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Research Article

Genetic analysis of yield related traits in 5×5 diallel crosses of spring wheat (*Triticum aestivum* L.)

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ABSTRACT

Wheat, a staple crop and an essential component of global food security, holds immense significance for Pakistan due to its historical roots, agricultural contributions, and socio-economic impact. The present study was conducted to reveal the genetics of various yield associated traits in spring wheat using 5 × 5 diallel cross scheme involving high yielding wheat varieties. A total of ten tillers per plant, 1000-grain weight, number of total grains per spike, peduncle length, length of spike, and yield of grain per plant were among the characteristics that were evaluated. Hybrid vigor can be a viable strategy for further improving these characteristics, as the graphical analysis for all characteristics per plant demonstrated supremacy form of gene activity. While additive action of gene with partial dominance dictated the transmission of peduncle length and number of tillers per plant, these features might be improved in early generations by selecting for attractive transgressive segregates. For all of the studied characteristics no epistasis was evaluated. This study is promising and has the potential to significantly impact wheat breeding programs, agricultural productivity, and food security in the coming years.

Keywords: Gene action, Gene manipulation, Heterosis, Population improvement, Polygenic traits, Quantitative traits.

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INTRODUCTION

The work of genetically modifying wheat crops to increase yield and strengthen resistance to common difficulties of drought, salt, disease and insect pest stressors is ongoing. Wheat is among the most widely grown grains and a major food crop in many countries, including Pakistan. As the primary source of carbs and proteins and the "versatile cereal food," wheat has taken center stage in Pakistan's economy. Since wheat is the staple grain of Pakistanis and is grown on the greatest acreages as a commercial crop, it plays a significant role in ensuring food security in our nation. Wheat was grown on 8.67 M. ha last year, and its average yield of 2714 kg/hectare was far lower than its potential. It increased GDP by 2.6% and added 12.5% to agricultural value added (Anonymous, 2011-12).

The need for wheat is rising in tandem with Pakistan's population growth. Consequently, there is a growing disparity between the supply and demand for wheat, necessitating the effective management of the resources at hand. This includes breeders' efforts to produce wheat varieties with high productivity even under stressful conditions and their investigation of the genetic diversity of earlier germplasm, as a different genetic base is necessary to attain sustainability and self-sufficiency. Despite the fact that wheat has long been the subject of extensive research focused on maximizing grain output, there remains a great deal of potential for genetic alteration.

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The most complicated trait in the breeding of wheat historically has been the plant's potential for yield, which is determined by a variety of polygenic factors including tillers per plant, length of spike, 1000-grain weight and grains per spike. These factors all ultimately affect the yield that the crop produces. While Rabbani et al. (2011) recognized supremacy of gene activity regulating the inheritance of the same trait. In terms of grain yield, Irshad et al. (2012) demonstrated a supplementary form of gene activity with partial dominance. Therefore, in order to initiate an effective breeding program and create varieties with improved yield gain, novel combinations of genes must be developed. According to Heyman (1954a,b) and Jinks (1955), the most widely used and practical method for determining the gene action responsible for trait expression starting in the F1 generation and studying the mode of inheritance of quantitative traits in self-fertilized crops like wheat is parallel mating design. In order to choose the optimal parents for a hybridization program and to create recombinants with the desired features, gene action research is essential.

To comprehend the genetic behavior of a few polygenic spring wheat traits, the current research were set up as a five parent diallel cross. Gene action research data can be successfully used to develop suitable plans for the ongoing genetic advancement of this important food crop.

