

GENETIC ANALYSIS FOR GRAIN QUALITY TRAITS IN PAKISTANI WHEAT VARIETIES

NASIR MAHMOOD MINHAS*, SAIF ULLAH AJMAL, ZAMMURAD IQBAL AHMED AND MUHAMMAD MUNIR

Department of Plant Breeding and Genetics, PMAS Arid Agriculture University, Rawalpindi, Pakistan

*Corresponding author e-mail: nmminhas@hotmail.com

Abstract

A set of eight parental diallel involving seven commercial wheat cultivars and one breeding line was made to investigate the nature of gene action determining inheritance pattern of grain quality characters. Highly significant differences were observed among the genotypes for 1000 grain weight, protein content, wet gluten and lysine content. Adequacy tests were employed to estimate the fitness of data sets to additive dominance model. Both the tests i.e. analysis of uniformity of W_r , V_r and joint regression analysis validated the data of these traits for genetic analysis.

Gene actions for grain quality traits were ascertained following Hayman's analysis of variance. Results of the genetic analysis revealed that both additive and dominance genetic components were involved in the manifestation of characters under study. However, additive gene effects were more pronounced in the genetic control of these traits. Non significance of b_1 , b_2 and b_3 values revealed the absence of directional dominance, symmetrical distribution of genes among the parental lines and absence of specific genes action respectively in all the traits. Maternal effects were also noted in 1000 grain weight, protein content and wet gluten percentage. It is concluded that additive effects are crucial in the expression of grain quality characters of wheat in germplasm under study and single plant selection may be recommended in segregating generations for effective improvement in these characters.

Introduction

World's population is increasing day by day at a quite rapid rate and there is a need for staggering increase in food production to feed huge population. Due to significant accomplishment made in agricultural research, thousands of new crop varieties have been released and the production has been remarkably increased throughout the world. A great deal of research work has been done in the domain of wheat breeding in Pakistan and the country has made tremendous progress in wheat production. During the year 2009-10, the production was 23.8 million tonnes (Anon., 2010). To keep pace with burgeoning population growing at the rate of approximately 2.0 % per year, it is necessary to further increase the productivity level to meet the requirement of 250 million people in the country up to the year 2020.

In Pakistan wheat breeding efforts remained focused on higher yields and resistance/tolerance against rust diseases. In this bidirectional breeding programme of the past, the potential for grain quality in wheat germplasm remained unexploited. Wheat is supreme among cereals largely due to the fact that its grain contains protein with unique chemical and physical properties. Therefore, there is a dire need to understand the inheritance pattern of wheat grain quality characters and to improve the genotypes on these aspects (Hussain *et al.*, 2012; Ali *et al.*, 2013). The knowledge of inheritance governing mechanisms provides the basis for architecting genotypes comprising of desirable genes.

The diallel cross technique as advocated by Hayman (1954) and Jinks (1954) offers a method especially in self fertilized crops like wheat to assess the crosses right in the F_1 generation and provides the necessary genetic information on the plant characters to determine the right breeding approach. Results of previous studies showed different pattern of inheritance. Siddique *et al.*, (2004), Awan *et al.*, (2005), Kamaluddin *et al.*, (2007) and

Dagustu (2008) reported that additive genetic effects were involved in the inheritance of 1000 grain weight. Whereas, certain other scientists have revealed dominance type of gene action for this character (Sanjeev *et al.*, 2005, Akbar *et al.*, 2009, and Cifci & Yagdi, 2010). Iqbal & Khan (2006) and Akram *et al.*, (2007) studied the gene action for protein content and found that it was under the genes acting additively. However, non additive type of gene action was reported by Budak (2001) and Sanjeev *et al.*, (2005). Rathod *et al.*, (2008) and Singh *et al.*, (2009) found that grain protein and other quality traits were conditioned by both additive and non additive gene effects. Akram *et al.*, (2007) revealed the dominance genetic effects governing wet gluten and lysine content.

