Research article

Gene action for pre and post harvest traits in F_2 wheat populations

Sultan Akbar Jadoon[1], Fida Mohammad[2], Hidayat Ullah[1]*, Iftikhar H Khalil[2]

[1]Department of Agriculture, The University of Swabi-Khyber Pakhtunkhwa, Pakistan
[2]Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar, Pakistan

*Email: shabkadar@yahoo.com

ABSTRACT

The inheritance mechanism for plant height, days to heading, spike length, grains spike^{-1} and biological yield traits in 8 × 8 half diallel F_2 wheat populations was studied at Agricultural University, Peshawar, Pakistan, during 2006-07. The experiment was laid out in randomized complete block (RCB) design having four replications. Each experimental unit was assigned a four-row plot of 5 m length with row-row space of 30 cm. Analyses of variance displayed significant genotypic differences for studied traits. Diallel analyses reflected significance of both additive and non-additive components in the inheritance of these traits, however, genetic components revealed the importance of a non-additive component. The average degree of dominance being greater than unity indicated involvement of over-dominance for phenotypic expression of all traits studied. Broad-sense heritability values were much higher than narrow-sense and thus delayed selection till advance generations are suggested.

Keywords: Wheat, diallel analysis, additive and non-additive gene effects

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important cereals not only in Pakistan but most parts of the world. It is a major staple food item that fulfills nutritional requirement of our population in the form of proteins and carbohydrates. Wheat occupies more acreage than any other crop in Pakistan as it is grown under irrigated as well as rainfed conditions all over the country. Wheat produced in the country fulfills most of the national requirement, but additional demands are met through costly imports.
To overcome the nutritional demands of this ever-increasing population, improvement in wheat production is still a major concern for wheat breeders in Pakistan. Diallel analysis is a useful tool that has been widely used by plant breeders for constructing their desirable plant type using available genetic resources. It provides useful information regarding the nature of gene action and inheritance patterns of a particular trait that directs plant breeders to practice selection in earlier generations, or delay until advanced generations. Researchers have reported the importance of additive, as well as non-additive, gene action for the inheritance of various traits among wheat populations.[1] reported additive gene action with partial dominance for spikelets spike^{-1}, while[2] identified non-additive gene action for grain yield. Similarly,[3] reflected additive gene control for grains spike^{-1}, number of tillers and grain yield. However,[4] reported transgressive segregation among all the F_2 wheat populations and F_5 single seed-decent lines. The present study was therefore formulated to investigate the inheritance mechanism involved in governing different traits among F_2 wheat populations.

MATERIALS AND METHODS
Plant Material and Experimental Design

The experimental material consisted of eight wheat cultivars/lines and their 28 F_2 progenies (direct crosses) obtained after one year of selfing of a full 8×8 diallel F_1 wheat crosses. The experiment was planted at Khyber Pakhtunkhwa Agricultural University, Peshawar, in RCB design having four replicates during 2006-07. Each experimental unit consisted of a four row plot of five meter length and a row-row space of 30 cm. Urea and DAP fertilizers were applied at 120 and 60 kg ha^{-1}, respectively. Half dose of urea and full dose of DAP were applied at the time of seedbed preparation, while the remaining half dose of urea was applied at the time of first irrigation. All other cultural practices were applied time to time as and when required.

Data Collection

Ten plants from parental cultivars/lines and thirty from F_2 generation were used to collect data on plant height, days to heading, spike length, grains spike^{-1} and biological yield. Plant height was recorded from ground level to tip of spike. excluding awns, while days-to-heading was recorded as the number of days taken from germination to 50% spike emergence. Spike length was measured from the base of 1st spikelet to tip of last spikelet, excluding awns. Grains spike^{-1} as an average of produce of thirty spikes obtained after manual threshing and biological yield as total biomass from each plot before threshing.

Statistical Analysis

Data after compilation was analyzed using statistical package 'SAS 6.12' following[5] to see whether significant differences existed among the wheat genotypes for further analysis. Traits showing significant differences were subjected to diallel analysis to study the nature of gene action controlling these genetic traits using computer software 'Dial-98' for half diallel F_2 wheat populations following[6] procedures.
In addition, t^2 test and regression analysis were carried out to test adequacy of additive dominance model. The model is considered fully adequate for a given set of data if it qualifies all tests, however, if one of the tests satisfy the conditions then the model is considered partially adequate. Scientists such as[7−9] have already advocated genetic components estimation for partially adequate model.