MATERIALS AND METHODS

Plant Material and Measuring Traits

The planned research of the gene activity of several plant morphological characteristics has been concluded. Five different spring wheat cultivars or lines were used as the trial material viz., Farid-2006, Manthar-2008, 9242, 9444 and 9317 and their F_1 crosses. The study involved planting F1 seeds and their parents in a field during Rabi season, crossing them in a diallel fashion. The seeds were planted in a RCBD method with three replications, each with 20 crosses and 5 parental lines. After germination, two seeds per hole were sown using a dibbler, and the seeds were thinned to single seedlings per site. All agronomic practices were uniformly adopted. At maturity, ten competitive plants from each line were randomly selected to record data on length of peduncle, tillers per plant, length of spike, yield of grain per plant, 1000-grain weight and grains per spike,

Statistical Analysis

The research study was conducted three times, and because of a non-significant heterogeneity test, the data collected for each experiment were combined. Every value listed here is the three replications' arithmetic mean. The recorded data was implemented to the ANOVA (Steel et al. 1997). The characteristics exhibiting substantial genotypic variances were additional analyzed by means of diallel analysis method governed by Hayman (1954) and Jinks (1955).

RESULTS AND DISCUSSION

ANOVA technique exposed highly significant genotypic differences for all the characteristics under study indicating that material used had significant genetic diversity (Table 1).

Table 1. Mean squares for different yield parameters of spring wheat in 5×5 diallel cross.

S.O.V	D.F	Peduncle length	Spike length	Tillers per plant	Number of grains per spike	1000-grain weight	Grain yield per plant
Replication	2	3.65^{NS}	2.53^{NS}	2.71^{NS}	2.83^{NS}	2.25^{NS}	1.14^{NS}
Genotypes	24	14.53**	13.09**	8.08*	25.43**	41.58**	24.72**
Error	48	0.19	0.19	0.392	2.15	2.14	0.875

NS = Non-Significant at P> 0.05 ** = Significant at P≤ 0.01 * = Significant at P≤ 0.05

Peduncle Length

Statistical evaluation demonstrated the improved type of action of gene with incomplete or partial dominance for peduncle length as the line of best fit crossed the covariance axis in the point of origin (Figure. 1). Since the line of best fit stayed true to unity, there was no evidence of epistasis. These findings correspond to those of Ajmal et al. (2011) and Nazeer et al. (2010), who similarly identified additive gene activity with partial dominance. However for the similar variable, Samiullah et al. (2010) observed a supremacy form of gene action.

As genotype 9317 is nearest to the origin and has the maximum dominant genes for peduncle length, genotype Farid-06 is farther away from the origin and has the most recessive genes (Fig. 1). This is further indicated by the distribution of display points along the line of best fit. For a decent enhancement of this characteristic, selection in the early generations could prove crucial. At 29.55cm, genotype 9317 has a larger display mean than genotype Manthar-08, which has the lowest display mean of 28.58cm (Table 2).

Table 2. Display means for various characters of spring wheat in 5×5 diallel cross.

Characters	Farid-06	Manthar-08	9444	9242	9317
Peduncle length (cm)	28.96	28.58	29.17	29.16	29.55
Spike length (cm)	14.57	14.00	15.05	14.85	14.64
Number of Tillers plant^{-1}	12.37	12.59	12.07	11.40	12.34
Number of grains spike^{-1}	57.25	60.38	59.78	56.64	60.23
1000-grain weight (g)	42.10	39.16	45.17	43.15	41.29
Grain yield plant^{-1} (g)	20.54	18.55	20.58	19.05	19.42

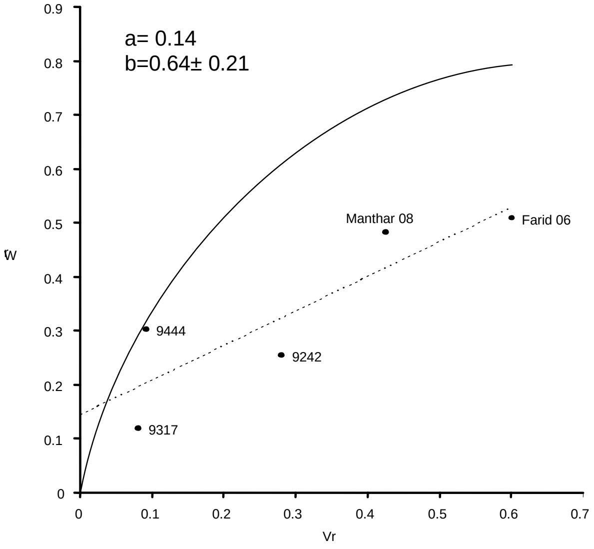

Figure 1. Wr/Vr graph for peduncle length.

