

Genetic analysis in wheat (*Triticum aestivum* L. Em. Thell.)

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ABSTRACT

In bread wheat ten genotypes were crossed in half diallel fashion to estimate gene action involved in the inheritance of grain yield and its component traits. The non-significance of 't²' values suggested that additive-dominance model was adequate for days to 50% flowering, plant height, number of effective tillers per plant, number of spikelets per main spike, days to maturity, number of grains per main spike, grain weight per main spike, 100 grain weight, grain yield per plant, biological yield per plant, harvest index and protein content. Additive (D) and both the dominance components (H₁, H₂) were significant for all for all the above said characters except 'D' for days to 50% flowering, number of effective tillers per plant, length of main spike, peduncle length of main spike, grain yield per plant, harvest index, total soluble sugar and chlorophyll content. The average degree of dominance (H_1/D)^{1/2} was greater than unity for all the traits indicating over dominance behavior of interacting alleles. Asymmetrical distribution of positive and negative genes in the parental lines was revealed from the estimate, H₂/4H₁ for all the characters except days to maturity and grain weight per main spike for which symmetrical distribution was evidenced. Narrow sense heritability estimates were less than 50 per cent for all the traits (except grain weight per main spike) indicating major role of dominance gene effect in the expression of grain yield and its component characters.

Key words : Wheat, gene action, genetic parameters, heritability, grain yield.

Wheat (*Triticum spp.*) is the second most important staple food crop next to rice, consumed by nearly 35% of the world population and providing 20% of the total food calories. Wheat breeding, in its fundamental form had many priorities, of which grain yield potential gain has been given a lot of attention. Progress in this endeavour is dependent on the understanding of the structure of genetic components in the wheat gene pool, and the understanding of the relationship between genotypic and phenotypic variation. A large number of new genetic combinations are, therefore, essential for the construction of high-resolution genetic maps, for implementation of efficient breeding methods and rapid development of superior varieties. The diallel analysis advocated by Hayman (1954) provides reliable method particularly in autogamous crops like wheat to work out the genetic system and gene action involved in the expression of matricate attributes. To understand the mode of expression of genes those are present in the experimental material, gene action studies is helpful as it aids in selection of

parents to be used in hybridization as well as appropriate breeding procedures for genetic improvement of various polygenic characters. Therefore, this study was undertaken to generate information about nature and magnitude of gene action involved in various characters. Information derived may be effectively exploited in developing and formulating an efficient breeding program for the evaluation of better quality and high yielding varieties.

MATERIALS AND METHODS

The experimental material consisted of ten genotypes/ varieties of bread wheat viz., GW-496, GW-322, LOK-1, GW-173, KYZ-300, RAJ-4136, HW-5018, K-604, UAS-281, HI-1544 and GW-366; these genotypes were crossed in all possible combinations using diallel mating design excluding reciprocal during Rabi 2010-11 at Wheat Research Station, Junagadh Agricultural University, Junagadh, Gujarat. A set of 56 entries, including 10 parents, their 45 crosses and one standard check (GW-366) were sown in randomized block design with three replications during

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Rabi 2011-12. Each entry was sown in a single row plot of 2.5 m length keeping row-to-row and plant-to-plant distance of 22.5 cm and 10 cm, respectively. Five competitive plants of each parents and hybrids were selected randomly for recording observations for sixteen characters viz., days to 50% flowering, plant height, number of effective tillers per plant, length of main spike, number of spikelets per main spike, peduncle length of main spike, days to maturity, number of grains per main spike, grain weight per main spike, 100-grain weight, grain yield per plant, biological yield per plant, harvest index, total soluble sugar, protein content and chlorophyll content. The genetic components and related parameters were computed according to Hayman (1954). Heritability in narrow sense was worked out following Mather and Jinks (1982).

RESULTS AND DISCUSSION

Knowledge about the magnitude and nature of genetic variation in a specific population is of prime importance for the prediction of the most effective breeding programme (Debnath, 1988). The t^2 test (Hayman, 1954) was employed to test the assumptions of diallel analysis for all the 16 characters. The non-significance of t^2 values suggested the fulfillment of basic assumptions underlying diallel analysis for all the characters except length of main spike, peduncle length of main spike, total soluble sugar and chlorophyll content which revealed that additive-dominance model was adequate and thereby components analysis was performed for all the characters except stated above.

