Inheritance Pattern of Five Yield Related Characters in F$_2$ Wheat Populations

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Authors' contributions

This work was carried out in collaboration between all authors. Authors SAJ and FM designed the study. Authors SAJ, FM and IHK analyzed, interpreted and prepared the manuscript. Author ZAS helped in proof reading and approved the first draft. All authors read and approved the final manuscript.

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ABSTRACT

Inheritance mechanism for earliness and yield influencing traits in 8 x 8 F$_2$ half diallel progenies was studied 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 F$_2$ populations for all traits revealing greater genetic variability and thus allowing for further analysis. According to genetic analysis, Vr/Wr graphs indicated over-dominance type of gene action for all traits among parental genotypes and their F$_2$ 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,

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respectively for plant height. However, cultivar Iqbal-2000, Ghaznavi-98, Margalla-99 and Tatara-96 possessed maximum dominant genes for days to heading, spike length, grains per spike and biological yield, respectively.

1. 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 crop that fulfills nutritional requirement of the population in the form of protein and carbohydrates. Wheat occupies more acreage than any other crop in Pakistan due to its suitability under irrigated as well as rainfed conditions all over the country (PBS-2015-16). Wheat produced in the country fulfills most part of our requirements; however, the increasing population demands further improvement in wheat production Jadoon et al. [1].

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 a,b [2]). 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 [3]. Additive type of gene action with partial dominance for spikelets per spike was reported by Ivanovska et al. [4] while Sangwan and Chaudhary [5] identified non-additive gene action for grain yield and related traits in wheat. Similarly Singh et al. [6] reflected additive gene control for grains per spike, number of tillers per plant and grain yield in wheat. However, Navabi et al. [7] reported transgressive segregation among all the F_2 wheat populations and F_5 single seed-decent lines in wheat. Moreover, Jadoon et al. [1], Rabbani et al. [8] and Akram et al. [9] 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. In light of past review, the present study was designed to investigate the inheritance mechanism involved in earliness and other yield related traits among eight parental genotypes and their F_2 wheat populations.

2. MATERIALS AND METHODS

2.1 Breeding Material and Procedure

The experimental material consisted of eight wheat cultivars/lines viz. Tatara-96, Wafaq-2001, Takbeer, Iqbal-2000, Margalla-99, Ghaznavi-98, Khattakwal and Inqalab-91, and their 28 F_2 progenies. The experiment was planted in RCBD having four replicates at The University of Agriculture, Peshawar-Pakistan during 2006-07. 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 at 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 uniformly as and when required to all treatments in the experiment to minimize the environmental effects.

2.2 Data Collection

Ten plants from parental cultivars/lines and thirty from F_2 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. Similarly, grains per spike were recorded as an average of produce of thirty spikes obtained after manual threshing and biological yield by weighing the selected plants from each sub-plot/replication in parental genotypes as well as F_2 populations after harvesting and sun drying.

2.3 Statistical Analysis

After compilation, data for all the traits were analyzed using statistical package 'SAS 6.12' following Steel et al. [10] to detect significant

differences among the genotypes. Traits showing significant differences were further subjected to "t^2" and "regression analysis" for adequacy of additive-dominance model and Hayman (a, b) [2] diallel analysis to study nature of gene action controlling these traits using computer software 'Dial-98' for half diallel F_2 wheat populations following procedures outlined by Morley-Jones [11].

3. RESULTS AND DISCUSSION

The analysis of variance and genotypic differences have been reported by Jadoon et al. [1]. The regression analysis to evaluate gene action is hereby presented.

3.1 Days to Heading

According to Hayman's genetic analysis, Vr-Wr graph reflected involvement of over-dominance for days to heading as the regression line cuts the Vr-axis below the origin (Fig. 1a). Cultivars Iqbal-2000, Wafaq-2001 and Tatara-96 possessed maximum dominant genes being closest to the origin. Ivanovska et al. [4], Mishra et al. [12] and Singh et al. [13] have reported over-dominance to be responsible for yield related traits in bread wheat population. Margalla-99 being farthest from origin possessed maximum number of 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 (Fig. 1a). 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 Vr+Wr values with parental values reflected the importance of recessive gene for controlling days to heading (Fig. 1b).

