The effects of dwarfing gene *Rht-8* on plant height and other agronomic traits in common wheat

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Abstract: A study was carried out to estimate the inheritance, genetic effects of dwarfing gene *Rht-8* on plant height and other agronomic traits in common wheat. Three tall elite cultivars of Jinmai 47, Xifeng 20 and Fengchan 3 were crossed with the *Rht-8* donor cultivar Jining 13 to produce F_1. The F_1 was self crossed to obtain F_2 seeds. Then the F_2 segregation populations were used to estimate the inheritance and genetic effects. For the plant height, the progeny of Fengchan 3 with Jining 13 attained the highest broad inheritability (74.32%) followed by the progeny of Xifeng 20 and Jinmai 47 with Jining 13 (69.49% and 67.60%, respectively). The effect of dwarfing gene *Rht-8* was more prominent in the progeny of Xifeng 20 with Jining 13, with plant height and peduncle length reduced by 30.26% and 19.20%, respectively. By contrast, in the progenies of Fengchan 3 and Jinmai 47 with Jining 13, plant height and peduncle length were reduced by 27.14% and 26.15%, 14.86% and 14.59%, respectively. There were no significantly negative effects of dwarfing gene *Rht-8* on the other agronomic traits except that it reduced the number of tillers per plant. Correlation analysis indicated that plant height was positively and significantly correlated with number of tillers (0.415, 0.355, and 0.489) and peduncle length (0.408, 0.450, and 0.500), but no significant correlations were observed among plant height and spike length, No. of spikelets per spike, and No. of grains per spike.

Keywords: wheat; inheritance; *Rht-8*; genetic effects; plant height; correlation

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小麦矮秆基因 *Rht-8* 对株高和其它农艺性状的遗传效应

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摘　要:分析矮秆基因 *Rht-8* 的遗传力及其对小麦株高及相关农艺性状的影响。利用三个小麦品种晋麦 47、西峰 20、丰产 3 号分别与 *Rht-8* 的供体亲本济宁 13 杂交,以其 F_2 分离群体分析 *Rht-8* 的遗传效应。结果表明,丰产 3 号和济宁 13 后代的遗传力最高(74.32%),西峰 20、晋麦 47 与济宁 13 后代的遗传力分别为 69.49%、67.60%。*Rht-8* 在西峰 20 和济宁 13 的 F_2 中具有较强的效应,株高和穗下节分别降低了 30.26%和 19.20%。在丰产 3 号和晋麦 47 与济宁 13 的 F_2 中,株高和穗下节分别降低了 27.14%和 26.15%、14.86%和 14.59%。*Rht-8* 减少了有效分蘖个数,对其他性状则无明显的不利影响。相关性分析表明株高与分蘖数显著正相关(r 为 0.415,0.355,0.489),与穗下节显著正相关(r 为 0.408,0.450,0.500);株高与穗长、每穗小穗数、穗粒数没有显著相关性。

关键词:小麦;遗传力;*Rht-8*;遗传效应;株高;农艺性状

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Wheat plant height is an important character, which can significantly influence not only lodging resistance, but also photosynthesis and assimilate distribution, therefore grain yield[1]. Most current wheat cultivars contain *Rht-B1b* (formerly *Rht-1*) or *Rht-D1b* (formerly *Rht-2*), which were GA (gibberellic acid) insensitive dwarfing genes and transferred from the Japanese line 'Norin 10'[2]. These two dwarfing genes had been located on homoeologous chromosome arms of 4BS and 4DS, and had pleiotropic effects on plant growth, causing reduction in coleoptiles length and seedling leaf area[3], and increase in ear productivity under favorable conditions. Sip and Skorpik[4] found that only the strong height reduction caused by *Rht-3* had a negative influence on yield, while dwarfing genes *Rht-8*, Rht-B1b and *Rht-D1b*, had no negative effect on yield. Significant effects of these genes on earliness and grain quality characters were not detected[2].

It is evident from different analyses that the effects of *Rht* alleles vary greatly with genetic background and environment[5]. Even though obtaining desirable bread-making quality does not seem to be a great problem with the commonly used Norin 10 genes, there still persist problems with obtaining broader adaptation and resistance to different stress factors. Poor emergence from depth because of shorter coleoptiles and lower adaptation, especially to dry environments, are known problems connected with the presence of the *Rht-B1b* and *Rht-D1b* alleles[6-7]. This has led to the examination of alternative *Rht* genes[6,8] and/or additional genes that increase coleoptile length in *Rht-B1b* and *Rht-D1b* backgrounds while maintaining semi-dwarf height[5].