RESULTS AND DISCUSSION

The data obtained from eight wheat cultivars/lines and their 28 half diallel F_2 populations reflected highly significant differences (P $\leq$ 0.01) among wheat genotypes, thus allowing for further analysis of data (Table 1). When data was subjected to adequacy tests for fitness of the additive-dominance model, traits such as plant height, days to heading and spike length were found partially adequate; qualifying one or the other test. While grains spike^{-1} and biological yield depicted full adequacy to the model, qualifying both tests (Table 2). Detailed description of results obtained for each trait can be seen below.

Table 1. Mean squares of indicated quantitative traits among F_2 half diallel wheat populations at Peshawar during 2006 – 07.

SOV	df	Plant height	Days to heading	Spike length	Grains spike^{-1}	Biological yield (kgha^{-1})
Reps	3	101.54**	9.57**	1.36**	65.95**	27,06997^{ns}
Genotypes	35	445.42**	11.69**	1.67**	79.11**	52,32400**
Error	105	42.93	2.26	0.34	8.91	13,1417

**, ^{ns}: Significance at 1% level of probability and Non-Significant respectively.

Table 2. Scaling tests of additive-dominance model for yield and associated traits in 8x8 F_2 half diallel wheat populations during 2006 – 07.

Parameters	t^2	Regression analysis (t value of b) b = 0	b = 1	Conclusions
Plant height	0.01^{ns}	1.82^{ns}	1.12^{ns}	Model was partially adequate
Days to heading	0.68^{ns}	1.11^{ns}	2.59*	Model was partially adequate
Spike length	0.30^{ns}	1.55^{ns}	0.83^{ns}	Model was partially adequate
Grains spike^{-1}	3.16^{ns}	6.72**	2.36^{ns}	Model was fully adequate
Biological yield	0.02^{ns}	2.45*	1.0^{ns}	Model was fully adequate

*: Significance at 5% level of probability
**: Significance at 1% level of probability
^{ns}: Non-Significant respectively

Results obtained from diallel analysis of variance are presented in Table 3. The data clearly indicates that both additive (a) and non-additive (b) genetic components were equally important in the inheritance of all traits as both components differed significantly during 2006-07. Significance of 'b$_1$' component depicted dominance deviation predominantly in one direction, while significance of 'b$_2$' value suggested asymmetric distribution of dominant and recessive alleles. This unequal distribution of genes clearly indicates that some parents have considerably more dominant alleles than others for plant height, days to heading, spike length, grains spike^{-1} and biological yield. Moreover, significance of 'b$_3$' values confirm residual dominance, due to specific genes/combination for all traits studied, except biological yield where non-significant 'b$_3$' value confirm the absence of residual dominance.

Table 3. Diallel analysis for some quantitative traits of F_2 half diallel wheat populations at Peshawar, 2006 – 07.

SOV	df	Plant height	Days to heading	Spike length	Grains spike^{-1}	Biological yield (kgha^{-1})
Replication	3	99.56	12.33	1.29	65.95	27,07008
a	7	814.21**	7.58**	1.26**	29.26**	73,40839**
b	28	350.89**	13.54**	1.04**	91.57**	47,05290**
b$_1$	1	1493.00**	180.96**	4.64**	1953.3**	66,380720**
b$_2$	7	202.81**	8.67**	1.14**	34.35**	31,22711**
b$_3$	20	345.61**	7.68**	0.82**	18.52**	21,75420*
Error	105	42.37	2.12	0.35	8.91	13,61417
Total	143	99.56				

Where 'a' stand for Additive and 'b' for Non-additive
**: Significance at 1% level of probability

The genetic components of variance revealed all variance components including additive (D), dominance (H$_1$ and H$_2$), F, h^2 and environmental variance (E) were significantly different for all traits, except days-to-heading, where additive component (D) and F were non-significant, and biological yield where only 'F' component was non-significant during 2006-07. Additive component was smaller in magnitude than both components of dominance (H$_1$ and H$_2$) for plant height, spike length, grains spike^{-1} and biological yield indicating preponderance of non-additive gene action for these traits (Table 4). Similarly, the non-significant value of additive component (D) for days to heading indicated the important role of non-additive gene action controlling this trait.[1,10,11] reported non-additive gene

Table 4. Genetic parameters and their standard errors for some quantitative traits of F_2 half diallel wheat populations at Peshawar, 2006–07.

