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Chromosomal Arm Location of A Dominant Dwarfing Gene Rht21 in Common Wheat Variety——XN0004*

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Abstract XN0004 is a new dwarf wheat variety derived from the progeny of Qing 431× Xiaoyan 6. The dwarfing effect is controlled by a partially dominant gene which reduces plant height by 13.8% on an average in heterozygotes as compared with that of tall parents and is insensitive to exogenous gibberelic acid. Results of CS nulli-tetrasomic and ditelosomic analysis indicated that the Rht gene is located on the short arm of chromosome 2A. It might be a new dominant dwarfing gene and therefore the gene symbol Rht21 is designated provisionally. According to a previous study, there were no any side effects on agronomic characters with XN0004 and the hybrids with XN0004 as one of their parents showed higher heterosis suggesting that XN0004 might be a useful source for conventional and hybrid wheat breeding.

Key Words *Triticum aestivum*. dominant: dwarfing gene. gene loction. hybrid wheat

1 Introduction

Several dwarfing genes have been succesfully used for lodging—resistance in wheat breeding, and dominant dwarfing genes have special advantages for hybrid wheat production. According to literatures, twenty Rht genes were found or located on relative chromosomes in *Triticum aestivum* of *T. durum*. Among them, Rht3, Rht5, Rht10, Rht12, Rht14, Rht16, Rht18, and Rht19 are dominant, and Rht1, Rht2, Rht4, Rht6, Rht7, Rht8, Rht9, Rht11, Rht13, Rht15, Rht17, and Rht20 are recessive. Rht1, Rht2, Rht3 and Rht10 are insensitive to exogenous gibberellic acid(GA) while the others are sensitive to GA. XN0004 is a new variety developed from the progeny of Qing431 crossed with Xiaoyan 6 at Northwestern Agricultural University. On the basis of previous investigation, the grain yield of XN0004 was as high as that of the control. Some hybrids from XN0004 showed higher heterosis on grain yield due to increases in number of kernels per spike, thousand—kernel weight and harvest index etc.. This paper reports on the inheritance of plant height by progeny investigation and on the chromosomal arm location of Rht21 gene in XN0004 by using CS nulli-tetrasomic and ditelosomic analysis.

2 Materials and methods

Dwarfing variety XN0004 and six tall varieties involving 88B124, 84-129, 84-1, 89F5774, Shaan213 and Chinese Spring were used in crosses for investigation of plant

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height inheritance. A set of CS nulli－tetrasomics and ditelosomic 2AS and 2AL were used for the determination of Rht gene－chromosomal arm location. Becouse of lacking CS 4B° 4D ^{m} and CS 4D° 4A^{m}, they were replaced by monosomic CS 4B and ditelosomic CS 4DS and 4DL respectively. All crosses were made in greenhouse and their progenies were grown in field plots spaced by 25cm × 10cm in a randomized design with three replications. For chromosomal location of Rht gene, all F1s were planted in spring but those from CS 2AS and 2AL were planted in autumn in 1991. For GA response to seedling test, seeds were put into petri dishes for germination in two days at 15－16℃, then transplanted to seed trays with vermiculite, and different concentrations of GA, 0, 1, 30 and 100 mg/kg, were added, 15 mL to each. After 5 days at 20℃ under dark condition, seedling lengths were measured. For adult response, Different GA concentrations, 0, 100, 150 and 250 mg/kg, were sprayed by 25 mL over each plot every one week beginning from three leave stage for three times. The plant heights were measured before maturity. In order to avoid influences of addition chromosome from CS tetrasomics, plant heights of the Fls were compared with those of the means between XN0004 and each CS *nulli*－tetrasomic for location analysis of Rht gene.

3 Results and discussion

3.1 Inheritance of plant height of XN0004

The plant heights in Fls of XN0004 crossed with six tall varieties including Chinese Spring were between that of their parents or slightly over the mid-parent valud by 4 cm on the average ranging form 1.0 to 6.8 cm. This indicated that the Rht gene in XN0004 was partially dominant. Comparing to their tall parents, the heights in Fls were about 14.6 cm (from 6.7 to 32.9 cm) or 13.8% (8.0 to 24.0%) shorter than those of the tall parents (Table 1).

