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Research Article

Regression analysis for yield components and quality traits in wheat

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Abstract

The objective of the experiment was to evaluate the genetic parameters of ten genotypes using half diallel analysis. The experiment was conducted at Crop Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut in randomized complete block design (RCBD) using three replications as blocks. The regression analysis using Haymans' approach for days to 50% flowering, days to maturity, number of productive tillers/plant and spikelets per spike revealed that positive intercepts of Wr-Vr regression line supported an additive gene action with partial dominance and the selection could be fruitful for these traits in early segregating generations. While, the regression analysis for traits viz., plant height, flag leaf area, spike length, grains per spike, 1000-grain weight, biological yield per plant, grain yield per plant, harvest index, ash content and gluten content revealed that negative intercepts of Wr-Vr regression line supported an over-dominance gene action and selection should be delayed to later generations.

Key words: Hayman method, graphical analysis, gene action, diallel analysis, bread wheat

1. Introduction

Bread wheat (*Triticum aestivum* L.) is one of the most important cereal crops of the world and it occupies a notable position among food grains of the world not only in terms of acreage and production but also for its versatility in adaptation to a wider range of agro-climatic conditions. Among the several approaches followed for the biometrical genetic analysis for quantitative traits, diallel analysis is most effective with proven merits for ascertaining the systematic genetic architecture of metric traits within a short period. The improvement in yield and quality of wheat varieties in a sustainable way mainly depend upon the genetic potential and desired inherent genetic variability that exists in the population with regards to grain yield.

Diallel mating design has been a useful tool for genetic analysis and used extensively by wheat breeders to analyse mating system in which a set of genotypes are inter-crossed in all possible combinations. However, the diallel analysis developed by Hayman (1954) provides information on genetic mechanism involved in early generations. The major objective of the present study was to generate information on gene action and magnitude of contributing yield and quality components using 10 x 10 diallel crosses excluding reciprocals. The information generated would be effectively exploited to develop an appropriate breeding strategy for continued genetic improvement in wheat crop, for evolving new genotypes with desirable yield and ultimate good quality for nutritional value.

2. Materials and methods

The study material comprising of ten wheat genotypes namely MP 1236, PBW 550, WH 1094, PBW 590, PBW 373, RAJ 3765, DBW 58, HD 2687, DBW 17 and WH 711 was sown at Crop Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut during *rabi* 2010-2011 for attempting of crossing programme in a diallel fashion (10x10). The pedigree details and other passport data showing diversity among these genotypes are given below in Table 1.

Following season (*rabi* 2011-2012) experimental material comprising total 55 genotypes (10 parental line and 45 F_1's) were planted in a Randomized Complete Block Design (RCBD) having three replications. Each of the parental lines and crosses were sown by hand dibbling method in two rows plot (3 m length keeping 25 cm spacing between row and 10 cm between plants). All the recommended agronomic practices were followed to raise good crop and for proper expression of material. Observations were recorded on 10 randomly selected competitive plants in each of three replications for fourteen different characters namely days to 50% flowering, days to maturity, number of productive tillers per plant, plant height (cm), flag leaf area (cm^2), spike length (cm), spikelets per spike, grains per spike, 1000-grains weight (g), biological yield per plant (g), grain yield per plant (g), harvest index (%), ash content (%) and gluten content (%). The data were analyzed statistically using graphical analysis (Wr-Vr) graph suggested by Hayman (1954). The expectations in biometrical scale for various statistics were worked out following Hayman (1954) approach.

Table 1. Pedigree and other passport details of parental lines used for present study

Parent	Parentage/pedigree	Area of adoption	Production condition	Origin
MP1236	GW276/PBW429/HI1077	CZ	IR,LS	JNKVV, Jabalpur
PBW550	WH 594/RAJ 3814//W 495	NWPZ	IR,TS	PAU, Ludhiana
PBW590	WH 594/RAJ 3814//W 485	NWPZ	IR,LS	PAU, Ludhiana
PBW373	ND/VG 1944//KAL/BB/3/YACO`S`4/VEE#5`S`	NWPZ	IR/LS	PAU, Ludhiana
DBW58	ATTILA/3*BCN//BAV92/3/TILHI	NWPZ	IR,TS	DWR, Karnal
DBW17	CMH 79A.95/3*CNO79//RAJ 3777	NWPZ	IR,TS	DWR, Karnal
RAJ3765	HD 2402/VL 639	NW/NEPZ	IR,LS/VLS	RAU, Rajasthan
HD2687	CPAN 2009/HD 2329	NWPZ	IR,TS	IARI, New Delhi
WH1094	WH337/HD2285//URES/BOW	NWPZ	IR,LS	CCSHAU, Hisar
WH711	S 308/ CHR//KAL	NWPZ	IR,TS	CCSHAU, Hisar