SOV	Plant height	Days to heading	Spike length	Grains spike^{-1}	Biological yield (kgha^{-1})
D	159.92* ± 33.48	1.36* ± 0.84	0.42* ± 0.17	8.84* ± 4.02	66,8975* ± 50,1786
H_1	324.64* ± 40.63	10.30* ± 1.69	0.88* ± 0.22	59.50* ± 7.88	31,41504* ± 81,0047
H_2	286.06* ± 32.64	8.92* ± 1.27	0.68* ± 0.16	53.26* ± 6.45	26,83971* ± 59,1291
F	133.31* ± 44.02	2.06* ± 1.40	0.56* ± .25	13.25* ± 6.42	41,6329^{ns} ± 73,6408
h^2	178.98* ± 62.74	22.04* ± 4.65	0.53* ± 0.33	239.4* ± 31.2	80,23906* ± 21,82826
E	11.45* ± 1.18	0.54* ± 0.05	0.09* ± 0.01	2.32* ± 0.24	35,1171* ± 37,613
$\sqrt{(H_1/D)}$	1.43 ± 0.13	2.80 ± 1.43	1.45 ± 0.25	2.59 ± 0.53	2.17 ± 1.08
kd/(kd + kr)	0.65 ± 0.03	0.66 ± 0.04	0.73 ± 0.04	0.65 ± 0.04	0.57 ± 0.08
h^2/H_2	0.72 ± 0.22	2.78 ± 0.43	0.89 ± 0.42	5.14 ± 0.35	3.42 ± 0.61
h	−13.55 ± 2.29	−4.72 ± 0.48	−0.76 ± 0.19	15.50 ± 0.99	2858 ± 381.90
uv	0.22 ± 0.01	0.21 ± 0.01	0.19 ± 0.02	0.22 ± 0.01	0.21 ± 0.02
h^2 (bs)	0.90 ± 0.01	0.83 ± 0.02	0.70 ± 0.04	0.86 ± 0.02	0.75 ± 0.04
h^2 (ns)	0.28 ± 0.04	0.10 ± 0.03	0.10 ± 0.05	0.06 ± 0.03	0.26 ± 0.06

'D' Additive; 'H_1 & H_2' Dominance; 'F' Frequency of dominant to recessive alleles in parents; 'h^2' overall dominance effect due to heterozygous loci; 'E' Environmental variance; '$\sqrt{(H1/D)}$' Average degree of dominance; kd/(kd + kr) Proportion of dominance & Recessive alleles in parents; 'uv' proportion of genes with positive and/or negative effects in the parents; 'h^2(bs)' Broad-sense heritability; 'h^2(ns)' Narrow-sense heritability;

action for some quantitative traits in F_2 wheat populations. However,[3,12–14] reported additive genetic effects for most traits. The average degree of dominance $(H_1/D)^{1/2}$ exceeded unity for all traits, which confirmed the greater role of non-additive gene action. These results confirmed the earlier findings of,[4] who reported transgressive segregation among all F_2 wheat populations and F_5 single seed-decent lines. Positive value of 'F' suggests that dominant alleles were more frequent than recessive ones for all traits and were also in increasing order as reflected by the high positive value of h^2. Difference in values of dominance components (H_1 and H_2) showed unequal distribution of dominant and recessive genes among the parent. The asymmetrical gene distribution among parents was supported by the ratio of $H_2/4 H_1$ being unequal to 0.25. Environmental variance (E) was positive and significant, indicating the important role of environmental conditions in the phenotypic expression of these traits, also reported by Ullah et al.[15] Positive value of 'h' clearly indicated an increase in number of grains spike^{-1} and biological weight among the progenies as compared to their parents. Similarly, negative value of 'h' for plant height, days-to-heading and spike length reflected a decrease in plant height, number of days to heading and spike length of progenies (Table 4). Broad-sense heritability values were higher than narrow-sense for all traits, indicating an important role of non-additive gene action. Maximum and minimum values of both types of heritabilities have been reported in many domesticated crops ([15,16]). Narrow-sense heritability values were low for days-to-heading, spike length and grains spike^{-1}, therefore selection would be effective in later generations.