Materials and Methods

The investigated plant material comprised of seven approved wheat cultivars; Rawal 87, Chakwal 97, Sarsabz, Wafaq 2001, GA-2002, Bhakkar 2002 and one advance breeding line. AUR111 for studying the genetic basis for grain quality traits. The genotypes were crossed in complete dialled fashion.

The seed of F_1 hybrids and the parental lines were planted in the research area of Arid Agriculture University Rawalpindi during Nov 2007. Randomized complete block design with three replications was followed single row of 5m length served as an experimental unit. Inter row and interplant distance were kept at 30 cm and 20 cm respectively. Fertilizer doze of NP at the rate of 100-40 kg ha⁻¹ was applied to the field.

The crop was harvested at maturity and the data were recorded for 1000 grain weight, protein content, wet gluten and lysine content.

Protein contents were determined by kjeldhal's method of nitrogen estimation and protein values were calculated as $N \times 6.25$ wet gluten percentage was measured by the method described by Kent & Evers (1994).

Similarly lysine content were estimated following the technique given by Miyahara and Jikoo (1967).

The data was subjected to statistical analysis following steel *et al.*, (1997). The data sets were validated through adequacy tests to check the fitness to additive dominance model. Analysis of uniformity of w_r - V_r and joint regression analysis were employed.

In first test, w_r , V_r is expected to be constant over arrays, if all the assumptions of additive dominance model were fulfilled. Heterogeneity of w_r , V_r arrays shows either one or more assumptions are not fulfilled for that character. Similarly in the second test regression coefficient (b) of a covariance on variance of each character is expected to be satisfactory different from zero and at the same time not significantly different from unity, if all the assumptions hold true.

The Hayman-Jinks method is considered as powerful tool for analysis of gene action due to the degree of the analysis that makes it more informative than the other methods of genetic analysis (Toledo & Kibbi, 1982). The same technique was used in the present study.

Results and Discussion

In present study an attempt was made to understand the genetic mechanism of grain quality traits in intervarietal crosses of eight wheat genotypes. These results provided useful information about the genetic basis of variation for important quality traits. The preliminary data on 1000 grain weight, protein content, wet gluten and lysine content were analyzed using ordinary analysis of variance technique. The mean squares of the analysis showed that genotypic differences for all the characters examined were highly significant (Table 1).

To test the adequacy of the data set to the simple additive-dominance model, the analysis of uniformity of w_r , V_r (t^2) and regression analysis were carried out. The results of both scaling tests are presented in Table 2. The regression slope deviated significantly from zero and was equal to unity suggesting that epistasis was absent and genes were distributed independently among the parents for all the grain quality characters. Similarly uniformity of w_r , V_r also suggested the indication of absence of non-

allelic interaction of genes. Therefore, both the tests suggested that additive-dominance model was adequate to proceed further for genetic analysis of these characters.

1000 grain weight: The result of Hayman's analysis of variance of diallel data for 1000 grain weight is given in Table 3. The significant 'a' and 'b' items exhibited the presence of additive and dominance genetic effects. The non significant 'b₁' revealed the absence of directional dominance. Similarly items 'b₂' and 'b₃' were also non significant indicating the uniform distribution of genes and the absence of specific gene effects respectively. Due to significant 'c' and 'd' items, maternal effects and reciprocal effects respectively were also present, and thus items 'a' was retested against 'c' and mean squares of 'b', 'b₁', 'b₂' and 'b₃' against 'd' mean square. After retesting 'a' item, which was previously highly significant had reduced to significant ($p \leq 0.05$) and thus indicated the preponderance effects of genes acting additively. The non significant values of 'b₁', 'b₂' and 'b₃' remained unchanged after testing against 'd'. However, the significant effects due to 'b' were reduced to non significant. This showed that general dominance effects were suppressed due to reciprocal effects.