Spike Length

The Wr/Vr statistical evaluation demonstrated supremacy form of gene activity for length of spike as the line of best fit interrupts the Wr-axis under the origin (Figure. 2). It is possible that there was no non-allelic interaction or lack of epistasis because the line of best fit's divergence from unity was not significant. Related same findings have also been reported by Nazeer et al. (2011) and Ajmal et al. (2011) while Samiullah et al. (2010) described supplementary foem of activity of gene with incomplete dominance for the similar trait.

The display's placement with line of regression indicates that, because genotype 9444 is located closer to the origin, it has the maximum number of dominant genes for spike length, while genotype 9317 is located farther away, meaning it has the greatest number of recessive genes (Figure. 2). Therefore, the current study suggests that selection may not be possible in the early generations and that it must wait until later generations. With an display mean of 15.05cm, genotype 9444 is an excellent overall combiner for this feature, whereas Manthar-08 has the smallest display mean value of 14.00cm (Table 2).

Number of Tillers per Plant

The statistical evaluation demonstrated that the partial dominance of additive gene action was prevalent, as indicated by the line of best fit's slope on the covariance axis being above the origin (Figure. 3). The lack of epistasis is suggested by the computed line of best fit's little deviation from the unit slope. The current findings are consistent with the findings reported by the Samiullah et al. (2010) and Ahmad et al. (2011). The line of best fit's scattered display points showed that parent 9242 had the maximum number of recessive genes, the furthest from the origin, whereas parent Farid-06 and Manthar-08 looked to have the majority of the dominant genes. Therefore, the possibility of improving this feature through selection in the early generations is strengthened by the existence of an additional form of gene action and incomplete dominance. Manthar-08 was determined to be an outstanding overall combiner with an outstanding display mean of 12.59, whereas genotype 9242 was shown to be a mediocre combiner with an display mean score of 11.40 (Table 2).

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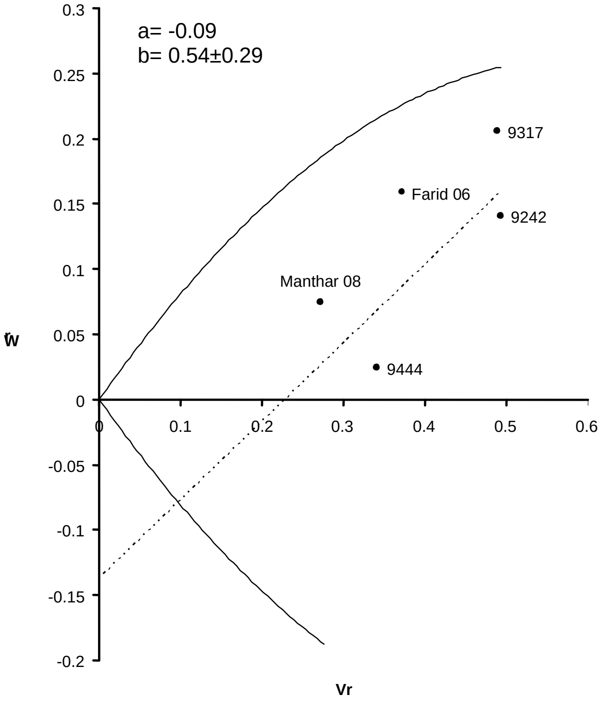

Figure 2. Wr/Vr graph of length of spike.