Where, NEPZ=North Eastern Plains Zone; NWPZ=North Western Plains Zone; CZ=Central Zone; IR=Irrigated; TS=Timely sown;LS=Late Sown; and VLS=Very Late Sown

Information about gene action was inferred by plotting the covariance of each array against its variance. The slope and position of the regression line fitted to the array points within the limiting parabola indicated the degree of dominance and the presence or absence of gene interaction. The position of regression line on Wr-Vr graph provides information about the average degree of dominance given below:

I. When the regression line passes through the origin, it indicates dominance ($D=H_1$).

II. When it passes above the origin cutting the Wr-axis, it shows that there is partial dominance ($D>H_1$).

III. When it passes above the origin, cutting Wr-axis and touching he limiting parabola, it suggests the absence of dominance.

IV. But when it passes below the origin, cutting the Vr-axis, it denotes the presence of over dominance.

3. Results and discussion

3.1 *Days 50% flowering:* The regression analysis for days 50% flowering revealed that positive intercepts of Vr/Wr regression line supported an additive gene action with partial dominance. This result suggests that the selection in early generation may be fruitful. Varieties HD 2687, DBW 58, DBW 17 and WH 711 possessed maximum dominant genes being nearest to the origin, while varieties MP 1236 and PBW 550 possessed maximum recessive genes being farthest from the origin. It means that genotypes are efficient for taking minimum time to reach the flowering stage when used in hybrid condition. The rest parents possessed equal proportion of dominant and recessive genes. The estimated regression line was not deviated significantly from the unit slope, this suggests the absence of non allelic interaction. Similar results were reported by Farshadfar *et al.* (2013).

3.2 *Days to maturity:* The graphical representation of Vr-Wr graph indicated the additive gene action with partial dominance for this character, as the regression line cuts Wr-axis just above the point of origin. The regression line did not deviate significant from unit slope. It is apparent from the graphic illustration that variety WH 711 being closest to the origin possessed maximum dominant genes whereas PBW 550 contained maximum recessive genes being farthest from the point of origin. Ullah *et al.* (2010) and Farshadfar *et al.* (2012) reported similar finding for most of the trait as given in the present study.

3.3 *Plant height:* The regression analysis for plant height revealed that negative intercepts of Vr-Wr regression line supported an over-dominance gene action. This results suggests that the selection in early generation may be unfruitful. Genotypes PBW 590 and RAJ 3765 possessed maximum dominant genes being nearest to the origin, while line DBW 58 possessed maximum recessive genes being farthest from the point of origin. The intercept of regression line on the covariance ordinate being below the origin, show a clear cut case of over-dominance. Similar findings were reported by Chowdhry *et al.* (2002), Adel and Ali (2013) and Farshadfar *et al.* (2013).

3.4 *Number of tillers/plant:* From Vr-Wr graph (Figure 1a), it was evident that regression line cut the Wr-axis above the origin revealing additive and partial dominance type of gene action. Epistasis was present as the regression line deviate significantly from unit slope. Parents DBW 58 and HD 2687 possessed maximum dominant genes being closest to the point of origin, whereas the parent WH 711 and WH 1094 had maximum recessive genes being farther from the origin. However for rest of the parents with equal frequencies of dominant and recessive genes occupy an intermediate position. Similar finding were reported by Adel and Ali (2013).

3.5 *Flag leaf area*: From Vr-Wr graph (Fig. 1b) for flag leaf area, it was evident that regression line passed through the Wr-axis below the origin revealing over-dominance type of gene action. Epistasis was absent as the regression line did not deviate significantly from unit slope. Saleem *et al.* (2005) reported similar type of gene action while studying this trait. HD 2687 and RAJ 3765 possessed maximum dominant genes being closed to the point of origin, whereas the genotype PBW 550 and MP 1236 had maximum recessive genes being farther from the origin. Due to the over-dominance shown by this trait, genotypes are more efficient in producing more leaf area in hybrid combinations and the selection in the early generation may not be fruitful for this trait.

3.6 *Spike length:* The graphical representation of Vr-Wr graph indicated the additive gene action with over-dominance type of gene action controlling the inheritance of spike length with a genotypes of unit slope and negative intercept of the regression line. Distribution of the array points in the graph represented the genetic constitution of the genotypes. It was observed that the HD 2687 and PBW 373 had the maximum dominant genes for spike length, while the genotype having the most recessive genes was MP 1236 followed by WH 711 and WH 1094. Reflecting more dominant and recessive genes occupy an intermediate position. These findings are also in agreement with the findings of Chowdhry *et al.* (2002) who also found over-dominance type of gene action for spike length.

