

## Inheritance of Protein Content and Maturity Traits in Spring Wheat (*Triticum aestivum* L. em Thell)

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### Abstract

Genetic parameters were estimated for protein content, days to 50% heading, days to 50% heading in growing degree days (GDD), days to 50% flowering, days to 50% flowering in growing° days (GDD), days to 50% physiological maturity, days to 50% physiological maturity in growing° days (GDD), Grain filling duration, Grain filling duration in growing degree days (GDD), no. of grains/spike, 1000 grain weight (g) and grain yield/plant (g) using diallel analysis involving 11 diverse parents and their F<sub>1</sub> and F<sub>2</sub> progenies of spring wheat. Additive and dominance gene action was found significant for expression of these traits. High heritability estimates in narrow sense was obtained for all the traits except grain filling duration in GDD, 1,000 seed weight, no. of grains/spike and seed yield/plant which showed moderate heritability in both generations. Biparental and diallel selective mating design would be valuable approach for further improvement of protein content with early maturity and acceptable level of grain yield in bread wheat.

**Key words :** Protein content, Inheritance, Wheat, Diallel analysis.

Wheat is one of the most leading source of vegetable proteins among food crops (1) and protein content in wheat grain governs its end use quality. Therefore, improvement in protein content of wheat kernel has been the most important objective of wheat breeder for a long time owing to its importance in human nutrition (2). Better understanding of inheritance of protein content and maturity traits will be valuable to make breeding strategies for rapid development of wheat varieties having high protein content with early maturity. In view of above facts, the present investigation was undertaken with the objective to determine inheritance of protein content and maturity traits in some important cultivars of spring wheat.

(The financial support given by University Grants Commission, New Delhi, Government of India in the form of fellowship to the first author during the course of this study is acknowledged).

### Methods

Eleven wheat genotypes of diverse origin namely

HP 1633, PBW 343, Bagula, Veery 'S', Pavon 76, HP 1731, HW 1084, HD 2285, HP 1102, K 9107 and KRL-1-4 were selected on the basis of variation present for their protein content and maturity traits from germplasm collection at Banaras Hindu University, Varanasi, India. This center (25.2°N and 83.0°E) has loam alluvial soil having neutral pH (7.2). Average minimum and maximum temperature was 10.9°C and 23.66°C during vegetative phase and 25.55°C and 32.9°C during reproductive phase of the crop, respectively. These genotypes were crossed in all possible combinations to produce F<sub>1</sub> and F<sub>2</sub> generations excluding reciprocals. The parental plants, F<sub>1</sub> and F<sub>2</sub> offspring's were then sown on *rabi* 2002 in randomized block design with three replications at research farm of this centre. Each entry was sown in three 3 m long rows at a spacing of 25 × 5 cm. Agronomic practices recommended for normal fertility (120 kg N : 60 kg P<sub>2</sub>O<sub>5</sub> : 40 kg K<sub>2</sub>O/ha) were followed to ensure good crops. Twenty plants each from parents and F<sub>1</sub> and 250 plants from F<sub>2</sub> generation were tagged randomly in each replication excluding the border plants prior

**Table 1.** Analysis of variance of parents, F<sub>1</sub>s and F<sub>2</sub>s for protein content and maturity traits in 11 × 11 diallel cross of spring wheat. \*, \*\* Significant at the 0.05 and 0.01 probability levels, respectively.

Characters	Source of variation					
	Parents (df10)	F <sub>1</sub> S (df54)	F <sub>2</sub> S (df54)	Parents vs F <sub>1</sub> S (df1)	Parents vs F <sub>2</sub> S (df1)	Errors (df 130)
Protein content	19.05**	9.03**	5.35**	33.90**	4.38**	1.21
Days to 50% Heading	158.69**	39.20**	73.22**	18.95**	32.71**	0.94
Days to 50% Heading in GDD	36799.01**	10044.44**	8223.22**	220.445**	10584.54**	359.63
Days to 50% flowering	146.60**	36.87**	42.19**	16.97**	24.26**	0.64
Days to 50% flowering in GDD	35805.07**	11854.04**	10439.26**	9375.74**	4068.18**	2091.70
Days to 50% Phy. Maturity	69.40**	9.09**	31.84**	247.19**	18.36**	0.62
Days to 50% Phy. Maturity in GDD	34531.89**	4599.54**	11347.76**	113447.15**	1599.01**	329.37
Grain filling duration	98.55**	45.95**	58.55**	139.03**	9.90**	0.79
Grain filling duration in GDD	24769.09**	13136.75**	19539.37**	145158.41**	17266.71**	2885.16
No. of grains/spike	131.69**	233.81**	268.19**	191.56**	278.34**	3.48
1000-grain weight	39.89**	48.71**	57.34**	42.18**	300.57**	0.32
Grain yield/plant	65.24**	45.62**	54.01**	636.47**	134.14**	0.21

to heading and observations were made for different traits on these plants only. The observations were recorded for quantitative traits viz. Days to 50% heading (in days), Days to 50% flowering (in days), days to 50% physiological maturity (in days), no. of grains/

spike, 1000-grain weight (g) and grain yield/plant (g). Grain filling duration was determined from the days to flowering to days to physiological maturity. Protein content (per cent) in wheat kernel was calculated by multiplying the total percentage of nitrogen by a