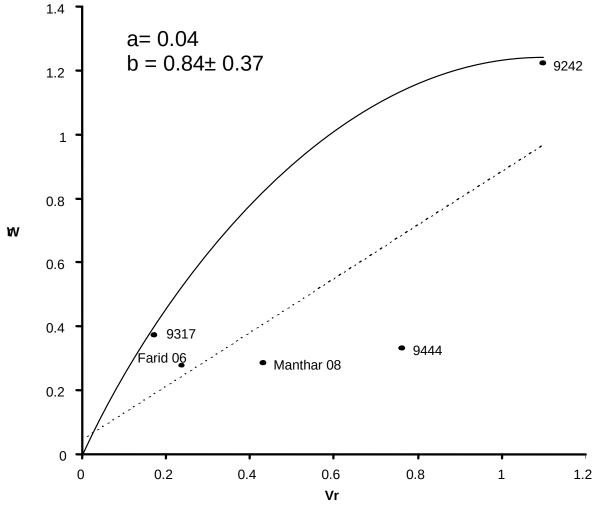

Figure 3. Wr/Vr graph for tillers per plant.

Number of Grains Per Spike

The Wr/Vr statistical evaluation demonstrated that the supremacy form of gene action governs the inheritance of the quantity of grains per spike, as the line of best fit intercepts the covariance axis under the point of origin (Figure. 4). The elevation of line of best fit unit suggested that there were no non-allelic interactions, which is consistent with findings from earlier research by Hussain et al. (2012), Rabbani et al. (2011). The dispersed display points throughout the line of best fit also show that, whereas genotype 9444 carries the majority of the recessive genes for plant height and is located far from the origin, genotype Manthar-08 has the majority of the dominant genes for grains per spike. In the early era, selection was challenging due to the predominance of the supremacy type of gene activity for grains per spike. These findings imply that because supremacy gene action is so common, selection will not be successful in the early stages of segregating generations. With a higher display mean value of 59.78, genotype 9444 is a promising candidate for general combiners, but genotype 9242 performed poorly with a smaller display mean value of 56.64.

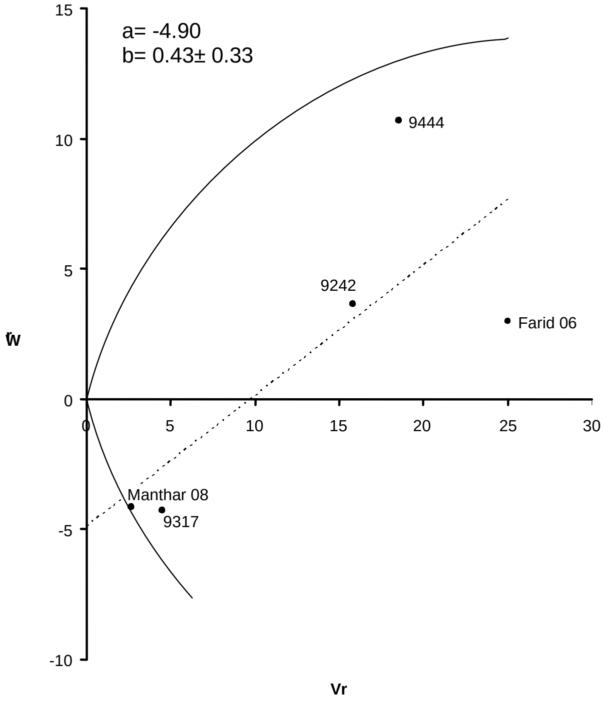

Figure 4. Wr/Vr graph for grains per spike.

1000-grain weight

The supremacy form of gene activity was identified by the statistical evaluation because the line of best fit's intercept on the covariance axis is under the point of origin (Figure. 5). Since there was no non-allelic interaction, the relationship between Wr and Vr was shown to be a straight line of best fit with a unit slope. These outcomes are consistent with the research conducted by Samiullah et al. (2011), Rabbani et al. (2009). According to the placement of the display points on the line of best fit, the genotype 9317 seems to have the majority of its dominant genes near the origin, but the parent Manthar-08 had an abundance of its recessive genes further from the origin. Thus, it may be inferred that the initial generations of selection would not yield fruit for 1000-grain weight due to the supremacy kind of gene activity. The genotype 9444 had the highest display mean value, 45.17 (g), based on the analysis of the display mean, whereas Manthar-08 had the lowest display mean, 39.16 (g) (Table 2).