The GA responsive (GAR) height-reducing gene *Rht-8* was introduced into Italian wheat from the Japanese landrace Akakomugi, and has been widely used in wheat adapted to southern and eastern European conditions. The *Rht-8* allele has been shown to reduce plant height and increase carbon-partitioning to grain to increase grain number and yield[6]. *Rht-8* has a smaller effect on height reduction (ca. 8% ~ 12%) than the GAI-dwarfing genes *Rht-B1b*, *Rht-B1c* and *Rht-D1b*[6,8]. *Rht-8* has been widely used in commercial wheat varieties identified with molecular markers[9], the distribution of the cultivars with *Rht-8* are in a range of environments, highlighting the potential of the other GAR-dwarfing genes for use in breeding of commercial varieties. A number of other GAR dwarfing genes have been identified with potential to reduce plant height without affecting seedling vigor[8,10]. Alleles at two of these loci, *Rht-8* and *Rht13*, show promise for use in breeding owing to their effects of decreasing plant height and stem lodging without reducing seedling vigor[10]. However, little is known on the effects of *Rht-8* on grain yield and grain yield components.

Following identification of a close linkage to *Rht-8*, microsatellite marker Gwm 261 has been used extensively to screen large numbers of diverse international germplasm. A192 bp allele at this locus has been taken as 'diagnostic' for *Rht-8* and used to infer the presence of *Rht-8* in wheat. In a previous study[11], Bonnett reported that several Australian wheat cultivars contained a 192 bp allele at the Xgwm 261 locus. Some cultivars comprised a mixture of genotypes at this locus, cultivars Mitre and Perenjori contained both 192 bp and 165 bp variants without apparent height differences[12]. Some authors stated that the presence of Xgwm 261 192 bp is only indicative of *Rht-8* in wheat cultivars that have inherited this allele from Akakomugi or a Strampelli wheat ancestor[13].

The aims of this study were to evaluate the inheritance of GAR dwarfing gene *Rht-8* in F2 segregation population of wheat and understand the effects of GAR dwarfing gene *Rht-8* on plant height and other agronomic traits.

1 Materials and methods

1.1 Materials

Three elite cultivars of Jinmai 47, Xifeng 20 and Fengchan 3 were crossed with the *Rht-8* donor Jining 13, respectively. The F_1 were selfed to obtain the F_2 seeds. The F_2 segregation populations were sown by single seed apart 10 cm with 20 rows per cross along with two rows for each parent. The row length was of 2 m with intervals of 0.25 m. The field experiment was conducted at the No.1 farm of Northwest A&F University, Yangling, Shaanxi, China.

1.2 Traits evaluation

Two hundred plants from each F_2 population and ten plants from each parental line were selected at random and indexed to record the data for quantitative traits.

Plant height (cm), peduncle length (cm), number of tillers per plant, spike length(cm), No. of spikelets per spike, and No. of grains per spike of the main stem of each individual were recorded accordingly at maturity.

1.3 Data analysis

All of the F_2 progenies and their parents were used to estimate genetic parameters of genetic variance(Vg) and coefficient of variation (CV), heritability percentage ($h_2\%$) of plant height as suggested by Falconer[14] and modified by Ansari et al[15].

To understand the effects of the dwarfing gene on plant height and other agronomic traits, all of the individuals among the F_2 population were sorted to three groups of tall, medium, dwarf, according to their plant height at the law of segregation, and then the effects of dwarfing genes were estimated. While for mean variance, significant level at 5% was used to declare difference. Data analysis was conducted in MS Office Excel 2007 and Statistical software SPSS 16.0.

2 Results and analysis

2.1 The distribution of plant height among the F_2 population

As for the three progenies namely Jinmai 47, Xifeng 20 and Fengchan 3 with Jining 13, the plant height of the two parents and among the F_2 population were significantly different and all of three progenies showed transgressive segregation(table 1).