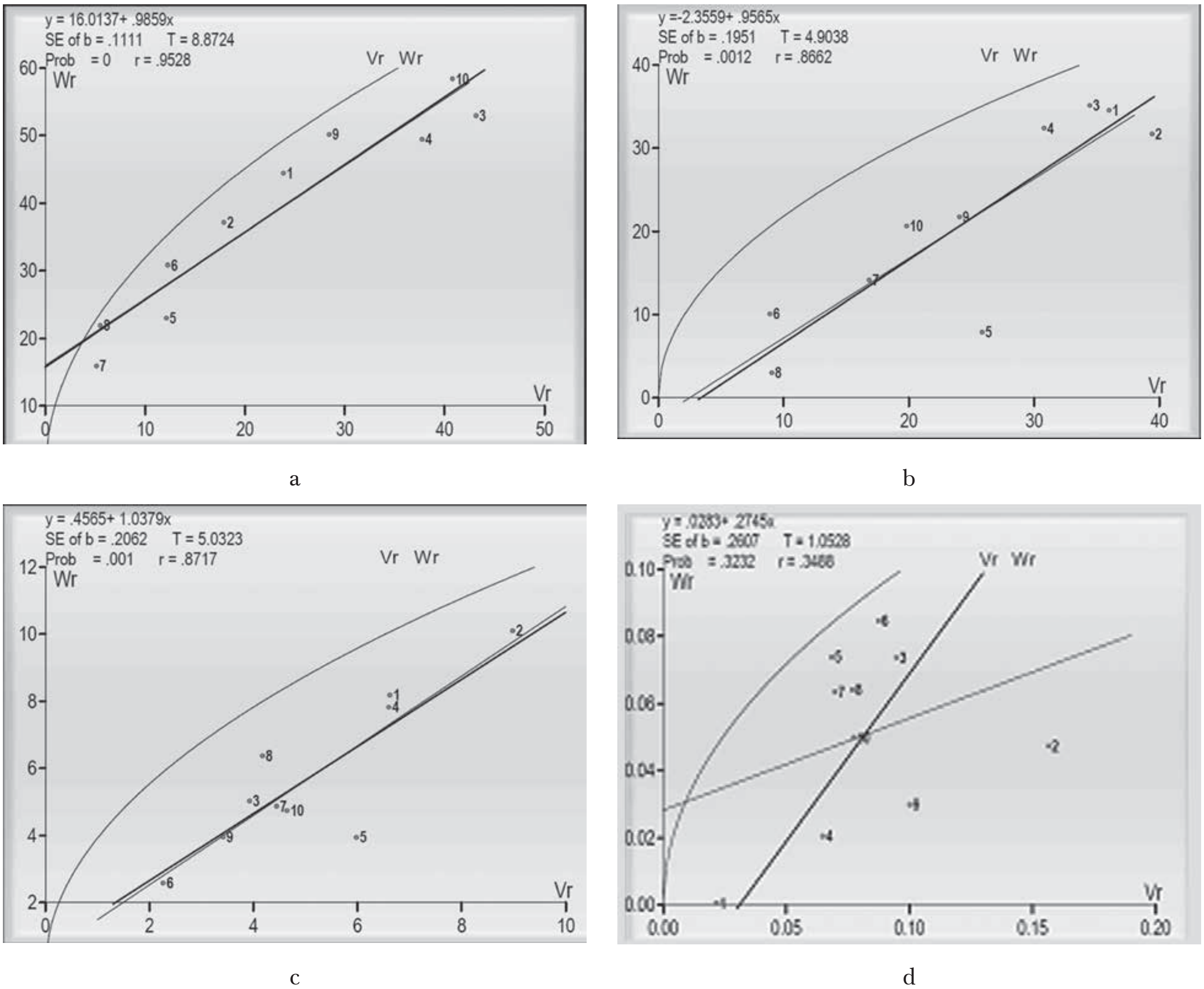

Fig. 1 Vr/Wr graph for a) number of productive tiller per plant b) flag leaf area c) grain yield per plant and d) gluten content

1: MP 1236, 2: PBW 550, 3: WH 1094, 4: PBW 590, 5: PBW 373, 6: RAJ 3765, 7: DBW 58, 8: HD 2687, 9: DBW 17, 10: WH 711

3.7 *Spikelets per spike:* The regression analysis for spikelets/ spike revealed that negative intercepts of Wr-Vr regression line supported a partial dominance gene action. The result suggests that the selection in early generation may be fruitful for this trait. Genotypes HD 2687 and DBW 17 possessed maximum dominant genes being nearest to the origin, while genotype PBW 590 possessed maximum recessive genes being farthest from the origin. The estimated regression line was not deviated significantly from the unit slope; this suggests the absence of non allelic interaction. Similar finding were reported by Khan *et al.* (1992) and Adel and Ali (2013).