Grain Yield per Plant

Through the analysis of graphical analysis, it became clear that the supremacy form of gene activity controlled the inheritance of grain yield per plant in the chosen genotypes (Figure. 6). Since the line of best fit does not stray from the base of slop, epistasis was not present. The present findings are consistent with the observations made by Ajmal et al. (2011) and Hussain et al. (2012), but the same feature was found to have additive gene action by Samiullah et al. (2010) and Irshad et al. (2012). Conferring to the location of the display points with the line of best fit, 9317 genotype has the maximum genes of dominant for grain yield when it comes near to the origin, whereas genotype Manthat-08 has the least dominant gene influence when it comes to yield when it comes closest to the origin. Because supremacy genes behave in certain ways, selection must wait until after subsequent generations. With a higher display mean value of 20.58 (g), genotype 9444—a possible universal combiner—performed better than Manthat-08, which had a minor display of 18.55 (g) mean value.

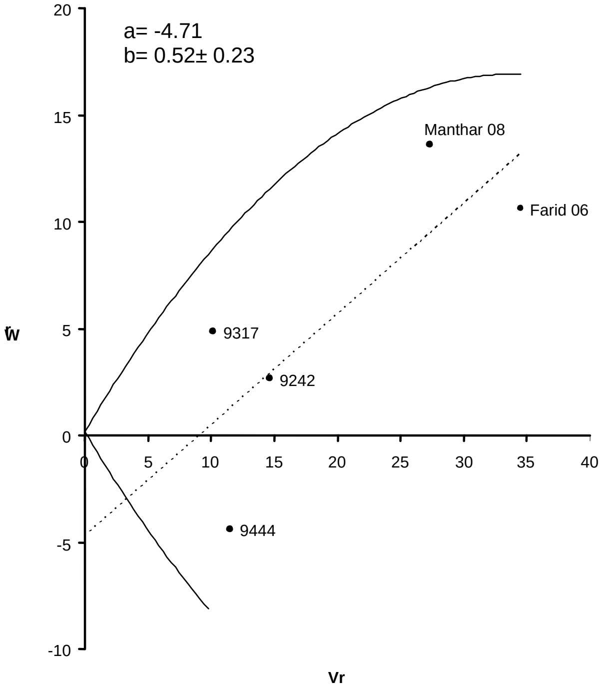

Figure 5. Wr/Vr graph for 1000-grain weight.

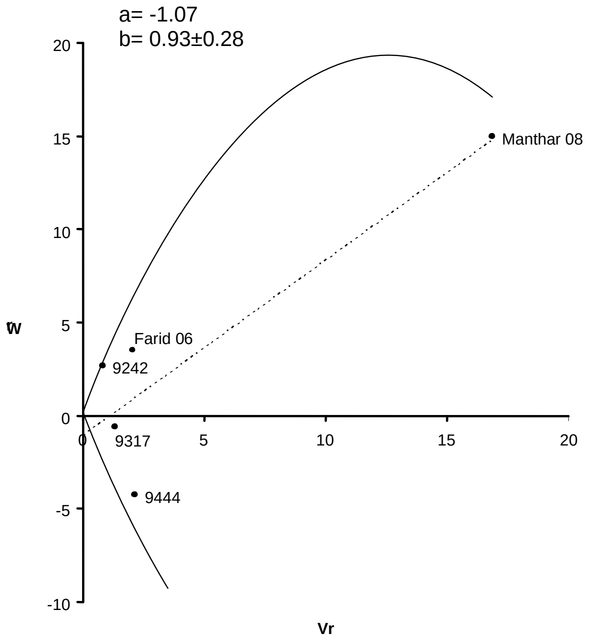

Figure 6. Wr/Vr graph of yield per plant.

