

Genetic Analysis of Branching angle in Rapeseed (*Brassica napus L.*) with Mixed Model of Major Gene Plus Polygene

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Abstract

Branching angle is one of the important agronomic characters in rapeseed to reflect plant type and it also has a great effect on population density. To make clear of the inheritance mechanism of branching angle will contribute a lot to rapeseed ideotype breeding. In this study, two lines with significant difference in branching angle were selected to hybrid to produce F₁, from which B₁, B₂ as well as F₂ were derived. Using the phenotype data of six generations to conduct a joint segregation analysis, the optimal genetic model was selected and genetic parameters were estimated. The result revealed that the branching angle in this cross was controlled by one major gene along with polygenes. Major gene shows no dominant effect but polygenes have negative effect, which lead to no heterosis but mid-parent value inclining to compact type in F₁. Additive effect of major gene and polygenes have an increasing effect on branching angle. The heritability of major gene and polygene in F₂ population are 23.97% and 16.59%, respectively. The results have implication for rapeseed breeding of branching angle that middle or later generation selection and large population will be more effective.

Key words: rapeseed, branching angle, major gene, polygene, genetic analysis

Introduction

In order to further expand the planting area and accelerate the mechanized process in China, the breeding for ideotype has aroused great attention in recent years. Branching angle, which is an important trait associated with the morphology of ideal plant type, it is not only related to population density and yield, but also has an effect on the occurrence of disease and insects. The previous studies on rapeseed revealed that branching angle showed no cytoplasmic effect and was mainly controlled by karyogene similar to yield trait, so reciprocal cross is of no concern when making cross combination (Zhang et al. 2000; Wang et al. 2005). F₁ performed mid-parent value inclining to compact type or negative over-parent heterosis. (Zhang et al. 2000; Wang et al. 2006;) Wang et al. (2005) found that branching angle was controlled by both additive and dominant effect. In addition, dominant gene has reducing effect on branching angle from his result. But all of them using the traditional quantitative genetics methods and statistic methods to analyse the genetic effect, while the major gene and polygene effect can't be separated. The objective of this study is to discuss the optimal genetic model and estimate the genetic parameters for the cross of 9548×520 by the major gene plus polygene mixed inheritance theory (Wang and Gai, 1998) in order to propose a breeding strategy for the selection of branching angle in rapeseed.

Material and methods

Materials: Two parent lines, 9548 and 520, showing significant difference on branching angle were selected by rapeseed breeding lab in Oil Crop Research Institute, Chinese Academy of Agriculture Science.

Experimental method: The cross was made in spring 2008 at Yangluo experimental field, Wuhan, China (Latitude 114°22'N, long 30°53'E). The F₁ seed was harvested in May 2009 and advanced to

produce F2, B1 and B2 population in summer 2009 at Xining, Qinghai, China (Latitude 101°44'N, long 36°35'E). In addition, the parents were bagged and self crossed in every growing season. All the P1, P2, F1, F2, B1 and B2 were planted at Yangluo in autumn 2009 with the population density of 120,000 plants per hectare and were evaluated in green-silique stage by measuring the third or fourth branching angle. The plant investigated should no less than 20 and 100 individuals for the non-segregation generations and segregation generations, respectively (Gai et al. 2003).

Statistical analyses: Analysis software was provided by Professor Wang in Crop Research Institute, Chinese Academy of Agricultural Sciences, China.

Results and discussion

The frequency distribution of branching angle in six generations: T-test for mean of two parents was conducted by SAS 7.0 and the result suggested that they had significant difference at 0.01 level ($t=5.895$, $t_{0.01,65}=2.654$). The phenotype value of F1 generation is 39.7° on average, showing no heterosis but tending to negative mid-parent value, which is consistent with previous studies (Wang et al. 2005; Zhang et al. 2000). Meanwhile, B1 and B2 population were unimodal distribution but deviated from normal distribution and F2 population showed bimodal distribution (Figure 1), which indicated major genes may be involved (Zhang et al. 2000).

able 1 Frequency distribution and basic statistics of branching angle in 6 generations derived from the cross of 9548×520

Generatio n	Gouping of branching angle(°)										Mea n	Standa rd error	
	16-20 65	21-25 66-70	26-30	31-35	36-40	41-45	46-50	51-55	56-60	61- 65			
P1				1	7	11	10	1	1			44.1	1.1
F1		6	14	41	35	11	1					39.7	0.5
P2		2	6	9	13	5	1					36.1	0.9
B1	1	1	7	31	65	60	36	11	2	0	1	41.2	0.5
B2	2	15	37	50	37	3	1	1				37.9	0.4
F2		6	16	56	73	40	26	1	3	1		38.6	0.5

AIC value Calculation and tests for goodness-of-fit. According to joint segregation of multi-generations analysis, we obtained maximum likelihood value and AIC value of twenty-four genetic models which were divided into five categories, that is one pair of major gene, two pair of major genes, polygene, one pair of major gene plus polygene and two pair of major genes plus polygene. Five models with relatively low AIC value were selected as the candidate models (Table 2). Then, tests for goodness-of-fit of five candidate models was conducted, including uniformity test ($U1^2$, $U2^2$, $U3^2$), Smirnov (nW^2) and Kolmogorov (D_n) test and the total number of significant statistic were counted (Table 2). From the results above, we can make a preliminary conclusion that branching angle in this cross was controlled by one major gene and polygene.

