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RESEARCH PAPER

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Estimation of genetic mechanism of stomatal traits influencing grain yield in hexaploid wheat (*Triticum aestivum* L.)

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Abstract

Efforts to improve wheat plant have been made at various plant characters. Yield component breeding and modification of the plant architecture offer possibilities to develop more efficient breeding systems for increased grain yield**.** A 6 × 6 diallel experiment was conducted to determine the genetic mechanism of stomatal traits influencing grain yield in hexaploid wheat. Graphical representation indicated the over-dominant type of gene action for 1000-seed weight, seed yield per plant, leaf venation, stomatal size, epidermal cell size and stomatal frequency suggesting that selection would be difficult in early segregating generation. Hence heterosis breeding may useful for genetic improvement for these traits. Non allelic interactions were found to be absent for all traits. The genotype Aas-11 contained maximum dominant genes for epidermal cell size while genotype 9515 for 1000-grain weight and seed yield per plant. The genotype 9516 possessed maximum dominant genes for leaf venation. Whereas, genotype Iqbal-2000 carried maximum dominant genes for stomata size.

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Introduction

Wheat is staple diet throughout the world. It belongs to a large family of plants named as Poaceae. Wheat has a significant importance among all the cereals. Its significance is enhancing to meet the demand of increased population of humans. Wheat yield is very complicated character and its yield cannot be improved through selection of genotypes on the phenotypic basis unless understanding about type of gene action controlling the grain yield and its related parameters. Over-dominance was important for stomatal size, epidermal cell size, leaf venation, and stomatal frequency (Hassaan and Khaliq; Chaudhry *et al.*, 2001). Whereas, partial dominant gene action for leaf venation and epidermal cell size (Subhani and Chowdhry, 2000; Chaudhry *et al.*, 2001). Chowdhry *et al.*, (2002) and Bakash *et al.*, (2004) observed the over-dominant type for 1000-grain weight. Similar finding were observed by Gurmani *et al.*, (2007); Munis *et al.*, (2012) for seed yield. Khan *et al.,* (2000) and Chowdhry *et al.*, (2001) observed the partial dominant gene action for 1000-grain weight. Seed yield is the ultimate goal and that was conditioned by over-dominant type of gene action (Asif *et al.,* 2000; Nazeer *et al.,* 2010) while partial dominant gene action was observed by Farooq *et al.,* (2010). It is necessary to get knowledge about genetic mechanisms of physio-morphic traits that is the basic requirement of any crop improvement program. Thus, precise and complete information about the nature of gene action and mode of inheritance is very important in expression of traits under selection. Hayman (1954a, 1954b) and Jinks (1955) developed diallel technique to well study of systems and actions of genetics related to the expression of genes for different plant traits. Stomata played an important role in exchange of gases between plant and the environment. Maintaining gas exchange in plants at normal rates is essential for maintaining and enhancing plant growth. Water stress is an un-favourable environmental condition which affects the wheat plant growth. Plant traits like, leaf venation, stomatal size, stomatal frequency and epidermal cell size played an important role in increasing efficiency of the plant to cope with unfavorable irrigation conditions. These traits played an important role in developing drought tolerant wheat varieties.

The present study was initiated to ascertain information on the stomatal traits using Diallel method and to search out the new genetic potential among available plant material. These new combinations will be produced and then utilized in further breeding program to enhance existing yield level.

Materials and methods

Plant material

Six wheat genotypes viz., Aas-11, Iqbal-2000, SH-95, 9512, 9515 and 9516 were crossed in a complete diallel fashion during March, 2012-13.

Experimental design

The parents and F_1’s including reciprocals were sown in a triplicated randomized complete block design in the field of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan, on 20th November 2013. The entries were assigned at random to experimental unit in each block and each row contained 20 plants. The row to row and plant to plant distance was maintained at 30 cm and 15cm respectively. All agronomic and plant protection measurements were adopted uniformly for the entire experiment.

Measurement of attributes

At physiological maturity, 1000-grain weight (g), and grain yield per plant (g) were taken. Data for physiological traits were recorded in the morning. The number of stomata per unit area counted from the upper surface of the third nodal leaf of each randomly selected plant. The leaf strips, which were taken from the middle part of the leaf, were dipped in methylated spirit to arrest stomatal movement and removal of chlorophyll from leaf tissues. After 24 hours the leaf strips were removed from solution, peeled off with razor and examined under 10X objective of microscope for counting the number of stomata and number of veins. Leaf strips were examined under the 40X objective of microscope with the help of ocular micrometer to measure stomata size (μm^2) and epidermal cell size (μm^2).

Statistical analysis

Analysis of variance was performed as suggested by Steel *et al.,* (1997) to evaluate the genetic differences among the wheat genotypes. Statistical significance was assumed at 5 level of probability where the mean squares were significant, data were further subjected to diallel analysis technique proposed by Hayman (1954 a, 1954 b) and Jinks (1955).