CONCLUSION

Significant genotypic variance was found for every characteristic in the current study design. Given the frequency of supremacy gene activity for 1000-grain weight, grains per spike, length of spike and yield of grain per plant, it appears that hybrid vigor might be a viable strategy for enhancing these characteristics. Whereas partial dominance and supplementary gene action governed the transmission of peduncle length and the number of tillers per plant, progressive selection in segregating generations can be useful for future development. The potential for identifying key genetic markers associated with high-yield traits in spring wheat, leading to the development of more efficient breeding strategies and the creation of new wheat varieties with improved yield potential. Additionally, this research could contribute to a better understanding of the genetic mechanisms underlying yield-related traits in wheat, paving the way for targeted genetic manipulation and enhanced crop productivity in the future.

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All authors contributed equally to this research.

REFERENCES

Ahmad, F., S. Khan, S.Q. Ahmad, H. Khan, A. Khan and F. Muhammad. 2011. Genetic analysis of some quantitative traits in bread wheat across environments. African Journal of Agricultural Research. 6(3): 686-692.

Ajmal, S., I. Khaliq and A. Rehman. 2011. Genetic analysis for yield and some yield traits in bread wheat (*Triticum aestivum* L.). J. Agric. Res. 49(4): 447-454.

Akram, Z., S.U.K. Ajmal, G. Shabbir, M. Munir and N.M. Cheema. 2009. Inheritance mechanism of some yield components in bread wheat. Pak. J. Agric. 22(1): 1-8.

Anonymous. 2011-2012. Economic Survey of Pakistan. Ministry of Food, Agriculture and Livestock, Economic Advisor Wing, Islamabad, Pakistan.

Hayman, B.I. 1954a. The theory and analysis of diallel crosses. Genetics. 39: 789-809.

Hayman, B.I. 1954b. Analysis of variance of diallel crosses. Biometrics. 10: 235-245.

Hussain, T., W. Nazeer, M. Tauseef, J. Farooq, M. Naeem, S. Freed, M. Iqbal, A. Hameed, M. A. Sadiq and H. M. Nasrullah. 2012. Inheritance of some spike related polygenic traits in spring wheat (*Triticum aestivum* L.). Afr. J. Agric. Res.. 7(9): 1381-1387.

Irshad, M., I. Khaliq, A. S. Khan and A. Ali. 2012. Genetic studies for some agronomic traits in spring wheat under heat stress. Pak. J. Agric. Sci. 49(1): 11-20.

Jinks, J. L. 1955. A survey of the genetical basis of hetrosis in a variety of diallel crosses. Heredity, 9: 223-238.

Nazeer, W., J. Farooq, M. Tauseef, S. Ahmed, M.A. Khan, K. Mahmood, A. Hussain, M. Iqbal and H.M. Nasrullah. 2011. Diallel analysis to study the genetic makeup of spike and yield contributing traits in wheat (*Triticum aestivum* L.). Afr. J. Biotechnol. 10(63): 13735-13743.

Nazeer, W., Z. Ali, A. Ali and T. Hussain. 2010. Genetic behavior for some polygenic yield contributing traits in wheat (*Triticum aestivum* L.). Pak. J. Agric. 48(3): 267-276.

Rabbani, G., A. Mahmood, G. Shabbir, K. N. Shah and Naeem-Ud-Din. 2011. Gene action in some yield attributes of bread wheat under two water regimes. Pak. J. Bot. 43(2): 1141-1156.

Rabbani, G., M. Munir, S.U.K. Ajmal, F. Hassan, G. Shabbir and A. Mahmood. 2009. Inheritance of yield attributes in bread wheat under irrigated and rainfed conditions. S.J.A. 25(3): 429-439.

Samiullah, A.S. Khan and W. Ashfaq. 2011. Genetic analysis of physio-morphological traits in bread wheat (*Triticum aestivum* L.) under water stress conditions. Cereal Research Communications. Commun. 39(4): 544-550.

Samiullah, A.S. Khan, A. Raza and S. Sadique, 2010. Gene action analysis of yield and yield related traits in spring wheat (*Triticum aestivum*). IJAB. 12: 125-128.

Steel, R.G.D., J.H. Torrie and D.A. Dickey. 1997. Principles and procedures of statistics. A biometrical approach. 3rd ed. McGraw Hill Book Co., NewYork.

https://doi.org/10.55627/agribiol.001.02.0653