3.2 Plant Height (cm)

Vr-Wr graph revealed that over-dominance was mainly responsible for controlling plant height as the regression line cuts the Vr-axis below origin (Fig. 2a). Ivanovska et al. [4], Mishra et al. [12] and Singh et al. [13] also reported over dominance for quantitative traits in F_2 wheat populations. However, Ali and Khan [14], Joshi et al. [15], Singh et al. [6] and Zwart et al. [16] 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
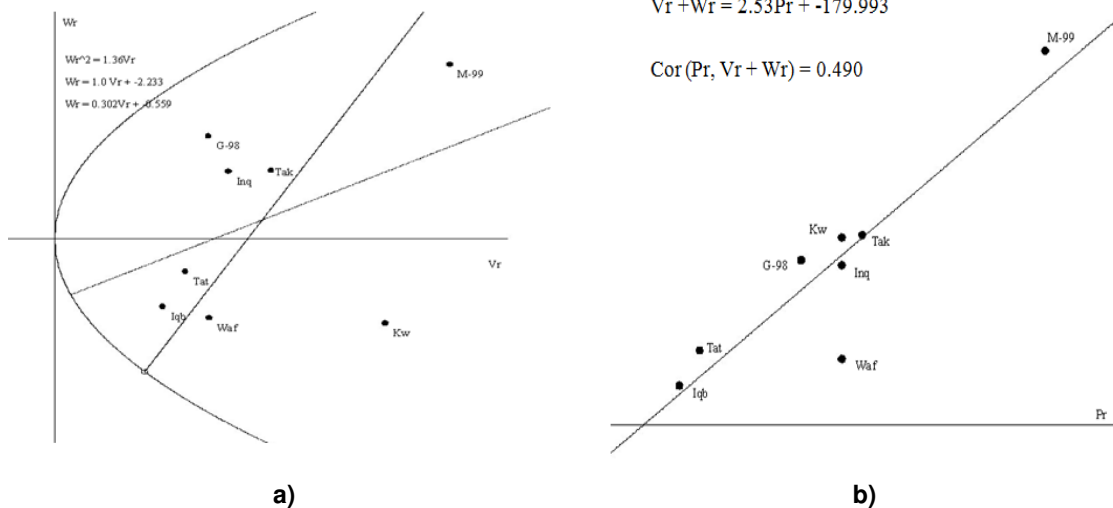

a)   **b)**

Fig. 1(a and b). Wr-Vr & Wr+Vr/P graphs for days to heading among F_2 wheat populations at Peshawar

Tat, Waf, Tak, Iqb, Mar, G-98, K-wal and Inq = Tatara-96, Wafaq-2001, Takbeer, Iqbal-2000, Margalla-99, Ghaznavi-98, Khattakwal and Inqalab-91, respectively

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recessive alleles (Fig. 2a). When Vr+Wr values were plotted against the parental values, positive correlation (r = 0.74) reflected involvement of recessive genes for plant height (Fig. 2b). 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.

3.3 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 Vr-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. [4], Mishra et al. [12] and Singh et al. [13] also reported similar results in their studies. However, contrary to present findings Khan and Ali [17] and Singh et al. [6] 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. [18] and Khan et al. [19] which could be attributed to residual heterozygosity among the parents. Positive correlation (r = 0.868) of Vr + Wr with parental genotypes reflected recessive gene control for spike length (Fig. 3b). Moreover, non-significant deviation of regression line may be an indication of additive gene action.

3.4 Grain Spike^{-1}

Hayman's genetic architecture revealed 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 in all studied cultivars. However, the landrace Khattakwal being farthest from origin exhibited excess of recessive genes. When Vr + Wr values were plotted against the parental values, negative correlation (r = -0.96) was observed which reflected dominant gene control for managing grains per spike (Fig. 4b). Similar results were reported by Khan and Ali [17], and Sangwan and Chaudhry [5] in their studies for tillers plant^{-1}, grains spike^{-1} and grain yield. Moreover, absence of non-allelic interactions was evident from non-significant deviation of regression line from unit slope.

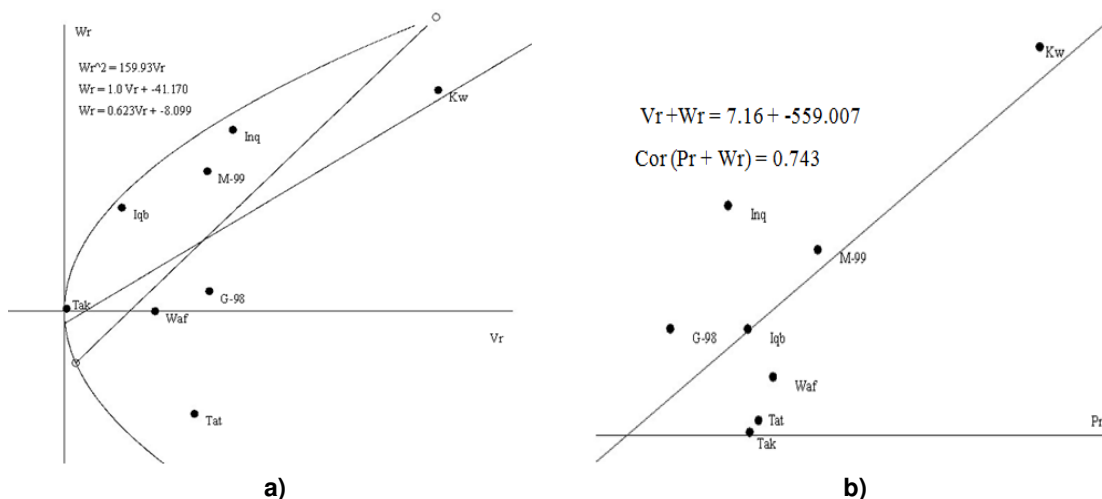a)   b)