Table 2 Maximum likelihood estimated value, AIC value and test for goodness-of-fit of candidate models calculated by joint segregation of multi-generations

Model code	Implication of model	Maximum likelihood estimated value	AIC value	The total number of significant statistic
B-1-2	1MG-AD	-2435.515	4883.030	2
C-1	PG-AD	-2434.891	4883.783	2
D-2	MX1-A-AD	-2432.640	4881.280	1
D-3	MX1-AED-AD	-2433.351	4882.702	1
D-4	MX1-AEND-AD	-2432.639	4881.278	1

MG: Major gene model; PG: Polygene model; MX1: Mixed one pair of major gene and polygene model; A: Additive effect; D: Dominant effect; E: Equal; N: Negative. e.g. model D-4, MX1-AEND-AD represents one pair of major gene with completely negative dominant effect and polygene with additive and dominant effect.

The selection of the optimal genetic model: The first order distribution parameters were estimated according to IECM algorithm and then the first order genetic parameters were calculated by the least square method based on its relation with the first order distribution parameters. The tests of significance for the first order genetic parameters (m, d, [d], [h]) were conducted referring to the method of Gai et al. (2003) (Table 3). The number of significant parameters under D-2 models were more than D-3 and D-4 model, so it was selected as the optimal genetic model, that is one pair of major gene with additive effect plus polygene with additive and dominant effect. The second order genetic parameters of model D-2 were estimated by the second order distribution parameters (Table 4). Under model D-2, the additive effect of major gene and polygene was 2.895 and 0.772, respectively. Therefore, The additive effect towards consistent direction to increase the branching angle. The heritability of B1, B2 and F2 were 40.0%, 7.3% and 40.6%, indicating that branching angle was partly influenced by environment, which is inconsistent with the research of Wang et al. (2005). The possible reason is the different evaluation methods and generations being used. In their study, they employed the method of diallel cross to estimate the heritability of F1 generation

Table 3 The test of significance for the first order genetic parameters of model D-2, D-3 and D-4

1st order parameter	D-2 model				D-3 model				D-4 model			
	Estimate	T value	$t_{0.05,5}$	$t_{0.05,5}$	Estimate	T value	$t_{0.05,3}$	$t_{0.05,3}$	Estimate	T value	$t_{0.05,3}$	$t_{0.05,3}$
m	39.723*	42.021	2.571	4.03	39.606*	65.543	3.182	5.84	39.696*	41.469	3.182	5.841
d	2.895*	3.267		2	0.437	0.620		1	2.272	3.113		
[d]	0.772	0.616			3.188	2.631			1.427	1.222		
[h]	-0.254	-0.141			-0.81	-0.655			1.992	1.038		

*** denotes significance difference at 1% level;

Table 4 Estimates of genetic parameters of branching angle in the cross of 9548×520 under D-2 model

Mode	1st order parameter	Estimate	2nd order parameter	Estimate(%)		
				B ₁	B ₂	F ₂
D-2	<i>m</i>	39.722	σ_p^2	43.996	28.478	44.415
	<i>d</i>	2.895	σ_{mg}^2	0.581	0.417	10.648
	<i>h</i>	0	σ_{pg}^2	17.017	1.663	7.370
	[<i>d</i>]	0.772	$h_{mg}^2(\%)$	1.322	1.465	23.974
	[<i>h</i>]	-0.254	$h_{pg}^2(\%)$	38.678	5.840	16.594

m: the mean of population; *d*: additive effect of the major gene; *h*: dominant effect of the major gene; [*d*]: additive effect of polygene; [*h*] dominant effect of polygene; σ_p^2 : phenotypic variance; σ_{pg}^2 : polygene variance; σ_{mg}^2 : major gene variance; $h_{mg}^2(\%)$: heritability of major gene; $h_{pg}^2(\%)$: heritability of polygene.

Conclusion

Branching angle is controlled by one pair of major gene with additive effect and polygenes with additive and dominant effect in the cross of 9548×520. F1 generation performed mid-parent value inclining to compact type, so two parents should have low branch angle in order to obtain compact hybrid. In addition, middle or later generation selection as well as large populations could be particularly necessary for branching angle breeding.

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