Protein content: The analysis of variance of diallel table showed that 'a' and 'b' items exhibited significant differences among the hybrids and parental lines for protein content (Table 4). The significant 'a' and 'b' items revealed the pronounced contributing of genes showing additive and dominance gene effects. Asymmetry of gene distribution among the parents was indicated by significant 'b₂' item ($p \leq 0.01$). Non significant values of 'b₁' and 'b₃' revealed the absence of directional dominance effects and specific genetic effects respectively. The effects due to 'c' were significant indicating the presence of maternal effects and also necessitated the retesting of 'a' against mean squares of 'c'. However, reciprocal effects were not found as variance due to item 'd' was non significant. After retesting the variance of additive component 'a', which was highly significant against its own interaction, remained unaltered.

Table 1. Analysis of variance for different wheat grain quality characters in an 8x 8 wheat diallel cross.

Parameters	Genotypic mean squares	Replication mean squares	Error mean squares
1000 grain weight (g)	26.236**	2.658	1.364
Protein content (%)	1.861**	0.335	0.154
Wet gluten (%)	13.531**	0.680	0.767
Lysine content (%)	0.387**	0.043	0.027

** = Significant at 1 % probability level

Table 2. Adequacy of data sets for grain quality characters to additive-dominance model through analysis of uniformity of w_r - V_r and Joint Regression Analysis.

Parameters	Analysis of uniformity of w_r - V_r (t^2)	Joint Regression Analysis		
		Regression coefficient \pm Standard error	Ho : b = 0	Ho : b = 1
1000 grain weight (g)	2.502	1.064 \pm 0.456	23.294**	1.399
Protein content (%)	0.086	1.007 \pm 0.059	17.036**	0.116
Wet gluten (%)	0.145	1.010 \pm 0.036	27.510**	0.269
Lysine content (%)	0.025	1.001 \pm 0.048	20.486**	0.012

** = Significant at 1 % probability level

Table 3. Hayman's analysis of variance for 1000 grain weight in 8 x 8 diallel cross of wheat.

Source of variation	D.F.	Mean squares	F. ratio	Retested against	
				c	d
a	7	209.7767	81.622 **	23.080**	
b ₁	1	4.354	5.342		1.780
b ₂	7	1.778	2.731		0.727
b ₃	20	2.632	0.444		1.076
b	28	2.481	2.417 **		1.014
c	7	9.089	6.624 **		
d	21	2.446	1.736		
Total	63	26.236			
B x a	14	2.574			
B x b ₁	2	0.815			
B x b ₂	14	0.651			
B x b ₃	40	1.168			
B x b	56	1.026			
B x c	14	1.372			
B x d	42	1.409			
Total interaction	126				

** = Significant at 1 % probability level

Table 4. Hayman's analysis of variance for protein contents in an 8 x 8 diallel cross of wheat.

Source of variation	D.F.	Mean squares	F. ratio	Retested against c
A	7	14.792	71.115**	17.443**
b ₁	1	1.5404	16.382	
b ₂	7	0.057	1.583	
b ₃	20	0.446	2.263	
B	28	0.388	2.536**	
C	7	0.847	9.976**	
D	21	0.109	0.673	
Total	63	1.862		
B x a	14	0.208		
B x b ₁	2	0.094		
B x b ₂	14	0.036		
B x b ₃	40	0.196		
B x b	56	0.153		
B x c	14	0.085		
B x d	42	0.162		
Total interaction	126			

** = Significant at 1 % probability level

This signified the pronounced effects of genes acting additively. These findings are in agreement with the result of Rathod *et al.*, (2008) and Singh *et al.*, (2009), who found the involvement of additive and dominance genes in the inheritance of protein content in wheat. However, the result of Iqbal & Khan (2006) and Akram *et al.*, (2007) suggested the role of genes acting additively for this character. The variation in finding might be due to difference in experimental material, their genetic back ground and the genotype environment interaction.