Table 1 Ranges and mean difference for plant height(PH) in F_2

Parents/Crosses	Dwarfing gene	Tall/cm	Dwarf/cm	Difference/cm	Range/cm
Jinmai 47	*rht-8*	103.50	—	19.40	—
Xifeng 20	*rht-8*	112.95	—	28.85	—
Fengchan 3	*rht-8*	108.65	—	24.55	—
Jining 13	*Rht-8*	—	84.10	—	
Jinmai 47 × Jining 13	*Rht-8/rht-8*	93.36	74.01	19.35	67.0~104.0
Xifeng 20 × Jining 13	*Rht-8/rht-8*	109.14	83.78	25.37	57.0~119.5
Fengchan 3 × Jining 13	*Rht-8/rht-8*	104.93	82.53	22.24	67.0~112.5
Mean of three crosses	*Rht-8/rht-8*	102.48	80.11	22.32	—

2.2 Inheritance of dwarf gene *Rht-8*

Genetic parameters of genetic variance coefficient of variability(Vg), environmental variance(CV), heritability percentage in broad sense($h_2\%$) of plant height in the studied F_2 progenies were estimated and shown in table 2.

Table 2 Genetic parameters estimated for plant height in three wheat F_2 progenies

F_2 cross	Vg	CV	VE	h_2/%
Jinmai 47 × Jining 13	38.65	13.23	18.52	67.60
Xifeng 20 × Jining 13	71.89	9.83	31.56	69.49
Fengchen 3 × Jining 13	58.21	11.30	20.11	74.32

For the plant height, the progeny of Fengchan 3 and Jining 13 revealed the highest heritability percentage ($h_2\% = 74.32\%$) followed by crosses Xifeng 20 ($h_2\% = 69.49\%$) and Jinmai 47 ($h_2\% = 67.60\%$) with Jining 13. This reflected the higher heritability of plant height, which offered the possibility of the improvement through selection in early generations[16].

2.3 The effects of *Rht-8* on plant height and peduncle length

Among the F_2 populations, the effects of dwarfing gene *Rht-8* on plant height were estimated and showed in table 3, as in the progenies of Jinmai 47, Xifeng 20 and Fengchan 3 with Jining 13, the plant height showed reduction of 27.92% in average, with stronger effects observed in the back ground of Xifeng 20. The effects of dwarfing gene *Rht-8* on peduncle length were calculated and listed in table 4. The peduncle length in the three progenies was reduced by 16.34% in average. It suggested that the dwarfing gene *Rht-8* had better effects on reducing plant height and peduncle length in wheat.

Table 3　Effects of the dwarfing gene *Rht-8* on plant height based F_2 population

Parents/Crosses	Tall/cm	Dwarf/cm	Difference/cm	Effect/%
Jinmai 47 × Jining 13	93.36	74.01	19.35	−26.15
Xifeng 20 × Jining 13	109.14	83.78	25.37	−30.26
Fengchan 3 × Jining 13	104.93	82.53	22.24	−27.14
Mean of three crosses	102.48	80.11	22.32	−27.92

Table 4　Effects of the dwarfing gene *Rht-8* on peduncle length based F_2 population

Parents/Crosses	Tall/cm	Dwarf/cm	Difference/cm	Effect/%
Jinmai 47 × Jining 13	27.24	23.77	3.47	−14.59
Xifeng 20 × Jining 13	36.43	30.56	5.87	−19.20
Fengchan 3 × Jining 13	36.39	31.68	4.71	−14.87
Mean of three crosses	33.35	28.67	4.68	−16.34

2.4　The effects of *Rht-8* on some agronomic traits

2.4.1　The effects of *Rht-8* on No. of tillers per plant

With regards to the effects of dwarfing gene (*Rht-8*) on No. of tillers per plant (table 5), negative effects were observed among the three progenies with a reduction of 24.11% in average. It suggested that the dwarfing gene could reduce the No. of tillers per plant.

Table 5　Effects of the dwarfing gene *Rht-8* on No. of tillers per plant

Parents/Crosses	Tall	Dwarf	Difference	Effect/%
Jinmai 47 × Jining 13	9.39a	5.82b	3.57	−23.47
Xifeng 20 × Jining 13	9.29a	5.94b	3.35	−22.00
Fengchan 3 × Jining 13	7.91a	4.56b	3.35	−26.86
Mean of three crosses	8.86a	5.44b	3.42	−24.11

2.4.2　The effects of *Rht-8* on spike length　As to the spike length, although negative effects were also observed in all the three populations with average of 4.94% (table 6), there were no significant differences. It indicated that *Rht-8* can reduce plant height while not affect the spike length.

