RECURRENT SELECTION BY USING DOMINANT MALE STERILITY IN *BRASSICA NAPUS* L.

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ABSTRACT

A base (C_0) population originated from 72 crosses produced from 75 genotypes with desired quality and agronomic traits has been synthesized after two times of random mating mediated by a dominant male sterile allele, Ms, in *Brassica napus*. The population contained 12 different types of cytoplasm. There were about 40% sterile plants segregating in each random mating generation. The differences of seed weight and quality traits were observed between sterile and fertile sub-populations in C_0 population. Obvious progress of selection for quality was obtained after one cycle of selection. Test of S_1 family lines selected from fertile plants in C_0 population showed that the synthesized population had wide variation and relative high potential in seed yield.

INTRODUCTION

It is well documented that recurrent selection is an efficient breeding method in cross-pollinated crops for improving quantitative characteristics, such as yield and its components (Hallauer, 1992). Because of the difficulty of cross pollinating the recurrent selection in self-pollinated crops were often conducted by use of recessive or dominant genic male sterility (Kaul, 1988). The objectives of this study were to construct a base population by use of the dominant male sterile allele for recurrent selection in *Brassica napus*, to characterize the population and to conduct a preliminary evaluation of selection to the synthesized base population.

MATERIALS AND METHODS

Accessions of *B. napus* used to constitute a base population included conventional varieties with good agronomic traits and adoptability to local growing conditions, and breeding lines with one or more expected quality traits. The plants with genotype of Msmsrfrf (male sterile) and various cytoplasms were used as pollen receptors (Zhou, 1993), and the selected accessions of *B. napus* were used as pollinators to make crosses with sterile plants. Equal numbers of seeds from each cross which performed segregation in fertility were taken and mixed, and then sown in the isolated plot. During flowering next spring the male sterile plants were tagged. The population was under a open-pollination condition. Equal numbers of Seeds from sterile plants of second cycle of random mating were pooled to form a base (C_0) population.

Plant growth and development stage in C_0 population were recorded. The individuals without disease infection and with most numbers of primary branches in the population during the late siliqua filling period were selected from both sterile and fertile plants, respectively. About 10% plants were selected from both sterile and fertile sub-populations for determination of seed weight and quality analysis. The seeds from selected male sterile plants were pooled to produce the next base population (C_1).

Fertile plants in base population of each cycle were selected based on their seed weight and quality performance and grown as S_1 families for yield evaluation.

RESULTS AND DISCUSSION

1 Characteristics of synthesized base population

Total of 72 crosses were produced from pollinators, different varieties and breeding lines, and Ms plants derived from lines with 12 different cytoplasms. Those crosses contained 75 genotypes, including Ms gene donors, various cytoplasmic donors and male parents for the crosses. The ratio of sterile plants versus fertile ones deviated from the expected ratio of 1:1 (Table 1). The reason for the deviation could be the presence of suppressor gene in a heterozygous status, either Ms_Rfrf or msmsRfrf, which might be introduced to the population when crosses were made (Zhou and Bai, 1994). The Rf gene will inhibit the expression of Ms gene and as a result their was a lower frequency of sterile individuals than expected in random-mating populations. The frequency of low erucic genotype did not change significantly in the consecutive generations (Table 1). This was an expected characteristic in a random mating population when the loci considered were heterozygous at the initial stage.

Table 1. Structure of random mating population and the frequency of low erucic genotypes in three successive generations

random mating time	population size (plants)	% of sterile plants	% of low erucic genotypes*
1 (R_1)	5978	36.5	8.534
2 (R_2)	8261	42.4	9.460
3 (C_0)	10134	38.4	9.676

* The percentage was calculated based on more than 1000 seeds sampled from mixed seeds from all sterile plants in each random mating generation.

The data from base (C_0) population (table 2) showed that quite large differences existed between fertile and sterile sub-populations in quality traits as well as seed weight per plant. For example, the fertile sub-population had lower erucic and glucosinolates and much higher frequencies of low erucic and low glucosinolate genotype than in sterile sub-population.

2 Evaluation of selection to the base population

Glucosinolate content in C_1 decreased to almost half of content in C_0 in sterile sub-population and the frequency of low glucosinolate individuals increased 10 times (Table 2 and 3). The same tendency was also found in the fertile sub-population. The oil content in sterile sub-population increased from 40.62% in C_0 to 43.48% and from 43.02% to 44.33% in fertile sub-population in C_1 (Table 2 and 3).

Variance analysis for seed yield in first cycle of S_1 family evaluation showed a significant difference ($\alpha = 0.05$) between 38 lines tested. Among the lines there were five having significant higher seed

yield than double low control, Huashuang2 (LSD test, α=0.05) and eight having higher seed yield than double high control, Zhongyou 821. Linear regression analysis revealed that the seed yield per plant in the progeny lines has a close relation to their parent plants (regression coefficient was significant at p=0.02).

Table 2. Comparison of seed weight per plant and some quality traits between fertile plants and sterile ones in base (C_0) population

traits	fertile (F) mean/frequency	sterile (S) mean/frequency	F-S
seed weight/plant (g)	12.27±0.25	7.20±0.23	5.07**
oil percentage	43.02±0.22	40.62±0.23	2.40**
glucosinolate (μmol/g)	72.77±1.72	106.58±2.01	-33.81**
% of plants low in glucosinolate (<40)	0.084	0.03	
erucic acid (%)	22.24±0.48	25.19±0.54	-2.95**
% of plants low in erucic acid	0.028	0.0072	

**: The difference is significant at 0.01 level under the un-paired t-test.

Table 3. Average performance of quality traits of selected plants from base population (C_0) and their derived population (C_1)

traits	selected plants from C_0	C1 population		F-S
		sterile (S)	fertile (F)	
oil percentage	43.98±0.34	43.48±0.28	44.33±0.23	0.85*
erucic acid (%)	22.57±0.02	25.25±0.60	20.21±0.78	5.04**
% of plants low null erucic acid	0.041	0.0024	0.058	
glucosinolate (μmol/g seed)	58.43±1.68	62.90±3.12	65.39±3.04	2.49
% of plants low in glucosinolate (<40)	0.21	0.32	0.24	

* or ** means a significant difference at 0.05 or 0.01 level under the un-paired t-test, respectively.

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REFERENCES

Hallauer A R. (1992) Recurrent selection in maize. In: Janick J (ed.), Plant Breeding Reviews. New York: John Wiley & Sons, Inc., Vol 9:115-180

Kaul M L H. (1988) Male Sterility in Higher Plants. Springer Verlag, Berlin Heidelberg.

Zhou Y. (1993) Recurrent selection in *Brassica napus* I.Transfer of dominant male sterile gene into genotypes with various types of cytoplasm. Acta Agronomica Sinica. 19:70-76

Zhou Y, and Bai H.(1994) Identification and genetic studies of the inhibition of dominant male sterility in *Brassica napus*. Plant Breed. (in press).