Table 1 Plant height in the Fls of XN0004 crossed with six tall varieties cm

Cross	SP	TP	F1	MP	F1-MP	F1-TP	RH%
XN0004/88B124	62.3±2.1	84.1±1.9	77.4±2.3	73.2	4.2	−6.7	8.0
XN0004/84-129	62.3±2.1	97.1±3.8	81.5±2.4	79.7	1.8	−15.6	16.1
XN0004/84-1	62.3±2.1	91.8±2.9	82.5±2.0	77.1	5.4	−9.3	10.1
XN0004/89F5774	62.3±2.1	86.5±2.4	79.5±2.1	74.4	5.1	−7.0	8.1
XN0004/Shaan213	62.3+2.1	95.7±2.9	80.0±2.6	79.0	1.0	−15.7	16.4
XN0004/CS	57.7±3.6	137.1±8.2	104.2±7.9	97.4	6.8	−32.9	24.0
Mean	61.4	98.7	84.1	80.1	4.0	−14.6	13.8

Table 2 Segregation of plant heights in the F2 and Bcls of XN0004/CS

Generation	No. of Plant	Mean height(cm)	distribution			ratio	$X^2_{1:2:1}$	$X^2_{1:1}$
			S	*M*	*T*			
F2	98	104.1	26	43	29	1:2:1	1.31	5.99
Bcl SP	84	82.3	44	40		1:1	0.11	3.84
Bcl TP	209	120.9		99	110	1:1	0.48	3.84

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The plant height of the individuals in the F2 population of XN0004/CS could be classified into three groups: short(*S*), medium(*M*) and tall(*T*). The segregation of the F2 was in the ratio of 1*T* : 2*M* : 1*S*. The ratios of segregation of the Bcl(F1/Short P) and Bcl'(F1/Tall P) were 1*M* : 1*S* and 1*M* : 1*T* respectively(Table 2), indicating that the short plant height of XN0004 was controlled by a partially dominant major gene.

3.2 GA response

Data of GA response of XN0004 and Chinese Spring were summarized in Table 3. The results showed that there were significant differences between the different treatments and the control(0 mg/kg) both at the seedling and the adult stages with CS, but no such results with XN0004, indicating that XN0004 was insensitive to GA treatment.

Table 3　Response of XN0004 and CS to GA treatment

Variety	Concentration of GA(mg/kg)				
	0	1	10	30	100
	Seedling Length(mm)				
XN0004	39.5	38.9(−0.6)	39.7(0.2)	39.7(0.2)	38.9(−0.6)
CS	60.8	65.6(4.8*)	66.2(5.4*)	68.0(7.2*)	65.2(4.4*)
	0	100	150	250	
	Adult height(cm)				
XN0004	57.6	58.3(0.7)	58.2(0.6)	56.8(−0.8)	
CS	137.2	141.8(4.6**)	149.0(11.8**)	149.1(11.9**)	

Note: figures in brackets are differences between the different concentrations of GA and 0 concentration.

* and * *, significant level at 0.05 and 0.01 respectively.

3.3 Chromosomal location of Rht gene in XN0004

When XN0004 was crossed with a set of CS nulli−tetrasomics, the plant heights in Fls of all crosses were over or near the mean heights of their two parents except that from XN0004/CS 2A° 2D^{m} in which the plant height of the F1 were significantly shorter (−3.1 cm) than the mid-parent value, indicating that the Rht gene was located on the chromosome 2A. On the contrary, when XN0004 was crossed to CS 2D° 2A^{m}, the plant height of the F1 was 5.5 cm significantly higher than midparent value due to 3 times of rht dosage existing in chromosome 2A, which which confirmed the results above.