Both additive (D) and dominance (H_1 , H_2) components were significant for all for all the characters except additive gene effect for days to 50% flowering, number of effective tillers per plant, length of main spike, peduncle length of main spike, grain yield per plant, harvest index, total soluble sugar and chlorophyll content (Table 1), for these characters only dominance gene effect was importance, while for the rest of the characters, both additive and dominance components were important in the inheritance of grain yield and its components traits. However, additive component was lower in magnitude than that of dominance components for all the characters which revealed over dominance effect in the expression of all the traits. Similar findings were also reported by Alam *et al.*, (1990), Kathiria and Sharma (1996b) and Khan *et al.* (2010).

The estimates of average degree of dominance (H_1/D)^{1/2} were greater than unity for all the traits (Table 1) indicating over dominance behavior of interacting alleles which suggested that heterosis breeding might be advantageous to get higher gain in bread wheat, however, the flower morphology of the crop and lack of working male sterility would not permit heterosis breeding, therefore segregating generations need to be followed for dilution of dominance and then selection may be applied for development of high yielding varieties. Similar finding was also reported by Sami *et al.*, (2010). The non-significant estimate of 'E' for all the traits except grain weight per main spike, grain yield per plant and biological yield per plant suggested that there was no considerable environment influence likely to modify the ability of genes to express respective characters.

The close to 0.25 $H_2/4H_1$ for days to 50 % flowering, length of main spike, days to maturity and grain weight per main spike and chlorophyll content revealed symmetrical distribution of increasing and decreasing alleles among the parental genotypes, while rest of the characters, an asymmetrical distribution was evidenced. The present findings are in parity with report of Kathiria and Sharma (1996b).

The positive sign of 'F' and more than one ration of K_D/K_R ratio for days to 50% flowering, plant height, number of effective tillers per plant, length of main spike, number of spikelets per main spike, peduncle length of main spike, number of grains per main spike, 100 grain weight, grain yield per plant, biological yield per plant, harvest index, total soluble sugar and protein content suggested an excess of dominant gene in the parents, while negative sign of 'F' and around unity ratio of K_D/K_R for days to maturity and grain weight per main spike indicated an equal proportion of recessive genes and dominant genes with the parents. The number of genes or group of genes exhibiting dominance for a particular character is important for the extent of genetic progress through selection. In the present investigation, the value of h^2/H_2 was very low for most of the characters, which suggested at least one dominant group of genes group could be involved in the inheritance of the studied characters.

High estimates of heritability in narrow sense was observed only for grain weight per main spike, while moderate values were observed for days to 50 % flowering, peduncle length of main spike, days to maturity, number of grains per main spike, 100 grain

Table 1 Estimation of genetic components of variation for different characters in bread wheat

Compo- nents/ Para- meters	Days to 50% flowering	Plant height	Number of effective tillers per plant	Length of main spike	Number of spikelets per main spike	Peduncle length of main spike	Days to maturity	Number of grains per main spike
D1	1.59 ± 9.64	22.48** ± 4.43	1.16 ± 0.89	0.23 ± 0.34	3.89** ± 0.62	4.13 ± 2.29	15.00* ± 7.48	44.67** ± 10.50
H ₁	66.30** ± 20.52	48.24** ± 9.43	6.83** ± 1.89	2.88** ± 0.72	10.26** ± 1.31	16.76** ± 4.86	62.12** ± 15.92	133.09** ± 22.35
H ₂	55.89** ± 17.44	36.88** ± 8.01	5.70** ± 1.61	2.47** ± 0.61	7.69** ± 1.11	12.24** ± 4.13	56.26** ± 13.53	102.75** ± 18.99
h ²	22.15** ± 3.44	8.11 ± 5.36	-0.10 ± 1.08	0.16 ± 0.41	0.05 ± 0.74	-0.02 ± 2.77	2.53** ± 9.05	24.94* ± 12.71
F	6.30 ± 22.25	30.54** ± 10.22	1.44 ± 2.05	0.53 ± 0.78	6.02** ± 1.42	5.36 ± 5.27	0.79 ± 17.25	49.58* ± 24.22
E	0.37 ± 2.90	0.88 ± 1.34	0.28 ± 0.27	0.10 ± 0.10	0.18 ± 0.19	0.52 ± 0.69	0.39 ± 2.25	1.55 ± 3.17
(H ₁ /D) ^{1/2}	2.39	1.47	2.43	3.52	1.63	2.04	2.04	1.73
H ₂ /4 H ₁	0.21	0.19	0.21	0.21	0.19	0.18	0.23	0.19
K _D /K _R	1.26	2.73	1.69	1.95	2.82	1.95	1.03	1.95
h ² /H ₂	0.40	0.22	-0.02	0.06	0.01	-0.001	0.05	0.24
Heritability (ns) %	35.40	14.10	19.9	7.4	9.4	31.50	41.00	31.80
t ²	2.68	0.45	5.23	7.33*	0.01	11.80*	5.20	0.03

