

## INHERITANCE OF Rht 8 DWARFING GENE IN WHEAT (*TRITICUM AESTIVUM* L.)

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### ABSTRACT

The inheritance of Rht 8 dwarfing gene was studied using a Chinese source (cv. Chuan Mai 18) as dwarf and 10 tall indigenous wheat cultivars. The study revealed that dwarfism caused by Rht 8 source is partially dominant. The crosses of this genotype with the tall parents like C 306, Hybrid 65, K 68, NP 824 and NP 846 can give desirable genotypes.

**Key words:** Dwarfing gene, Rht 8, wheat.

Significant increments in wheat yield has primarily been realized through the introduction of Norin 10 dwarfing genes. Presently, most of the wheat cultivars possess the dwarfing genes derived from the Norin 10 source (Rht 1 and Rht 2) either singly or together. However, the potential of Norin 10 genes has been fully exploited. Another dwarfing gene, Rht 3, causes drastic reduction in plant height [1]. Severe yield reduction has also been noticed due to incorporation of Rht 3 dwarfing gene [2, 3]. Likewise, Rht 4 [4], Rht 5 [5], Rht 6 [6] and Rht 7 [7] are of little commercial value as they also drastically reduce the plant height (24–50%) as well as grain yield [2]. It is, therefore, essential to search for additional sources of dwarfism to improve wheat yields further and create a broader genetic bases for dwarfism. In this context, the present investigation has been carried out to collect informations on the inheritance pattern of the new Rht 8 dwarfing gene. Rht 8 is a spontaneously induced Akakomugi gene [8] and extensively used in Italian wheat breeding programme [2]. Presently, it is also being used in the breeding programme of CIMMYT.

### MATERIALS AND METHODS

Ten crosses were made between ten tall wheat cultivars, namely, K 65, K 68, Hybrid 65, NI 5439, C 306, C 591, NP 710, NP 824, NP 846 and NP 875 (used as females) with the Chinese

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variety Chuan Mai 18 (CM 18) which possess the Rht 8 dwarfing gene (S. Rajaram, personal communication). The parents used in the crosses are characterized by a wide range of variability for different characters, viz., plant height, 1000-grain weight and grain yield (Table 1). The tall parents are good in respect of attractive grain colour, grain size, quality aspects and stable yielding ability but suffer due to lodging, whereas CM 18 is semidwarf with stiff stem and compact ear heads but poor quality grain. Reciprocal crosses were also made to verify the cytoplasmic effect on the expression of plant height. The F<sub>1</sub>s of both the direct and reciprocal crosses were raised together at the off-season summer nursery in Lahaul Valley, Himachal Pradesh. The parent strains, F<sub>1</sub> and F<sub>2</sub> populations were grown in randomized block design with three replications. Each parent and F<sub>1</sub> were represented by a single row of 3 m length, whereas each F<sub>2</sub>s had six rows in each replication. The spacing was 22.5 x 20 cm. The data recorded on five random plants in each parent and F<sub>1</sub> and on all the plants in each F<sub>2</sub> population were subjected to statistical analysis as per the standard procedures [9].

## RESULTS AND DISCUSSION

The analysis of variance showed the presence of sufficient variability among parents, F<sub>1</sub> and F<sub>2</sub> populations.

The mean values of different characters in the parents are presented in Table 1. The plant height in the tall parents ranged from 94 cm (NI 5439) to 126 cm (NP 846). Grain yield per plant and 1000-grain weight were in the range of 19.6 g (K 68) to 30.9 g (NP 875) and 31.0 g (NP 846) to 46.0 g (NP 875), respectively. The semidwarf parent CM 18 gave the highest grain yield of 34.9 g per plant. The observations (Table 2) indicated that there was practically no difference between the plant height of F<sub>1</sub> in the direct and reciprocal crosses. This suggested that plant height is controlled by nuclear genes only. The plant height of F<sub>1</sub> plants (Table 2) was close to the midparental values, except in the cross NP 875 x CM 18, where it was nearer to the dwarf parent. This suggested that dwarfism caused by Rht 8 gene in wheat is partially dominant. Similar results were reported regarding the inheritance of Rht 1 dwarfing gene in wheat [10]. Deviations from midparental values in F<sub>1</sub> can be caused by modifier genes in different parents

**Table 1. Mean values of different characters of wheat genotypes used in crosses**

Parent	Plant height (cm)	1000-grain weight (g)	Grain yield per plant (g)
K 65	102	42.1	25.2
Hybrid 65	105	39.8	22.3
K 68	107	33.1	19.6
NI 5439	94	37.4	26.2
C 306	111	34.8	30.5
NP 846	126	31.0	32.2
NP 875	113	46.0	30.9
NP 710	111	31.7	21.0
NP 824	101	42.6	27.5
C 591	103	36.4	22.6
CM 18 (Rht 8)	74	37.2	34.9

Table 2. Mean values of different characters in F<sub>1</sub> generation of wheat crosses

Cross	Plant height (cm)			1000-grain weight (g)	Grain-yield per plant (g)
	mid-parent	F <sub>1</sub>	reciprocal		
K 65 x CM 18	88.0	82	84	37.5	29.1
K 68 x CM 18	90.5	90	91	45.0	30.2
Hybrid 65 x CM 18	89.5	88	93	42.8	26.0
NI 5439 x CM 18	84.0	81	79	42.2	30.7
C 306 x CM 18	92.5	92	93	51.8	30.0
NP 846 x CM 18	100.0	94	96	41.4	35.3
NP 875 x CM 18	93.5	80	84	37.3	27.3
NP 710 x CM 18	92.5	87	89	38.9	25.7
NP 824 x CM 18	87.5	81	86	43.2	29.4
C 591 x CM 18	88.5	91	88	36.1	26.8

interacting with the Rht 8 dwarfing gene, as was also observed while studying the interaction of Norin 10 dwarfing genes [11]. Mean, range and coefficient of variability for plant height in F<sub>2</sub> are presented in Table 4. The F<sub>2</sub> segregation pattern confirmed the partially dominant nature of Rht 8 dwarfing gene in controlling plant height as it fits well in 1:2:1

Table 3. Segregation pattern in F<sub>2</sub> generation for plant height in ten wheat crosses

Cross	Total No. of plant analysed	Segregation (observed)			$\chi^2$ (1:2:1)	P
		tall	inter-mediate	dwarf		
K 65 x CM 18	260	70	117	73	2.06	0.50-0.25
K 68 x CM 18	263	73	116	74	3.65	0.25-0.10
Hybrid 65 x CM 18	258	60	122	76	3.11	0.10-0.05
NI 5439 x CM 18	262	62	129	71	0.68	0.75-0.50
C 306 x CM 18	260	70	134	56	1.75	0.50-0.25
NP 846 x CM 18	265	60	140	65	1.02	0.75-0.50
NP 875 x CM 18	262	72	112	78	5.78	0.10-0.05
NP 710 x CM 18	265	60	146	59	2.97	0.25-0.10
NP 824 x CM 18	260	70	114	76	4.21	0.10-0.05
C 591 x CM 18	254	72	126	56	2.03	0.50-0.25
Pooled	2609	669	1256	684	3.85	0.25-0.10

ratio (Table 3). The mean plant height in F<sub>2</sub> of each cross was either close to the respective F<sub>1</sub> or the dwarf parent CM 18. In most of the crosses, transgressive segregations were observed with greater proportions of semidwarf genotypes. This suggests the presence of minor genes in the tall varieties which may reduce the plant height. Similar observations were made while studying the inheritance of Rht 1, Rht 2 and Rht 3 dwarfing genes in wheat by Sastry [10]. Higher values of CV for plant height in F<sub>2</sub> were observed in the crosses involving parents like Hybrid 65, NP 824, K 68, C 306 and NP 846 (Table 3), indicating that there is ample scope of selection in these crosses towards obtaining semidwarf, high yielding genotypes.

**Table 4. Mean, range and coefficient of variation for plant height (cm) in F<sub>2</sub> generations of wheat crosses**

Cross	Mean	Range	C.V.
K 65 x CM 18	76	68-108	12.6
K 68 x CM 18	87	54-116	29.6
Hybrid 65 x CM 18	70	43-110	36.5
NI 5439 x CM 18	80	74-96	13.2
C 306 x CM 18	64	36-118	28.8
NP 846 x CM 18	81	57-135	27.4
NP 875 x CM 18	76	70-121	22.3
NP 710 x CM 18	84	75-115	14.2
NP 824 x CM 18	68	40-110	32.3
C 591 x CM 18	82	78-104	13.7

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