For arm location of Rht gene on chromosome 2A, CS ditelosomic 2AS and 2AL were crossed to XN0004. The results showed that the plant heights in F1 were 12.7 cm higher than the mean of that of its parents when XN0004 was crossed to 2AS, but 3.6cm significantly shorter than the mean of its parents when XN0004 was crossed to 2AS. but 3.6 cm significantly shorter than the mean of that of its parents when XNOOO4 was crossed to 2AL. Such different results were due to the corresponding rht gene existing in the former but not in the later so that the Rht gene of XN0004 must be on the short arm of chromosome 2A(Table 4).

Since none of the 20 Rht genes known are located on chromosome 2A except Rht7,

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and since Rht7 is sensitive to GA and has harmful effects on reducing yields, whereas the Rht gene of XN0004 is insensitive to GA and has no any side effects on agronomic traits. It is very probable that it is a new Rht gene, hence provisionally designated as Rht21. Whether or not Rht21 is allelic to Rht7 is unknown.

Table 4 Plant height in F1 from XN0004 crossed with Chinese Spring nulli—tetrasomics and ditelosomics

Parent	P	MP	F1	F1—MP
XN0004	38.7 (57.6)			
CS 21″	105.6	72.1	72.2	0.1
	(145.1)	(101.3)	(109.4)	(8.1)
1A° 1D″	91.4	65.1	70.6	5.1
2A° 2D″	94.5	66.6	63.5	−3.1*
3A° 3D″	103.7	71.2	71.3	0.1
4A° 4D″	62.0	50.4	67.7	17.3
5A° 5D″	(143.4)	(99.4)	(101.6)	(2.2)
6A° 6D″	84.9	61.8	72.1	10.3
7A° 7D″	82.5	60.6	77.2	16.6
1B° 1D″	91.4	65.1	75.0	9.9
2B° 2D″	86.3	62.5	78.4	15.9
3B° 3D″	89.6	64.2	69.3	5.1
4B	63.2	47.0	51.0	4.0
5B° 5D″	85.8	62.3	67.5	5.2
6B° 6D″	(122.8)	(89.1)	(103.9)	(14.8)
7B° 7D″	81.5	60.1	69.8	9.7
1D° 1A″	93.9	66.3	66.2	−0.1
2D° 2A″	81.6	60.2	65.7	5.5*
3D° 3A″	80.2	59.4	66.0	6.6
4DS	90.0	64.4	74.1	9.7
4DL	99.7	69.2	68.3	−0.9
5D° 5A″	64.9	51.8	62.3	10.5
6D° 6A″	90.6	64.7	69.3	4.6
7D° 7A″	99.0	68.9	72.5	3.6
2AS	(134.0)	(94.7)	(107.4)	(12.7)
2AL	(147.4)	(101.4)	(97.8)	(−3.6*)

Note: The figures in brackets were obtained from Autumn sown plots in 1992 and others form spring sown plots in 1991; * : Significant level at 0.05.

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矮秆小麦 XN0004 的矮秆基因 Rht21 的染色体臂定位

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摘　要　XN0004 是育 431 与小偃 6 号杂交选育的一个新的具有部分矮秆显性效应的小麦新矮源品系。和高秆亲本相比，其杂种 F1 代的降秆作用平均为 13.8%，对外源赤霉酸反应不敏感，在杂种小麦研究中，其配合力优良，增产显著，穗粒数增加，抗倒能力增强，收获指数提高等，无某些矮源对杂种 F1 产生的不良效应，是杂种小麦比较理想的矮秆亲本，可作为常规育种的优良矮秆品种资源。用中国春缺一四体和双端体分析的方法，对 XN0004 丰矮秆显性基因进行了染色体定位，证明其矮秆显性基因位于 2A 染色体的短臂上，是一个不同于世界上已定位的 20 个 Rht 基因的新矮源，故暂定名为显性矮秆基因 Rht21。

关键词　小麦，显性矮秆基因，基因定位，杂交育种　染色体、育种

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