Results and discussion

Analysis of variances for all traits indicated that there were highly significant differences among all genotypes as shown in Table. 1.

Table 1. ANOVA of various physio-morphic traits of bread wheat in a 6 x 6 diallel cross

Traits	SF	LV	SS	ECS	1000-GW	GY
Replications (df=2)	1.56	0.58	3661.58	22827	14.83	17.95
Genotypes (df=35)	23.77**	2.30**	16019.84**	147826.41**	42.50**	49.43**
Error (df=70)	0.7	0.16	3000.41	5862.23	11.43	6.66

**= Highly significant (0.5%).

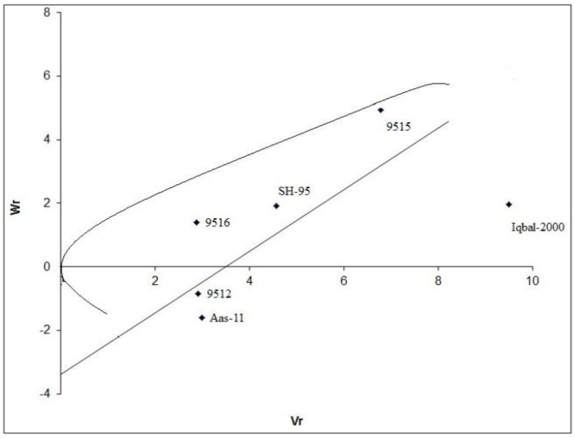

Fig. 1. Stomata frequency.

Inheritance of physiological traits

Stomatal frequency is an important trait where plants need to maintain its high relative water potential in leaf to carry out the normal physiological function. Therefore, less number of stomata will lead to less transpiration of water from leaves and plant can withstand in limited amount of water. Graphical presentation of data indicated the over-dominance type of gene action as the line cuts the Wr-axis on the negative side. Non-allelic interaction was absent. Similar results were found by Chaudhry *et al.,* (2001) and Hassan *et al.,* (2008). The distribution of array points in the graph displayed that genotypes 9512 and Aas-11 followed by 9516 carrying maximum dominant genes for stomatal frequency while genotypes 9515 and Iqbal-2000 were with maximum recessive genes as shown in Fig. 1. Over-dominant type of gene action suggested that selection for this trait would be difficult in early segregating generations.

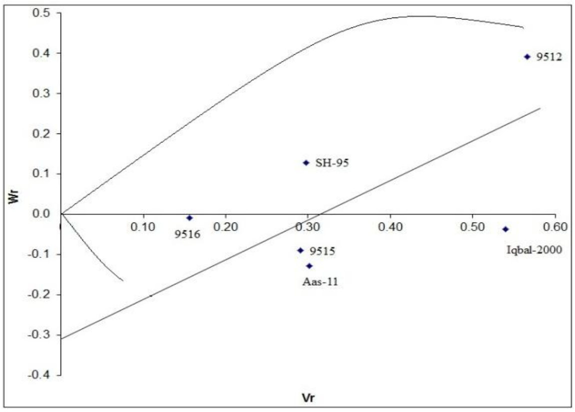

Fig. 2. Leaf venation.

Leaf venation is also one of the important trait. Stomata are arranged inside the veins of leaf. Therefore, more number of veins in leaf then more will be number of stomata. A greater frequency of stomata will lead to more loss of water from the surface of leaf. Wr/Vr graph for leaf venation indicated over-dominant gene action as regression line cut the Wr-axis on the negative side as displayed in Fig. 2. As the regression line followed unit slope so epistasis was absent for this trait. These results are in accordance with those of Subhani and Chowdhry, (2000) and Hassan *et al.,* (2008). The distribution of array points in the graph displayed that genotype 9516 possessed the maximum dominant genes while genotype 9512 carried least dominant genes for this trait.

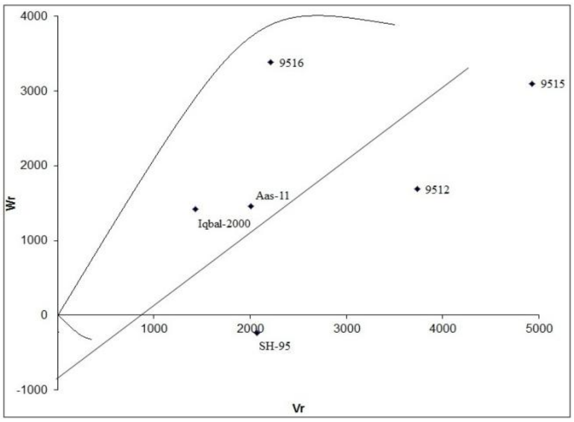

Fig. 3. Stomata size.

Graphical analysis indicated over-dominant type of gene action for stomatal size as the regression line cut the Wr-axis on the negative side. Similar finding has been reported by Hassan *et al.,* (2008). The distribution of array points in graph displayed that genotypes Iqbal-2000 possessed maximum dominant gene while genotype 9515 was the repository of the most recessive genes.