Wet gluten percentage: The data for wet gluten percentage were subjected to Hayman's analysis of variance and the results regarding this analysis are presented in Table 5. The significant differences for items 'a' and 'b' indicated the substantial role played by additive and dominance gene effects. The 'b₁' item was found to be non significant showing the absence of directional dominance. Non significant 'b₂' component

suggested symmetrical genes distribution among the parental lines. Similarly the 'b₃' item was also found to be non significant which indicated the absence of specific gene effects.

The maternal effects 'c' and other reciprocal effects 'd' were found significant suggesting their role in the expression of gluten content. Finding 'c' and 'd' components significant, the mean squares of 'a' and 'b' were retested against 'c' and 'd' respectively. After retesting, the value of 'a' remained unaltered. The significant 'b' became non significant which indicated that effects of 'd' reciprocal other than maternal effects has masked the dominance gene effects. The values of 'b₂' and 'b₃' remained non significant as before retesting. However, the non significant 'b₁' item has been altered to significant ($p \leq 0.05$). The finding of Akram *et al.*, (2007), however, do not agree with the present result and showed the involvement of non additive gene effects in the inheritance of gluten percentage.

Table 5. Hayman's analysis of variance for wet gluten in an 8 x 8 diallel cross of wheat.

Source of variation	D.F.	Mean squares	F. Ratio	Retested against c
a	7	108.831	82.136**	47.093**
b ₁	1	7.024	6.339	
b ₂	7	0.415	1.273	
b ₃	20	0.163	0.190	
b	28	1.899	2.590 **	
c	7	2.312	4.847 **	
d	21	1.014	1.402	
Total	63	13.53		
B x a	14	1.325		
B x b ₁	2	1.108		
B x b ₂	14	0.326		
B x b ₃	40	0.857		
B x b	56	0.733		
B x c	14	0.477		
B x d	42	0.723		
Total interaction	126			

** = Significant at 1 % probability level

Table 6. Hayman's analysis of variance for lysine content in 8 x 8 diallel cross of wheat.

Source of variation	D.F.	Mean squares	F. Ratio
a	7	3.114	81.947**
b ₁	1	0.189	9.400
b ₂	7	0.022	1.375
b ₃	20	0.040	1.481
b	28	0.041	1.708*
c	7	0.081	2.314
d	21	0.042	1.501
Total	63	0.387	
B x a	14	0.038	
B x b ₁	2	0.020	
B x b ₂	14	0.016	
B x b ₃	40	0.027	
B x b	56	0.024	
B x c	14	0.035	
B x d	42	0.028	
Total interaction	126		

** = Significant at 1 % probability level

* = Significant at 5 % probability level

Lysine content: The analysis of variance following additive dominance model was performed for lysine content and the results pertaining to this analysis are given in Table 6. The significant 'a' item revealed the pronounced contribution of genes showing additive effects. Similarly the 'b' item being significant ($p \leq 0.05$) predominated the role of dominance variance. The items 'b₁' 'b₂' and 'b₃' divulged non significant effects, showing the absence of directional dominance and uniform distribution of genes among the parents and unimportant specific genes effects respectively. The non significant values of 'c' and 'd' showed the absence of maternal effects and other reciprocal effects. Hence retesting of 'a' and 'b' against 'c' and 'd' was worthless

and the previous significance of additive and dominance variances stood valid.

The results of genetic analysis following the hybridization among eight wheat genotypes having contrasting grain quality attributes gave very useful information. Both additive and non additive genetic effects were found important in governing the inheritance of most of the characters investigated. However, additive gene action predominated for all the traits. Although pedigree method could effectively be practiced to utilize the genetic variability arising due to additive gene effects, better segregants with desirable character combinations can be selected in early segregating generation.