Fig. 2(a andb). Wr-Vr & Wr+Vr/P graphs for plant height among F$_2$ wheat populations at Peshawar

Tat, Waf, Tak, Iqb, Mar, G-98, K-wal and Inq = Tatara-96, Wafaq-2001, Takbeer, Iqbal-2000, Margalla-99, Ghaznavi-98, Khattakwal and Inqalab-91, respectively
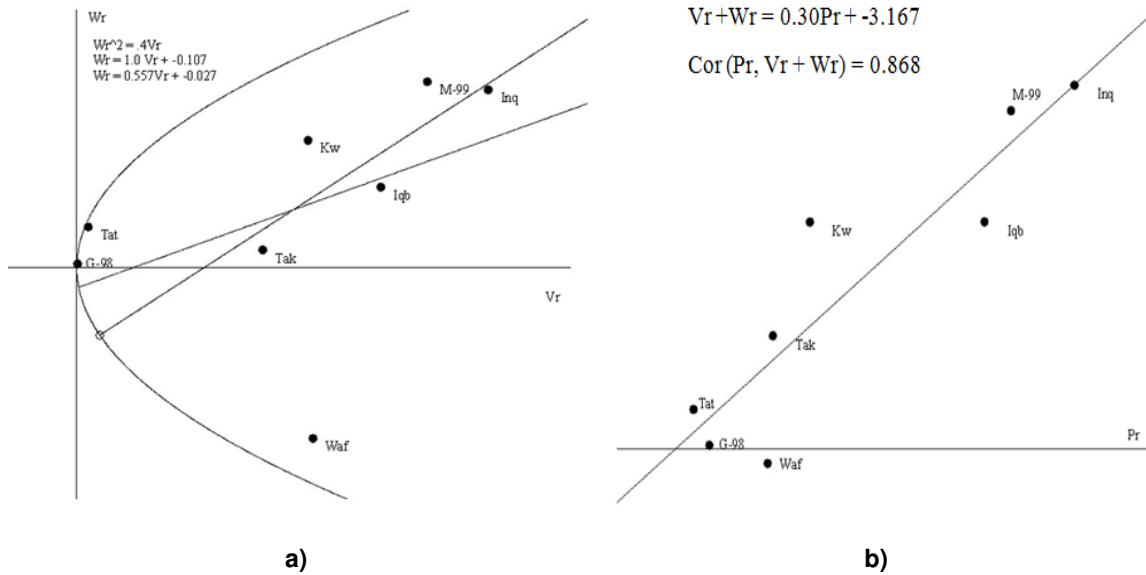
a)

b)

Fig. 3 (a and b). Wr-Vr & Wr+Vr/P graphs for spike length among F$_2$ wheat populations at Peshawar

Tat, Waf, Tak, Iqb, Mar, G-98, K-wal and Inq = Tatara-96, Wafaq-2001, Takbeer, Iqbal-2000, Margalla-99, Ghaznavi-98, Khattakwal and Inqalab-91, respectively

a)

b)

Fig. 4(a and b). Wr-Vr & Wr+Vr/P graphs for grains spike^{-1} among F$_2$ wheat populations at Peshawar