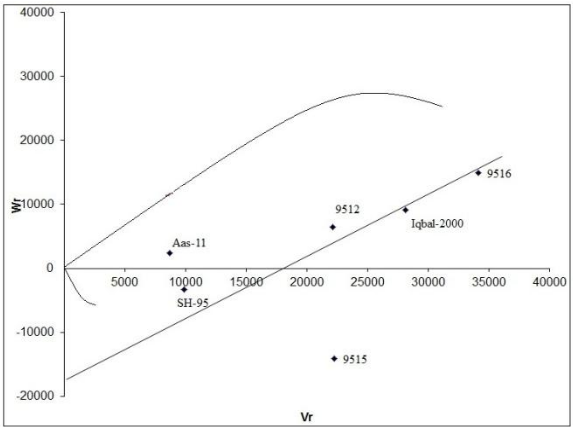

Fig. 4. Epidermal cell size.

Graphical presentation for epidermal cell size indicated over dominant gene action as the regression line cut the Wr-axis on negative side. Hassan *et al.,* (2008) also reported similar results. The position of array points in graph revealed that genotypes Aas-11 followed by SH-95 contained maximum dominant genes while genotype 9516 had minimum dominant genes for this trait.

Inheritance of morphological traits

1000-seed weight is one of the significant yield related parameters. Wr/Vr graph for this trait indicated the over-dominant gene action as the regression line cuts the Wr-axis on the negative side as shown in Fig. 5. Epistasis was found to be absent. These results are in accordance with those of Chowdhry *et al.,* (2001); Chowdhry *et al.,* (2002); Bakhsh *et al.,* (2004); Gurmani *et al.,* (2007); Rashid *et al.,* (2012) and Nazeer *et al.,* (2013). Distribution of array point in the graph displayed that genotype 9516 followed by genotype 9515 carrying maximum dominant genes while SH-95 having most recessive genes.

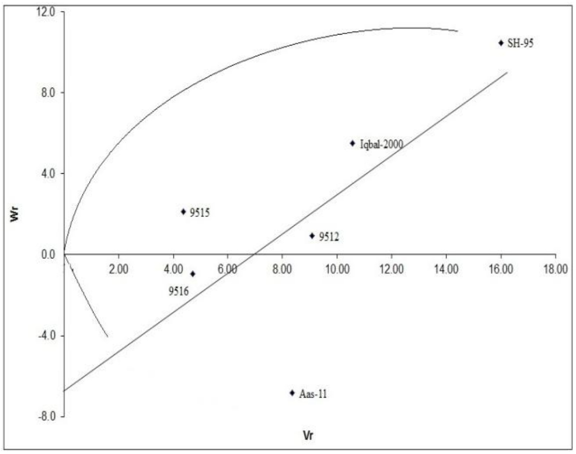

Fig. 5. 1000-Grain weight**.**

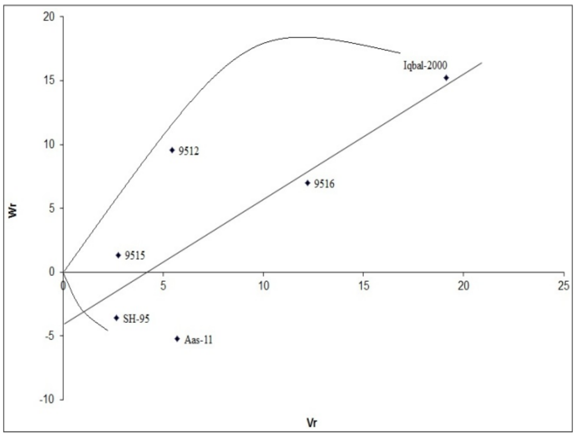

Fig. 6. Grain yield.

Highest yield potential is the ultimate goal of any breeding program so seed yield per plant is very important plant trait that should be given due consideration during selection of genotypes. Graphical presentation for this trait revealed the over-dominant gene action as the line cuts the Wr-axis on the negative side as shown in Fig. 6. These results were similar to the conclusion of Sheikh *et al.,* (2000); Asif *et al.,* (2000); Chowdhry *et al.,* (2001); Chowdhry *et al.,* (2002); Saleem *et al.,* (2005); Dere *et al.,* (2006); Inamullah *et al.,* (2006); Gurmani *et al.,* (2007); Nazeer *et al,*. (2010); Munis *et al.,* (2012): Nazeer *et al.,* (2013). The location of array points in the graph showed that the genotypes 9515 and SH-95 carried maximum dominant genes while Iqbal-2000 possessed maximum recessive genes. In view of over-dominant type of gene action effective selection would be fruitful in later generations for this trait. The results explored that the parental genotype Aas-11 being the potential general combiner and also hold the maximum dominant genes for important yield related traits may prove beneficial to generate desirable combination in future breeding strategies. The crosses Aas-11 × 9516, Aas-11 × 9512 and 9512 × Iqbal-2000 may produce transgressive segregants in the subsequent generations which can be selected and improved.

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