Table 6　Effects of the dwarfing gene *Rht-8* on spike length

Parents/Crosses	Tall/cm	Dwarf/cm	Difference/cm	Effect/%
Jinmai 47 × Jining 13	11.04a	10.76a	0.28	−2.60
Xifeng 20 × Jining 13	11.73a	10.97a	0.76	−6.93
Fengchan 3 × Jining 13	10.40a	9.88a	0.52	−4.94
Mean of three crosses	11.06a	10.54a	0.52	−4.94

2.4.3　The effects of *Rht-8* on No. of spikelets per spike　As for the effects of dwarfing gene *Rht-8* on No. of spikelets per spike (table 7), no significant differences were observed in all the three populations.

Table 7　Effects of the dwarfing gene *Rht-8* on No. of spikelets per spike

Parents/Crosses	Tall	Dwarf	Difference	Effect/%
Jinmai 47 × Jining 13	20.76a	20.96a	−0.20	0.95
Xifeng 20 × Jining 13	21.09a	20.64a	0.45	−2.18
Fengchan 3 × Jining 13	19.00a	18.80a	0.20	−1.06
Mean of three crosses	20.28a	20.13a	0.15	−0.75

2.4.4　The effects of *Rht-8* on No. of grains per spike

Regards to the effects of dwarfing gene *Rht-8* on No. of grains per spike (table 8), significant reduction effect was observed in the progeny of Xifeng 20 and Jining

13 with 8.76%, but there were no significant differences observed in the progenies of Jinmai 47 and Fengchan3 with Jining 13. It suggested that the effects on No. of grains per spike varied with the background of tall parents. However, it should be combined with spike characters when introducing *Rht-8* to breeding new wheat cultivars using different genetic background.

Table 8 Effect of the dwarfing gene *Rht-8* on grains per spike

Parents/Crosses	Tall	Dwarf	Difference	Effect/%
Jinmai 47 × Jining 13	56.07a	53.64a	2.43	-2.21
Xifeng 20 × Jining 13	36.43a	30.56b	5.87	-8.76
Fengchan 3 × Jining 13	54.43a	52.84a	1.59	-1.48
Mean of three crosses	48.98a	45.68a	3.30	-7.22

2.5 Relationships between plant height and other agronomic traits

The correlation coefficients between plant height and the other agronomic traits were estimated as shown in table 9. In general, it indicated that plant height was positively and highly correlated with number of tillers (0.415, 0.355 and 0.489) and peduncle length(0.408, 0.450, 0.500), but no significant correlations were observed between plant height with spike length and No. of spikelets per spike and No. of grains per spike. While in the progenies of Xifeng 20 and Fengchan 3 with Jinjing 13, plant height was highly significant and positively correlated with spike length (0.208, 0.191). It also suggested that dwarfing gene had negative effects on number of tillers per plant, but no significant effects on the number of spikelets per spike and number of grains per spike.

Table 9 Correlation coefficients between plant height(PH) and other agronomic traits

Traits	Jinmai 47 × Jining 13	Xifeng 20 × Jining 13	Fengchan 3 × Jining 13
No. of tillers per plant	0.415**	0.355**	0.489**
Spike length	-0.03	0.208**	0.191**
Peduncle length	0.408**	0.450**	0.500**
No. of spikeletsper spike	-0.013	0.127*	0.041
No of grains per spike	0.078	0.083	0.096

Note: ** and * indicates correlation significant at the 0.01 and 0.05 level (1-tailed), respectively.

3 Discussion

Heritability of a trait reflects its response to selection. In broad sense heritability, the environment plays a significant role in the expression of the phenotype[16]. Analysis on plant height in the three progenies of dwarfing gene *Rht-8* revealed higher broad sense heritability, which are in accordance with those previously reported by Jedynski[17], Patel & Jain[18], Kumar et al[19] and suggests that selection at an early segregating generation is efficient for plant height, which will be beneficial for selecting superior wheat lines with dwarfing gene.