References

- Akbar, M., J. Anwar, M. Hussain, M. H. Qureshi and S. Khan. 2009. Line x tester analysis in bread wheat (*Triticum aestivum* L.). *J. Agric. Res.*, 47(1): 21-30.
- Akram, Z., S.U. Ajmal, A.A. Kiani and M. Jamil. 2007. Genetic analysis of protein, lysine, gluten and flour yield in bread wheat (*Triticum aestivum* L.). *Pak. J. Biol. Sci.*, 10(12): 1900-1995.
- Ali, N., M. Iqbal, S. Yasmin, I. Ahmed and M. Asif. 2013. Genetic variation at loci controlling quality traits in spring wheat. *Pak. J. Agri. Sci.*, 50: 637-647.
- Anonymous. 2010. Agricultural Statistics of Pakistan. 2010. Ministry of Food and Agriculture, Islamabad, Pakistan.
- Awan, S.I., M.F.A. Malik and M. Siddique. 2005. Combining ability analysis in intervarietal crosses for components traits in hexaploid wheat. *J. Agric. Soc. Sci.*, 1(4): 316-317.
- Budak, N. 2001. Genetic analysis of certain quantitative traits in the F₂ generation of an 8x8 diallel durum wheat population. *Ege. Uni. Ziraat Fak. Derg.*, 38(2-3): 63-70.
- Cifci, E. A. and K. Yagdi. 2010. The research of the combining ability of agronomic traits of bread wheat in F₁ and F₂ generations. *J. Agric. Faculty, Uludag Univ.*, 24(2): 85-92.
- Dagustu, N. 2008. Genetic analysis of grain yield per spike and some agronomic traits in diallel crosses of bread wheat (*Triticum aestivum* L.). *Turk J. Agric.*, 32: 249-258.
- Hayman, B.I. 1954. The Theory and analysis of diallel crosses. *Genet.*, 39:789-809.
- Hussain, M., A.S. Khan, I. Khaliq and M. Maqsood. 2012. Correlation studies of some qualitative and quantitative traits with grain yield in spring wheat across two environments. *Pak. J. Agri. Sci.*, 49: 1-4.
- Iqbal, M. and A.A. Khan. 2006. Estimation of combining ability effects for plant biomass, grain yield and protein content in wheat (*Triticum aestivum* L.). *Intl. J. Agric. Biol.*, 8(5): 688-690.
- Jinks, J. L. 1954. The analysis of continuous variation in a diallel cross of *Nicotiana rustica* varieties. *Genet.*, 39: 767-788.
- Kamaluddin, R., M. Singh, L.C. Prasad, M.Z. Abdin and K. Joshi. 2007. Combining ability analysis for grain filling duration and yield traits in spring wheat (*Triticum aestivum* L. em. Thell). *Genet. Mol. Biol.*, 30(2): 411-416.
- Kent, N.L. and A.D. Evers. 1994. Wet milling: Starch and Gluten. In: Technology of Cereals. Elsevier Science Ltd. Oxford, U.K.
- Miyahara, S. and K. Jikoo. 1967. Examination of the method of calorimetric determination of lysine. *J. Jap. Soc. Food Sci. Technol.*, 14: 512-513.
- Rathod, S.S.K., L. Dobariya, L.L. Jivani and H.P. Ponkia. 2008. Analysis for test weight, protein content and grain yield in six crosses of bread wheat (*Triticum aestivum* L.). *Advances in Plant Sci.*, 21(1): 99-101.
- Sanjeev, R., S.V.S. Prasad and M.A. Billore. 2005. Combining ability studies for yield and its attributes in *Triticum durum*. *Madras Agric. J.*, 92(1-3): 7-11.
- Siddique, M., S. Ali, M.F.A. Malik and S.I. Awan. 2004. Combining ability estimates for yield and yield components in spring wheat. *Sarhad J. Agric.*, 20(4): 485-487.
- Singh, K., P.K. Gupta and N. Tewari. 2009. Combining ability analysis for yield and quality traits in spring wheat (*Triticum aestivum* Linn. Emend Thell). *Progressive Agric.*, 9(2): 235-241.
- Steel, R.G.D., J.H. Torrie and D.A. Dickey. 1997. Principles and Procedures of Statistics: A Biometrical approach. (3rd Ed.). McGraw Hill Co. Inc., New York, USA.

(Received for publication 8 March 2013)