*,** Significant at 0.05 and 0.01 probability level, respectively

Table 1 Contd.

Compo- nents/ Para- meters	Grain weight per main spike	100 grain weight	Grain yield per plant	Biological yield per plant	Harvest index	Total soluble sugar	Protein content	Chlorophyll content
D	0.05* ± 0.02	0.26** ± 0.04	2.21 ± 2.58	123.90** ± 45.11	109.18 ± 89.38	285.30 ± 5521.96	0.56** ± 0.11	0.0012 ± 0.0036
H ₁	0.08** ± 0.03	0.46** ± 0.08	23.97** ± 5.50	785.41** ± 96.02	963.02** ± 190.25	44178.13** ± 11754.01	1.59** ± 0.23	0.026** ± 0.0077
H ₂	0.08** ± 0.03	0.34** ± 0.07	16.16** ± 4.67	568.86** ± 81.61	756.35** ± 161.69	35998.82** ± 9989.60	1.19** ± 0.19	0.023** ± 0.0065
h ²	0.009 ± 0.02	-0.002 ± 0.05	2.70 ± 3.13	47.37 ± 54.63	-1.14 ± 108.23	1042.90 ± 6686.65	0.11 ± 0.13	0.0023 ± 0.0044
F	-0.0007 ± 0.04	0.32** ± 0.09	7.81 ± 5.96	299.59 ± 104.09	235.45 ± 206.22	342.18 ± 12740.82	0.42 ± 0.25	0.0022 ± 0.0083
E	0.009 ± 0.005	0.01 ± 0.01	1.61* ± 0.78	1.66** ± 13.60	8.60 ± 26.95	68.66 ± 1664.93	0.02 ± 0.03	0.0003 ± 0.001
(H ₁ /D) ^{1/2}	1.34	1.31	3.29	2.52	2.97	12.44	1.69	4.64
H ₂ /4 H ₁	0.23	0.19	0.17	0.18	0.20	0.20	0.19	0.22
K _D /K _H	0.99	2.74	3.31	2.85	2.14	1.10	1.57	1.49
h ² /H ₂	0.11	-0.005	0.17	0.08	-0.002	0.03	0.09	0.09
Heritability (ns) %	50.70	21.20	16.40	12.4	16.90	30.90	46.10	13.70
t ²	3.66	0.31	0.46	2.15	5.17	207.76**	0.93	39.04

* ** Significant at 0.05 and 0.01 probability level, respectively

weight, total soluble sugar and protein content. On the other hand, plant height, number of effective tillers, grain yield per plant, biological yield per plant, harvest index per plant, chlorophyll content displayed low heritability. Very low heritability was observed in case of length of main spike and number of spikelets per main spike. In general, narrow sense heritability was found to be less than 50 per cent for all the traits except grain weight per main spike, indicating prime role of dominance gene effect in the expression of grain yield and its attributes. High narrow sense heritability for grain weight per main spike indicated that the major part of phenotypic variability was due to additive component, and possibility of fixing this character by pedigree method of selection.

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