**Table 2.** Genetic components of variation for protein content and maturity traits in 11 × 11 diallel cross of spring wheat in F<sub>1</sub> and F<sub>2</sub> generations. \*, \*\* Significant at the 0.05 and 0.01 probability levels, respectively.

Characters	Generations	D	H <sub>1</sub>	H <sub>2</sub>	E	F	b <sup>2</sup>
Protein content	F <sub>1</sub>	6.35**	15.04**	6.78**	0.02	5.2	4.08**
	F <sub>2</sub>	6.35**	35.80**	22.00**	0.02	10.53**	0.05
Days to 50% heading	F <sub>1</sub>	52.58**	382.54**	55.53**	0.32	200.32**	2.17
	F <sub>2</sub>	52.61**	430.40	285.01	0.29	134.32	3.84
Days to 50% heading in GDD	F <sub>1</sub>	12146.96**	21847.44**	13829.72**	119.52	18414.45**	-11.72
	F <sub>2</sub>	12224.82**	71946.10**	46254.14**	41.66	33601.23**	1257.27
Days to 50% flowering	F <sub>1</sub>	48.65**	96.36**	51.82**	0.22	72.50**	1.98
	F <sub>2</sub>	48.71**	318.44**	120.79**	0.15	128.49**	2.87
Days to 50% flowering in GDD	F <sub>1</sub>	11237.82**	23181.55**	14566.78**	697.23	17969.00**	895.23
	F <sub>2</sub>	11834.37**	78974.86**	53831.31**	100.68	31876.71**	456.35
Days to 50% phy. maturity	F <sub>1</sub>	22.93**	81.23**	19.15**	5.21	51.03	29.64**
	F <sub>2</sub>	17.01	115.53**	101.77**	6.12*	55.23	-2.02
Days to 50% phy. maturity in GDD	F <sub>1</sub>	11400.81**	44858.86**	9454.62**	149.60	23808.48**	13597.51**
	F <sub>2</sub>	11352.85**	95118.24**	46265.68**	257.55	22008.40**	143.00
Grain filling duration	F <sub>1</sub>	32.56**	87.44**	60.78**	0.29	52.98**	16.62
	F <sub>2</sub>	32.63**	445.51**	318.23**	0.23	160.09**	1.12
Grain filling duration in GDD	F <sub>1</sub>	7294.85**	21989.49**	16224.10**	961.77	11249.24**	17131.79**
	F <sub>2</sub>	7368.08**	126636.84**	91812.49**	888.27	28391.66**	1781.52
No. of grains/spike	F <sub>1</sub>	43.11**	325.88**	276.63**	0.79	52.92	230.01**
	F <sub>2</sub>	42.55	1502.26**	1453.75**	1.35	250.70	334.15**
1000-grain weight	F <sub>1</sub>	13.13**	51.76**	41.49**	0.17	9.76	5.02
	F <sub>2</sub>	13.27	215.53**	210.11*	0.03	45.56	36.12
Grain yield/plant	F <sub>1</sub>	21.65**	317.59**	53.18**	0.01	28.74**	76.48**
	F <sub>2</sub>	21.68**	444.12**	331.78**	0.07	86.28**	161.23**

**Table 3.** Proportion of genetic components of variation for protein content and yield contributing traits in 11 × 11 diallel cross of spring when in F<sub>1</sub> and F<sub>2</sub> generations.