3.8 *Grains per spike:* Over-dominance was noted as the regression line of unit slope intersected the Wr-axis below the point of origin. The distribution of array points showed the concentration of dominant genes in bread wheat genotype DBW 58 followed by DBW 17, HD 2687 and RAJ 3765. PBW 550 studied farthest from the origin was carrying maximum recessive genes. Rest parents with equal frequencies of dominant and recessive genes occupy intermediate position. Almost similar trend of involvement of over-dominance gene action has also been reported by Chowdhry *et al.* (2002).

3.9 *1000-grains weight:* Vr-Wr graph indicated that 1000-grains weight was governed by additive type of gene action with over-dominance, as the regression line intercepted the Wr-axis well below the point of origin. The regression line did not deviate significantly from unit slope. DBW 17, HD 2687, PBW 590 and WH 711 possessed maximum dominant genes being closed to the origin, whereas the variety MP 1236 had maximum recessive genes being farther from the origin. The array points on the regression line indicated the genetic diversity among parents. The findings are in conformity with Chowdhry *et al.* (2002), Kashief and Khaliq (2003) and Farshadfar *et al.* (2013).

3.10 Biological yield: Graphical representation revealed that the regression line intercepted the Wr-axis just below the point of origin which indicated the presence of over dominance type of gene action for biological yield. Genotypes PBW 373 possessed maximum dominant genes being closest to the origin, whereas the variety PBW 550 had maximum recessive genes being for the trait being father from the point of origin. The result of this study was in agreement with Rabbani *et al.* (2011).

3.11 Grain yield per plant: From results presented in (Fig. 1c) it was observed that regression line intercepts the Wr-axis on the negative side of the origin, so, this indicates the over dominance type of gene action. Variety RAJ 3765 possessed maximum dominant genes whereas the parent PBW 550 had maximum recessive genes for grain yield. The regression line deviate significantly from unit slope, this indicates that present of non-allelic interactions. According, to the pattern of inheritance for yield seems too difficult to fix and the progress in selection will be inherently slow. Such types of findings of over-dominance type of gene action were also reported by Chowdhry *et al.* (2002), Kashief and Khaliq (2003), Adel and Ali (2013) and Farshadfar *et al.* (2013).

3.12 Harvest index: Graphical analysis of the data depicted an over-dominance type of gene action with a line of unit slope and negative intercept of the regression line. Distribution of the array points in the graph represented the genetic constitution of the parental lines. It was observed that DBW 58 had the maximum dominant genes for HI. The parents containing the most recessive gene was PBW 373. Rest of genotypes had intermediary gene constitution. Present findings are supported by the results of Rabbani *et al.* (2011)

3.13 Ash content: The graphical analysis of Vr-Wr graph depicted an additive type of gene action with over-dominance controlling the inheritance of ash content with a line of unit slope and positive intercept of the regression line. Distribution of the array points in the graph represented the genetic constitution of the parental lines. It was observed that the DBW 58, PBW 373 and RAJ 3765 had the maximum dominant genes for ash content, while the genotypes containing the most recessive and the least dominant genes was PBW 550. In earliar studies role of over-dominance type of gene action were reported by Farshadfar *et al.* (2013).

3.14 Gluten content: The regression coefficient did not differ significantly from unity. The regression line cuts the Wr-axis below the point of origin (Fig. 1d) indicating the control of over dominance for this trait. The position of the varietal array on the graph showed that MP 1236 contained the maximum number of dominant genes while RAJ 3765 the most recessive genes. Similar finding were reported by Kashief and Khaliq (2003).

Graphical analysis indicated that days to 50% flowering, days to maturity, number of productive tiller/plant and spikelets per spike were controlled by additive gene action with partial dominance in the absence of non-allelic interaction suggested that selection in early segregating generations may be heriatable and fruitful for these traits. The characters such as plant height, flag leaf area, spike length, grains per spike, 1000-grain weight, biological yield per plant, grain yield per plant, harvest index, ash content and gluten content were governed by over-dominance type of gene action suggested that the selection should be postponded to later generations for these traits. In genotypes namely, RAJ 3765, HD 2687, PBW 373, DBW 58, DBW 17 and PBW 590 distribution along with the regression line showed that maximum dominant genes for almost all the traits, while the regression line revealed that maximum recessive genes for most of the characters were present in PBW 550, MP 1236, WH 711 and WH 1094. Therefore, findings of present investigation will help multiple traits breeding programme to develop high yielding and better quality genotypes.

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