Reducing plant height is a key objective in wheat breeding programs worldwide[5]. *Rht-8* is reported with a smaller effect on height reduction (ca. 8%~12%) than the GAI-dwarfing genes *Rht-B1b*, *Rht-B1c* and *Rht-D1b*[6,8]. Despite this, *Rht-8* has been identified in commercial wheat varieties[9], highlighting the potential of the GAR-dwarfing genes for use in breeding of commercial varieties. The *Rht-B1b* and *Rht-D1b* alleles reduce stem internode length through a decreased sensitivity of vegetative tissues to endogenous gibberellins[8,20-21], thus decreasing overall plant height. This finding showed that GA3 insensitive dwarfing genes (*Rht-B1b* and *Rht-D1b*) reduced the plant height of wheat by approximately 20%~30%, while dwarfing gene (*Rht-8*) reduced the plant height by only 18%, which was not agreement with the results obtained in this study. Comparisons among the three populations in this study demonstrated stronger genetic effects on plant height reduction associated with dwarfing alleles *Rht-8*(27.92%). The disagreement of these results with previous findings may be caused by environmental effect or presence of some other alleles in these populations.

Agronomic performance is a key consideration in assessment of new alleles for use in breeding. It has been reported that *Rht-8* reduced plant height, but had no effect on coleoptile length and seedling vigor compared with GA – insensitive dwarfing genes *Rht-B1b* and *Rht-D1b*[8]. Rebetzke et al[22] reported that *Rht-8* had little effect on grain number (–1%). In this study, considerable genotypic variation was observed for all agronomic traits measured in each population. Negative effect (24.11%) of dwarfing gene *Rht-8* was observed in number of tillers per plant, no significant effects were observed for the other traits as spike length, number of spikelets per spike and number of grains per spike. But the variations in the effects of dwarfing gene *Rht-8* were observed among different crosses, which suggest the back ground of tall parents also play very important role on the agronomic traits. However, the modest height-reducing gene *Rht-8* may be more suitable to reduce final plant height without affect spike characters.

Correlation analysis indicated that plant height was positively and highly correlated with number of tillers per plant and peduncle length in all the three populations, but only positively correlated with spike length in two populations, not correlated with number of spikelets per spike, and grains per spike. The results are in agreement with the findings of Nirala and Jha[23], Khan and Mohammad[24] and Mohsin et al[25].

The effect of dwarfing gene *Rht-8* on plant height, and a number of agronomic traits were evaluated. It showed that *Rht-8* has higher heritability on plant height, which offered the possibility of the improvement through selection in early generations. *Rht-8* has significantly reduced plant height by almost 30% in the three F_2 populations. However, *Rht-8* has no significant effect on yield components except the number of tillers per plant. It indicates that *Rht-8* is suitable for wheat improvement. However, when introducing the dwarf gene *Rht-8* to breeding new wheat cultivars, it should be combined with other agronomic traits (such as grain size, harvest index, coleoptile length, root characters or flag leaf area) to select ideal plant type. In addition, large population with different genetic background carrying *Rht-8* should be used in further studies to acquire a thorough understanding of the effects of *Rht-8* on plant height and yield components under different environments. The present findings will be helpful for better understanding of *Rht-8* in wheat.

参 考 文 献 References:

[1] Kertesz Z, Flintham J E, Gale M D. Effects of Rht dwarfing genes on wheat grain yield and its components under eastern European conditions [J]. Cereal Res Commun, 1991,19:297-304.

[2] Gale M D, Youssefian. Dwarfing genes in wheat[C]//GE Russed. Progress in Plant Breeding Vol 1. London: Butterworths, 1985:1-35.

[3] Rebetzke G J, Appels R, Morrison A, et al. Quantitative trait loci on chromosome 4B for coleoptile length and early vigour in wheat (*Triticum aestivum* L.)[J]. Aust Agric Res, 2001,52:1221-1234.

[4] Sip V, Skorpik M, Performance trials with spring wheat lines, isogenic for the dwarfing genes[J]. Genetika a Slechteni, 1993,29(1):1-10.

[5] Mathews K L, Chapman S C, Trethowan R, et al. Global adaptation of spring bread and durum wheat lines near isogenic for major reduced height genes[J].Crop Sci, 2006,46:603-613.

[6] Rebetzke G J, Richards R A. Giberellic acid – sensitive dwarfing genes reduce plant height to increase kernel number and grain yield of wheat[J]. Aust J Agric Res, 2000,51(2):235-245.

[7] Trethowan R M, Singh R P, Huerta-Espino J, et al. Coleoptile length of near isogenic Rht lines of modern CIMMYT bread and durum wheats [J]. Field Crops Res, 2001,70:167-176.