Characters	Genera- tion	h <sup>2</sup> NS	Degree of domi- nance and recessive		h <sup>2</sup> /H <sub>2</sub>	H <sub>2</sub> /4H <sub>1</sub>
			domi- nance	genes		
Protein content	F <sub>1</sub>	38.90	1.53	1.72	0.60	0.25
	F <sub>2</sub>	62.69	0.59	5.63	0.002	0.15
Days to 50% heading	F <sub>1</sub>	33.68	2.69	5.80	0.03	0.03
	F <sub>2</sub>	55.85	0.71	-1.36	0.01	0.18
Days to 50% heading in GDD	F <sub>1</sub>	75.64	1.34	35.99	-0.0008	0.15
	F <sub>2</sub>	90.00	0.60	-16.05	0.02	0.16
Days to 50% flowering	F <sub>1</sub>	67.18	1.40	3.27	0.03	0.13
	F <sub>2</sub>	75.29	0.63	-8.41	0.02	0.09
Days to 50% flowering in GDD	F <sub>1</sub>	58.41	1.43	3.51	0.06	0.62
	F <sub>2</sub>	73.76	0.64	-478.45	0.008	0.17
Days to 50% phy maturity	F <sub>1</sub>	30.98	1.88	3.89	1.54	0.05
	F <sub>2</sub>	39.83	0.65	-9.13	0.01	0.22
Days to 50% phy maturity in GDD	F <sub>1</sub>	34.49	1.98	3.22	1.43	0.05
	F <sub>2</sub>	45.12	0.72	5.05	0.003	0.12
Grain filling duration	F <sub>1</sub>	47.76	1.63	2.97	0.27	0.17
	F <sub>2</sub>	50.27	0.92	-7.12	0.003	0.71
Grain filling dura- tion in GDD	F <sub>1</sub>	33.33	1.73	2.59	1.05	0.18
	F <sub>2</sub>	25.95	1.03	27.35	0.01	0.18
No. of grains/ spike	F <sub>1</sub>	13.71	2.74	4.16	0.83	0.21
	F <sub>2</sub>	14.26	1.48	237.50	0.73	0.24
1000-grain weight	F <sub>1</sub>	23.51	1.98	1.46	0.12	0.20
	F <sub>2</sub>	29.76	1.00	12.53	0.17	0.24
Grain yield/plant	F <sub>1</sub>	23.64	4.14	1.38	1.43	0.03
	F <sub>2</sub>	24.12	1.13	15.57	0.48	0.18

factor of 5.7 (3) while nitrogen content (per cent) in wheat grain was estimated following the method of Linder (4). The number of days from sowing to 50% heading, sowing to 50% flowering and sowing to 50% physiological maturity was converted to growing degree days. Degree days for a particular period were calculated as  $T_n = (T_{max} + T_{min})/2 - T_b$ , where  $T_{max}$  and  $T_{min}$  are the maximum and minimum daily temperature, respectively and  $T_b$  is the base temperature, below which no grain development occur. Data obtained for each trait were subjected to analysis of variance and variances were tested by *F*-test. Gene actions involved in the inheritance of the traits were analysed using Hayman's approach (5). Narrow sense heritability for protein content and other traits was also computed from the diallel following Mather and Jinks (6). The statistical analysis was carried out us-

ing the INDOSTAT program.

## Results and Discussion

Analysis of variance showed significant differences among parents, F<sub>1</sub>'s and F<sub>2</sub> progenies for all the traits (Table 1) indicating that the material used in the study had significant genetic diversity. Table 2 shows that both additive and dominance gene action was responsible for the expression of all the traits. These findings are in agreement with the finding of Tiwari and Marker (7). It was also observed that the magnitude of dominance component was larger than additive component for all traits in both the generations. The *F*-value was positive for all the traits indicating an excess of dominant alleles as compared to recessives alleles. The degree of dominance was greater than 1 in F<sub>1</sub> generation for protein content, days to 50% heading, days to 50% heading in GDD, days to 50% flowering, days to 50% flowering in GDD, days to 50% physiological maturity, days to 50% physiological maturity in GDD, GFD and 1,000 seed weight while it was greater than 1 in both generation for GFD in GDD, No. of grains/spike and seed yield/plant suggesting over dominance whereas degree of dominance was less than 1 for protein content, days to 50% heading, days to 50% heading in GDD, days to 50% flowering, days to 50% flowering in GDD, days to 50% physiological maturity, days to 50% physiological maturity in GDD and GFD in F<sub>2</sub> indicating partial dominance and was showed complete dominance in F<sub>2</sub> for 1,000 seed weight (Table 3). High heritability estimates in narrow sense was obtained for protein content, days to 50% heading, days to 50% heading in GDD, days to 50% flowering, days to 50% flowering in GDD, days to 50% physiological maturity, days to 50% physiological maturity in GDD and grain filling duration while moderate values occurred for grain filling duration in GDD, 1,000 seed weight, no. of grains/spike and seed yield/plant in both generations (Table 3) which indicates again that most of these traits are governed primarily by additive gene action. This suggested that the selection for these traits might be effective in early segregating generations. These findings are in agreement with the results of Iqbal et al. (8) and Kamaluddin et al. (9).

Results obtained in this study suggest that both additive and non-additive gene action played an im-

portant role in expression of these traits, although additive genetic variance was predominant. Therefore, biparental mating and diallel selective mating which may allow intermating of the selects in different cycles and utilize both additive and non additive gene effect could be effective in developing wheat cultivars having high protein content and early maturity with optimum yield. Dominance genetic effect shall be valuable in wheat breeding programs when hybrid seed production is made economically feasible through an efficient cytoplasmic male sterility system Pickett (10).

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