CONCLUSIONS

Though both of the gene interaction and behavior are of prime importance, using diallel analyses non-additive components are equally important to that of additive components for yield traits in segregating population of wheat. Maximum value for degree of dominance showed the involvement of over-dominance for phenotypic expression. Moreover, a greater magnitude of broad-sense, in comparison to narrow- sense, delayed selection until advanced generations would be preferred.[17] reported significant GCA & SCA for agronomic and yield traits of wheat. Both additive and non-additive genetic components are involved in the inheritance of the studied traits.

REFERENCES

[1] Ivanovska S, Stojkovski C, Marinkovic L. Inheritance mode and gene effect on spikelets number per spike in wheat. *Macedonian Agri. Review.* 2000;47(1/2):1–8.

[2] Sangwan VP, Chaudhary BD. Diallel analysis in wheat (*Triticum aestivum* L.). *Annals Biol. Ludhiana.* 1999;15(2):181–183.

[3] Singh SP, Singh LR, Yadav VK, Kumar R, Singh PB, Singh G. Combining ability analysis for yield traits in bread wheat. (*Triticum aestivum* L. em Thell). *Progressive Agric.* 2002;2(2):119–121.

[4] Navabi A, Singh PR, Tewari PJ, Briggs GK. Inheritance of high levels of adult-plant resistance to stripe rust in five spring wheat genotypes. *Crop Science.* 2004;44(4):1156–1162, doi:10.2135/cropsci2004.1156.

[5] Steel RGD, Torrie JH. *Principals and procedures of statistics.* New York, USA: McGraw Hill Book Co. 1980.

[6] Jones MR. Analysis of variance of the half-diallel table. *Heredity.* 1965;20(1):117–121, doi:10.1038/hdy.1965.12.

[7] Johnson LPV, Askel R. The inheritance of malting quality and agronomic characters in a diallel cross of Barely. *Can J Genet Cytol.* 1964;6(2):178–200, doi: 10.1139/g64-024.

[8] Wilson ND, Weibel DE, McNew RW. Diallel analyses of grain yield, percent protein and protein yield in grain Sorghum. *Crop Science*. 1978;18(3):491–495, doi:10.2135/cropsci1978.0011,183X0018,00030,035x.

[9] Azhar FM, McNeilly T. The Genetic Basis of Variation for Salt Tolerance in Sorghum bicolor (L.) Moench Seedlings. *Plant Breeding*. 1988;101(2):114–121, doi: 10.1111/j.1439-0523.1988.tb00275.x.

[10] Singh SP, Singh M, Yadav HK. Diallel analysis for seed yield and its component traits in Cuphea procumbens. *Genetika*. 2006;38(1):9–22, doi:10.2298/GENSR060,1009S.

[11] Mishra PC, Singh TB, Nema DP. Combining ability analysis of grain yield and some of its attributes in bread wheat under late sown condition. *Crop Res. Hisar*. 1994;7(3):413–423.

[12] Zwart RS, Thompson JP, Godwin ID. Identification of quantitative trait loci for resistance to two species of root-lesion nematode (Pratylenchus thornei and P. neglectus) in wheat. *Aust J Agri Res*. 2005;56(4):345–352, doi:10.1071/AR04223.

[13] Joshi SK, Sharma SN, Singhania DL, Sain RS. Combining ability in the F1 and F2 generations of diallel cross in hexaploid wheat (*Triticum aestivum* L. em. Thell). *Hereditas*. 2004;141(2):115–121, doi:10.1111/j.1601-5223.2004.01730.x.

[14] Khan AS, Ali Z. General and specific combining ability estimates for plant height and some yield components in wheat. *Pakistan J. Agri. Sci*. 1998;35:3–4.

[15] Ullah H, Khalil IH, Rahman HU, Muhammad F, Khalil IA, Khalil SH. Environmental influence on heritability and selection response of morpho-physiological traits in mungbean. *Pakistan J Bot*. 2011;43(1):301–310.

[16] Khan NU, Hassan G, Marwat KB, Farhatullah, Kumbhar MB, Parveen A, Aiman U, Khan MZ, Soomro ZA. Diallel analysis of some quantitative traits in *Gossipium hirsutum* L. *Pakistan J Bot*. 2009;41(6):3009–3022.

[17] Zare-kohan M, Heidari B. Estimation of genetic parameters for maturity and grain yield in diallel crosses of five wheat cultivars using two different models. *J Agri Sci*. 2012;4(8):74–85, doi: 10.5539/jas.v4n8p74.