[8] Ellis M H, Rebetzke G J, Condon A G, et al. The effect of different height reducing genes on early growth characteristics of wheat[J]. Funct Plant Biol, 2004,31:583-589.

[9] Zhang X, Yang S, Zhou Y, et al. Distribution of the Rht-B1b, Rht-D1b and *Rht-8* reduced height genes in autumn-sown Chinese wheats detected by molecular markers[J]. Euphytica, 2006,152:109-116.

[10] Rebetzke G J, Ellis M H, Bonnett D G, et al. The Rht13 dwarfing gene reduces peduncle length and plant height to increase grain number and yield of wheat[J]. Field Crops Res, 2011,124(3),323-331.

[11] Bonnett D G. Quantitative trait loci on chromosome 4B for coleoptile length and early vigour in wheat(*Triticum aestivum* L.)[J]. Aust J Agric Res, 2001,52(12),1221-1234.

[12] Schmidt A L, Gale K R, Ellis M H, et al. Sequence variation at a microsatellite locus(XGWM261) in hexaploid wheat (Triticum aestivum) varieties[J]. Euphytica, 2004,135(2):239-246.

[13] Ellis M H, Bonnett D G, Rebetzke G J. A 192 bp allele at the Xgwm261 locus is not always associated with *Rht-8* dwarfing gene in wheat (*Triticum aestivum* L.)[J]. Euphytica, 2007,157:209-214.

[14] Falconer D S. Introduction to quantitative genetics[M]. England Harlow: Pearson Education Limited, 1989:129-185.

[15] Ansari K A, Ansari B A, Khund A. Extent of heterosis and heritability in some quantitative characters of bread wheat. Indus[J]. Pl. Sci., 2004,3:189-192.

[16] Bhatt G M, Derera N F. Genotypex environment interactions for, heritabilities of, and correlations among quality traits in wheat[J]. Euphytica, 1975,24(3):597-604.

[17] Jedynski S. Heritability and path-coefficient analysis of yield components in spring wheat[C]//Grupy Problemowej Wodowli Pszenicy. Proceeding of Symposium. Poland: Zakopane, 2001:203-209.

[18] Patel A K, Jain S. Studies of genetic variability in wheat under rainfed condition[J]. JNKVV Research Journal, 2002,3:25-28.

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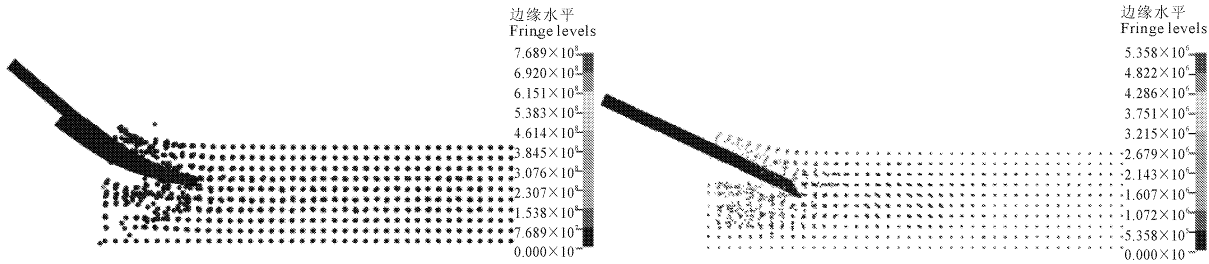

（a）仿生铲片 Bionic shovel （b）普通铲片 Nomal shovel

图 8 0.1918 s 仿生铲片切削土壤仿真过程

Fig.8 Simulation process of 0.1918 s bionic shovel cutting soil

由图 8a 和 8b 可看出，两种铲片挖削土壤时对土壤的应力不同，图 8a 中仿生铲片对土壤应力较集中，且铲尖处应力较大，更利于土壤的破碎；图 8b 中普通铲片挖削土壤时对土壤应力较分散，土壤的应力分布于挖削的土壤上，最大应力值较小，不利于土壤的破碎，这是造成阻力较大的原因。因此，在对两种铲片对比中发现，仿生铲片具有优良的挖削性能。

图 9 为仿生铲片与普通铲片挖削土壤时的阻力曲线对比图。从图中可知普通铲片挖削土壤时的阻力明显大于仿生铲片，且其阻力波动大。仿生铲片较普通铲片挖削土壤时的阻力减小近 61%。因此，说明仿生铲片较普通铲片更具挖削减阻效果。

