshawar