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Inheritance of *Rht5* dwarfing gene in common wheat (*Triticum aestivum* L.)

***Goudia D. Bachir*[1] *and Hu Yin-Gang*[1-2]**

[1]College of Agronomy, Northwest A&F University, Yangling, Shaanxi, 712100, China

[2]Institute of Water Saving Agriculture in Arid Regions of China, Northwest A&F University, Yangling, Shaanxi, 712100, China

ABSTRACT: The objective of this study was to estimate the inheritance of Rht5 dwarfing gene in wheat. Two tall elite cultivars Ningchun10 and Jinmai47 were crossed with Rht5 donor parent Marfed M, to produce F_1. The F_1 was allowed to self in order to obtain F_2 seeds. Then the segregation populations were evaluated for some genetic parameters viz., coefficient of variability (CV), genetic variance (Vg), heritability percentage (h2 %) and genetic advance (GA) in 5 quantitative characters (Plant height, spike length, number of spikelets spike^{-1}, number of fertile tillers and number of grains spike^{-1}). All the characters were quantitatively inherited with varying degrees. The progeny Jinmai47 and Marfed M exhibited the highest heritability associated with a moderate genetic advance for plant height (h2% 66.65% and GA 17.46). The highest heritability with low genetic advance for spike length, number of spikelets spike^{-1} was observed in the progeny Jinmai47 and Marfed M. The two progenies showed high heritability associated with high genetic advance for number of fertile tillers and number of grains spike^{-1}. In the two progenies plant height showed highly positive and significant correlation with spike length (0.73 & 0.71), number of spikelets spike^{-1} (0.55 & 0.52) and number of grains spike^{-1} (0.71 & 0.59).

The present findings suggest that the inheritance of Rht5 dwarfing gene is high although there is variation between different backgrounds of tall parents. It suggests that the selection at early segregation generation could be efficient for selecting superior lines of wheat with the target dwarfing gene. However, the use of molecular marker techniques could increase the efficiency of selecting superior lines with Rht5.

KEYWORDS: Coefficient of variability, genetic advance, heritability, Rht5, *Triticum aestivum*.

1 INTRODUCTION

Since the Green revolution, semi-dwarf wheat sources have been emphasized in most wheat improvement programs to increase grain yield [1]. The dwarfing and semi dwarfing genes have played important roles in reducing plant height, increasing harvest index, improving lodging resistance, and increasing grain yield. Nowadays, most of the wheat cultivars possess one or two dwarfing genes (Rht-1 and Rht-2) derived from "Norin". Another dwarfing gene, Rht3, causes drastic reduction in plant height [2]. Severe yield reduction has also been noticed due to incorporation of Rht3 dwarfing gene [3]; [4]. Likewise, Rht4, Rht5, Rht6, Rht7, Rht8, Rht12 and Rht13 [5]; [6]; [7]; [8] also reduce the plant height (7-55%) as well as grain yield. The dwarf character usually does not appear until the F_2 generation, although some researchers have observed dwarfs in the F_1 [9]. The presence of dwarf in the F_2 and later generations has usually been explained on the basis of a 2-factor difference - one, a dominant dwarfing factor, the other an inhibiting factor. Clark and Hooker [10] in a Marquis X Hard Federation cross and [11] in a Federation X Marquis cross, explained their results on the 2-factor basis.

Wheat breeders are utilizing available genetic resources to reconstruct the ideotype of plant to meet the ever increasing requirements of the population. In this regard heritability estimates plays an important role for planning the breeding strategy. The heritability of the character determines the extent to which it is transmitted from one generation to the next and it is most valuable tool when used in conjunction with other parameters in predicting genetic gain that follows in the

Corresponding Author: Goudia D. Bachir (bachirgaoh@gmail.com) selection for that character [12]; [13]; [14]; [15]. The heritability values become a measure of the genetic relationship between parents and progeny; hence considerable research work has been carried out to incorporate the desirable genes in present wheat varieties to increase the productivity of the crop. Similarly, the semi dwarfing or reduced height genes have been extensively exploited for developing high yielding varieties with grain yield associated trait [16]; [17]. It is, therefore, essential to search for additional sources of dwarfism to improve wheat yields further and create a broader genetic base for dwarfism. In this context, the present investigation has been carried out to collect informations on the inheritance pattern of the Rht 5 dwarfing gene. Rht-5 is a gibberellin acid-responsive (GAR) dwarfing gene that reduces plant height without affecting early growth [18].

2 MATERIALS AND METHODS

2.1 PLANT MATERIALS

In this study, two tall cultivars Ningchun10 and Jinmai47 used as female parents were crossed to male parent Marfed M with dwarfing gene Rht5. F_2 segregation populations were used to estimate the inheritance of dwarfing gene Rht5. Ningchun10 is a tall wheat cultivar in the dryland spring wheat region and without any known dwarfing genes detected. Jinmai47 is a tall winter wheat cultivar in the Northern winter wheat region of China and carries dwarfing gene Rht8. Marfed M is a mutation-derived line with dwarfing gene Rht-5, with strong winter habit, very small spike and late heading and maturity.

2.2 FIELD EXPERIMENT PROCEDURES

The experiment was conducted during the two winter wheat growing seasons of 2010–2011 and 2011–2012 at the experimental farm of Northwest A&F University (Shaanxi, P.R. China). The altitude of the area is 525 m and the climate is semi-humid prone to semi-arid with an average annual temperature of 13◦C and aver-age annual rain fall of 600 mm. The parental crosses were carried out during the 2010 – 2011 growing season and F_2 individuals were sown by single seed dibbler method during the 2011 – 2012 growing season in a uniform field in a row 1.67 m long with an interval of 25 cm between rows and 10 cm between plants within a row. There were 20 – 30 lines per F_2 cross and two rows for each parent.

2.3 MEASURED TRAITS

133 plants from Ningchun10 x Marfed M F_2 progeny, 140 plants from Jinmai47 x Marfed F_2 progeny and ten plants from each parental line were selected at random and indexed to record data for quantitative traits. Data on plant height (cm), spike length (cm), number of spikelets spike^{-1} (N), number of grains spike^{-1} (N) and number of fertile tillers plant^{-1} (N) were recorded.

3 STATISTICAL ANALYSIS

To evaluate the inheritance, Genetic parameters viz., heritability percentage (h2%), genetic variance (Vg) and coefficient of variation (CV) were calculated for the quantitative traits as suggested by [19] and modified by [14] by using the following formulas:-

$$\text{Coefficient of variability (CV)} = \frac{SD \times 100}{X}$$

$$\text{Genetic variance (Vg)} = VF_2 - Ve$$

$$\text{Environmental variance (Ve)} = (VP_1 + VP_2)/2$$

$$h_2 = \frac{VF2 - (VP1+VP2)/2 \times 100}{VF2}$$

Where, V = variance, F_2 = second filial generation and P = parent, Ve = Environmental variance, Vg = Genetic variance, Vp1 = Variance of parent one, Vp2 = Variance of parent two, h_2% = Heritability percentage in broad sense, S.D = Phenotypic standard deviation.

The genetic advance (GA) was calculated according to Allard (1960), and was estimated from the following formula: GA = K x δ_P x h2b , were K-the selection differential in standard units in the present study and it was 2.06 at 5% level of selection; δ_P - standard deviation of the phenotypic variance of F_2; h2b – heritability in broad sense. All analysis was worked out with the help of statistical software (SPSS 16.0).

4 RESULTS AND DISCUSSION

The mean values along with standard deviation (SD) for the tall and dwarf parents and their F_2 progenies were estimated and showed in Table 1. The highest values for standard deviation in the dwarf groups were observed for number of fertile tillers (9.47 and 12.46), number of grains spike^{-1} (11.61 and 12.13), and plant height (12.75 and 14.14), which suggested, greater magnitude of variability among the F_2 populations for these traits and the potential for selection of good lines with better agronomic traits and semi-dwarf architecture.

As for the character plant height is concerned, the two tall parents Ningchun10 and Jinmai47 were significantly taller than the Rht*5* donor parent Marfed M in the two crosses. The spike length of the tall parents was longer than that of the dwarf parent Marfed M while the number of fertile tillers plant^{-1} of the dwarf parent was more than that of tall parents in the two crosses. The number of spikelets spike^{-1} and number of grains spike^{-1} of the tall parents were more than that of the dwarf parent which indicated that the tall parent had greater yield potential than the dwarf parent. The plant height, spike length, number of spikelets spike^{-1} and number of grains spike^{-1} of the F_2 progenies were nearer to the dwarf parent values which suggest that dwarfism caused by Rht*5* gene in wheat is dominant. The mean plant height in the F_2 of each cross was close to the dwarf parent Marfed M. This suggests that Rht5 dwarfing gene may reduce the plant height. This was confirmed by a study conducted by [7]; [8] where Rht5 dwarfing gene was associated with a plant height reduction of 23.16 % and 25.84%. Distribution of phenotypic values of plant height, in the F_2 populations is presented in Fig.1 indicating continuous distributions for this trait.

Table 1: Mean values for the studied traits in F_2 generations of the two crosses

Cross		**Plant height**	**Spike length**	**Spikelets no. spike^{-1}**	**No. fertile tillers plant^{-1}**	**Grains no. spike^{-1}**
Ningchun10	P_1	129.88±13.15	14.14±1.16	20.50±1.05	13.78±2.54	55.75±6.31
x	P_3	71.2±10.52	7.67±0.77	18.62±1.22	27±7.03	28.15±2.74
Marfed M	F_2	82.78±14.15	9.64±1.91	19.62±2.67	17.81±9.47	29.95±12.13
Jinmai47	P_2	87.89±0.44	10.30±0.11	19.40±0.57	10.10±2.69	58±6.51
x	P_3	58.12±10.32	7.14±0.26	16.13±0.50	22.87±4.12	23.63±1.38
Marfed M	F_2	75.72±12.65	8.73±1.45	19.87±2.11	22.71±12.46	32.41±11.61

P_1 = female parent (Ningchun10), P_2 = female parent (Jinmai47), P_3 = male parent (Marfed M)

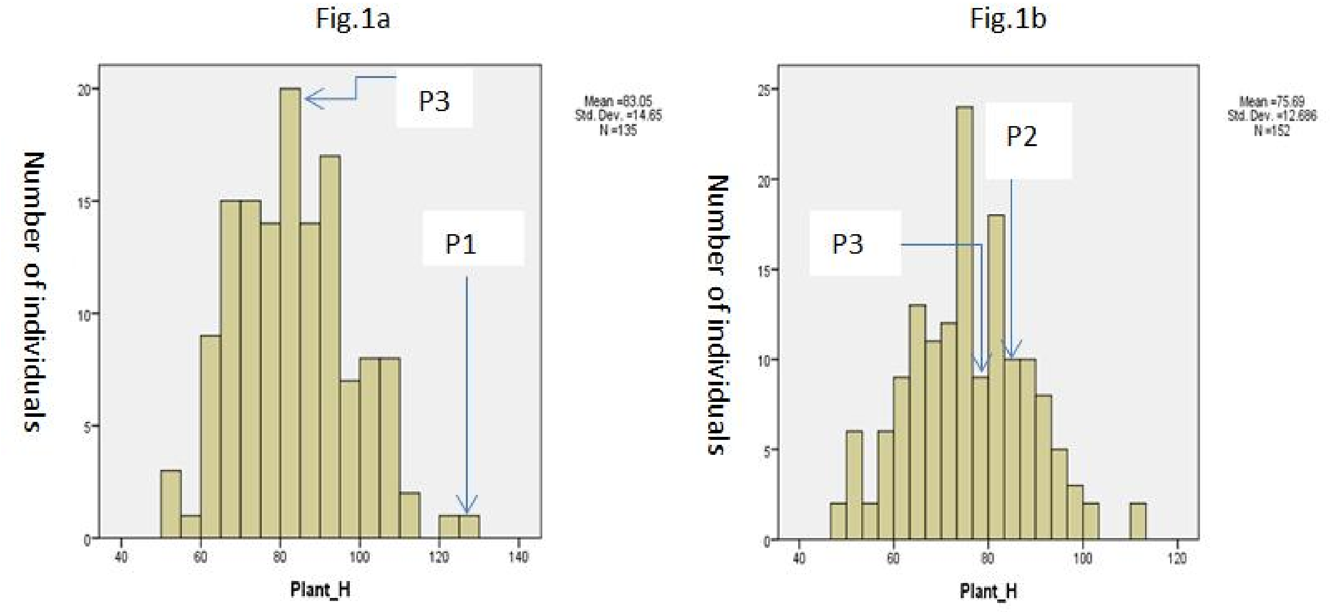

Fig 1a&b: Frequency distribution of plant height among the F_2 populations of Ningchun10 (P1) x Marfed M (P3) and Jinmai47 (P2) x Marfed M (P3)

Correlation analysis between plant height and other traits (table 2) revealed that in the two progenies plant height had highly positive and significant correlation with spike length, spikelets no. spike^{-1} and grains no.spike^{-1}. [7] reported highly positive and significant correlation between plant height and spike length, number of spikelets spike^{-1} and number of grains spike^{-1} in wheat $F_{2:3}$ lines with Rht5. Plant height had highly positive and significant correlation with number of tillers plant^{-1} in the progeny Ningchun10 x Marfed M, whereas no significant correlation was found between plant height and number of tillers per plant in the progeny Jinmai47 x Marfed M.

The genetic variability of plant height, spike length and number of spikelets spike^{-1} (Table 3) were 17.09, 19.78 and 11.56 in the cross Ningchun10 and Marfed M and 16.71, 16.58 and 10.63 in the progeny of Jinmai47 and Marfed M. High genetic variability was observed in the two progenies for number of fertile tillers and number of grains spike^{-1}. High values of CV for number of grains spike^{-1} in the F_2 progenies indicates that there is ample scope of selection in these crosses towards obtaining dwarf, high yielding genotypes.

The efficiency of selection from a population for a particular trait depends largely upon the genetic and non-genetic factors affecting the expression of phenotypic differences among genotypes in the population. Heritability thus is a significant parameter for the selection of an efficient population improvement method. Single plant selection in the earlier generations may be much effective for a character that is highly heritable as compared to that character which is less heritable. Furthermore, environment may also interact with the genotypic constitution to influence heritability [20]. The genetic selection parameters viz., genetic variance coefficient of variability (Vg), environmental variance (CV), heritability percentage in broad sense (h_2 %) and genetic advance (GA) are shown in Table 3. Genetic parameters studied in F_2 progenies were calculated according to the method described by [21].

For plant height, the cross between Ningchun10 and Marfed M resulted in low heritability associated with low genetic advance (h_2% 29.16 and GA 8.45) whereas the progeny of Jinmai47 and Marfed M expressed higher heritability and moderate genetic advance (h_2% 66.65 and GA 17.46) for plant height indicating that selection would be effective for this trait. The low heritability associated with low genetic advance in Ningchun10 and Marfed M could be due to genetic background of the tall parents and environmental conditions. In a study conducted on the inheritance of *Rht-B1b* dwarfing gene [22] reported high heritability associated with high genetic advance for plant height in Jinmai47 x Zhoumai17 and

Fengchan3 x Zhoumai17 F_2 progenies. The progeny Ningchun10/Marfed and Jinmai47/Marfed M exhibited high heritability along with low genetic advance for spike length and number of spikelets spike^{-1} which is indicative of non-additive gene action. High heritability with high genetic advance in wheat has been observed by various researchers for spike length and spikelet per spike [23]; [24]; [25]; [26].

For the number of fertile tillers and number of grains spike^{-1}, the broad sense heritability values and genetic advance were higher in both progenies, reflecting the large heritable variances offered the possibility of the improvement through selection [14]. [27] reported high heritability percentage along with high genetic advance linked with Rht1 and Rht2 for number of tillers per plant and grains per spike in the progeny Marvi-2000 x Soghat-90 and Soghat-90 x Sarsabz of spring wheat.

The present study suggested that the lines with Rht5 exhibiting high heritability with moderate to high genetic advance in most of the studied traits may be selected for evolving high yielding genotypes. Therefore, the improvement of these characters is possible through selection.

Table 2: Correlation coefficients between plant height and other traits in the F_2 progenies of Ningchun10 x Marfed M and Jinmai47 x Marfed M

Traits	Ningchun10 x Marfed M	Jinmai47 x Marfed
	F2 progeny	F2 progeny
No. fertile tillers plant^{-1}	0.26**	-0.1
Spike length	0.73**	0.71**
Spikelets no. spike^{-1}	0.55**	0.52**
Grains no.spike^{-1}	0.71**	0.59**

***Correlation is significant at the 0.01 level.*

** Correlation is significant at the 0.05 level.*

Table 3: Genetic variance (Vg), coefficient of variability (CV), environmental variance (Ve), heritability percentage (h_2%) in broad sense and genetic advance (GA) for the studied traits of the two F_2 progenies.

Cross		**Plant height**	**Spike length**	**Spikelet no. spike^{-1}**	**No. Fertile tillers plant^{-1}**	**Grains no. spike^{-1}**
Nigchun10 x Marfed M	Vg	58.35	2.66	3.84	61.64	123.35
	CV	17.09	19.78	11.56	53.16	40.48
	Ve	141.78	0.98	1.3	27.96	23.67
	h2 (%)	29.16	73.08	74.71	68.79	83.9
	GA	8.45	2.87	3.51	13.46	20.97
Jinmai47 x Marfed M	Vg	106.66	2.05	4.17	143.17	112.67
	CV	16.71	16.58	10.63	54.86	35.82
	Ve	53.38	0.04	0.29	12.1	22.11
	h2 (%)	66.65	98.09	93.5	92.2	83.6
	GA	17.46	2.93	4.09	23.61	20.09

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