Tat, Waf, Tak, Iqb, Mar, G-98, K-wal and Inq = Tatara-96, Wafaq-2001, Takbeer, Iqbal-2000, Margalla-99, Ghaznavi-98, Khattakwal and Inqalab-91, respectively
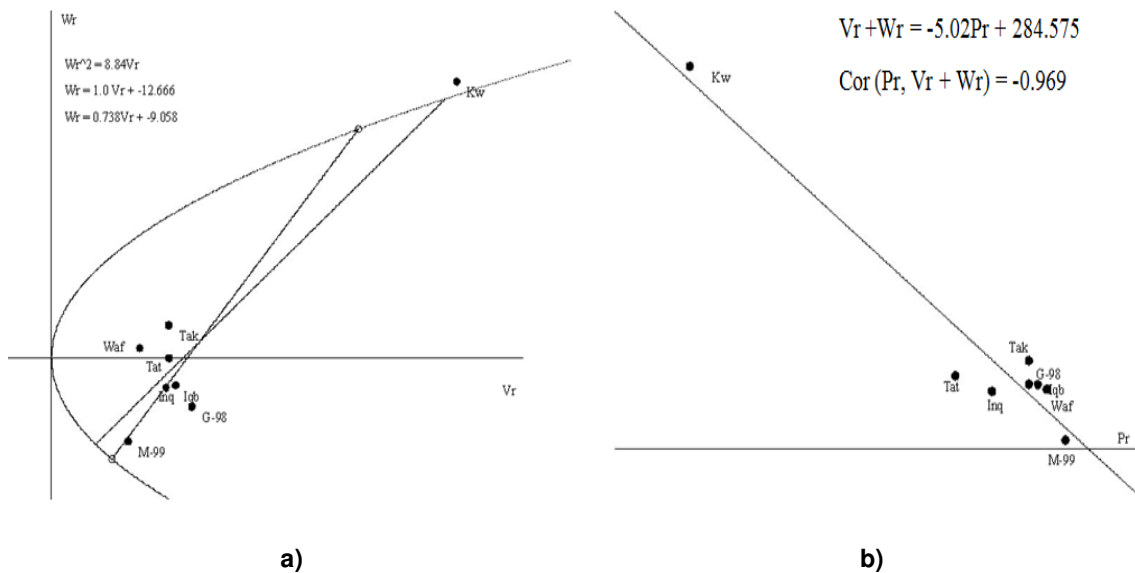
3.5 Biological Yield (kg ha^{-1})

Like other parameters, the biological yield in parental genotypes and their F$_2$ populations was under the control of over-dominance as the regression line cuts Vr-axis below the origin (Fig.

5a). Cultivars Tatara-96, Iqbal-2000, Ghaznavi-98 and Wafaq-2001 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,
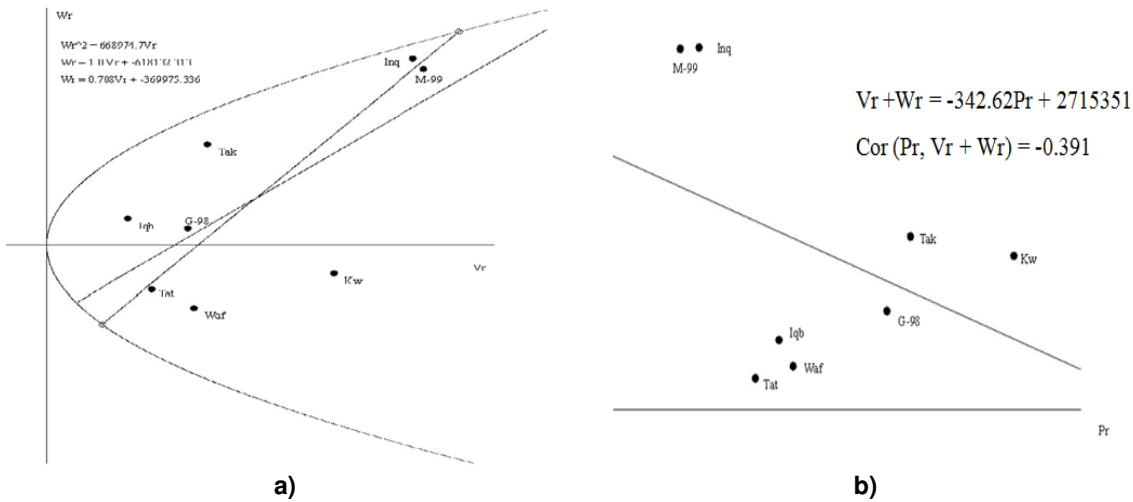
Fig. 5(a and b). Wr-Vr & Wr+Vr/P graphs for biological yield among F₂ wheat populations at Peshawar

Tat, Waf, Tak, Iqb, Mar, G-98, K-wal and Inq = Tatara-96, Wafaq-2001, Takbeer, Iqbal-2000, Margalla-99, Ghaznavi-98, Khattakwal and Inqalab-91, respectively

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 (Fig. 5a). Negative correlation (r = -0.39) among parental genotypes and Vr+Wr values suggested that inheritance pattern for this trait was controlled by dominant genes (Fig. 5b). Over-dominance type of gene action for biological yield and grain yield was also reported by Asif et al. [20], Biranvand et al. [21] and Pall and Kumar [22]. However, Salehi et al. [23] observed that average degree of dominance was less than unity and therefore, suggested partial dominance effects for this trait in wheat genotypes.

4. CONCLUSION

Over-dominance was mainly responsible for inheritance of studied traits among F₂ wheat populations which indicated that selection would be least effective for improvement in earlier generations. 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.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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