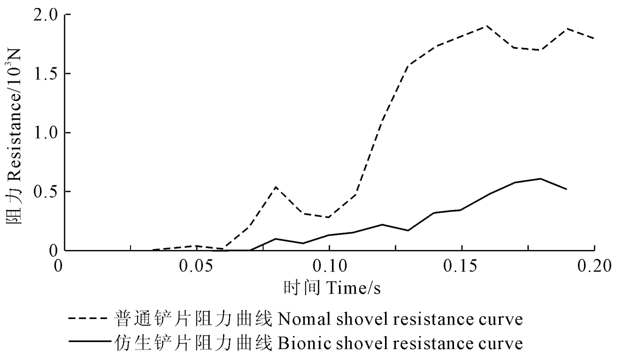

图 9 两种铲片挖削土壤时的阻力曲线对比

Fig.9 Comparison with resistance curves of 2 kinds of shovel cutting soil

5 结 论

1）基于 LS－DYNA 仿真模拟仿生铲片与普通铲片挖削土壤过程发现，普通铲片对土壤应力比较分散，最大应力值较小；而仿生铲片对土壤应力较集中，且铲尖处应力最大。因此，仿生铲片更具有优良的挖削性能。

2）仿真结果表明，仿生铲片较普通铲片土壤阻力减小近 61%。仿生挖掘铲片的设计成功为马铃薯挖掘机挖掘铲减阻技术要求提供了一种解决思路，且结构新颖。

参 考 文 献：

［1］ 鲁 振.小型马铃薯收获机械技术问题的探讨［J］.农业技术与装备，2007，(8)：26.

［2］ 任露泉，李建桥，陈秉聪.非光滑表面的仿生降阻研究［J］.科学通报，1995，40(19)：1812-1814.

［3］ 郭志军，周志立，徐 东，等.高效节能仿生深松部件的试验［J］.河南科技大学学报，2003，24(23)：1-3.

［4］ 郭志军，杜 干，周志立，等.土壤耕作部件宏观触土曲面减阻性能研究现状分析［J］.农业机械学报，2011，42(6)：47-52.

［5］ 任露泉，徐晓波，陈秉聪.典型土壤动物爪趾形态的初步分析［J］.农业机械学报，1990，21(2)：44-49.

［6］ Lewis B A. Manual for LS－DYNA soil material model 147［R］. USA：Federal Highway Administration，2004.

［7］ 郝好山. ANSYS12.0/LS－DYNA 非线性有限元分析从入门到精通［M］.天津：机械工业出版社，2012：360-364.

［8］ 蒋建东，高 洁，赵颖娣，等.基于 ALE 有限元仿真的土壤切削振动减阻［J］.农业工程学报，2012，28(增刊 1)：33-38.

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［19］ Kumar S，Dwidevi V K，Tyagi N K. Genetic variability in some metric traits and its contribution to yield in wheat(*Triticum aestivum* L.)［J］. Progressive Agriculture，2003，3：152-153.

［20］ Hoogendoorn J，Rickson J M，Gale M D. Differences in leaf and stem anatomy related to plant height of tall and dwarf wheat(*Triticum aestivum* L.)［J］. J. Plant Physiol，1990，136：72-77.

［21］ Keyes G J，Paolillo D J，Sorrells M E. The effects of dwarfing genes Rht1 and Rht2 on cellular dimensions and rate of leaf elongation in wheat［J］. Ann Bot，1989，64：683-690.

［22］ Rebetzke G J，Ellis M H，Bonnett D G，et al. Height reduction and agronomic performance for selected gibberellin-responsive dwarfing genes in bread wheat(*Triticum aestivum* L.)［J］. Field Crops Res.，2012，126：87-96.

［23］ Nirala RBP，Jha P B. Path coefficient analysis and selection indices in intervarietal crosses of wheat(*Triticum aestivum* L.)［J］. Res. Birsa Agric. Univ.，1997，9：129-132.

［24］ Khan H A，Mohammad S. Character associations and path coefficient analysis of grain yield and yield components in wheat［J］. Crop Res.(Hisar)，1999，17：229-233.

［25］ Mohsin T，Khan N，Naqvai F N. Heritability，phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat［J］. Food Agri. Environ.，2009，7：278-282.