Heterotic patterns in rapeseed (*Brassica napus* L.) using exotic germplasm

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Abstract

Chinese semi-winter rapeseed is highly different from spring and winter rapeseed. This study was conducted, 1) to evaluate the potential of semi-winter rapeseed for hybrid breeding in spring and winter rapeseed, and vice versa; 2) to asses the genetic effects involved and 3) to estimate the correlation of parental genetic distance (GD) with hybrid performance. Four spring male sterile lines of NPZ-Lembke[®] (MSL) from Germany and Canada, and four winter MSL lines from Germany were crossed with 13 Chinese rapeseed lines to develop F_1 -hybrids, which were evaluated together with their parents and commercial hybrids in two years. 8 spring growing environments in Europe and Canada for spring × semi-winter combinations, 4 winter growing environments in Germany for winter × semi-winter combinations and 3 semi-winter growing environments, with poor seed yield per se, the combinations exhibited high heterosis and seed yield potential. In the spring growing environments, about 92% and 68% combinations overcame the mean performance of their parents for seed yield and oil content, respectively; half of the combinations were superior to the local commercial hybrids for seed yield in the 2 winter growing environments in the first year; and the winter × semi-winter flowered later and had a shorter period to develop seed than the latter. Additive genetic effects mainly contributed to hybrid performance as judged from high GCA/SCA ratios. A weak association between parental GD and heterosis was found, but the correlation between GCA_(f+m) and hybrid performance was high.

Introduction

Chinese semi-winter rapeseed differs from spring and winter rapeseed from other parts in the world mainly due to the introgression from Chinese *B. rapa*. Recent researches have shown that some alleles from Chinese semi-winter rapeseed and Chinese *B. rapa* can favourably contribute to rapeseed seed yield (Qian et al. 2003, Qian et al. 2005; Udall et al. 2006). The main objectives of this study are, 1) to investigate the genetic changes by comparing normal rapeseed with new type rapeseed introgressed the genomic components of Chinese *B. rapa*, 2) to evaluate the potential of semi-winter rapeseed for hybrid breeding in spring and winter rapeseed, and vice versa, 3) to estimate the genetic effects involved, and 4) to estimate the correlation of parental genetic distance (GD) with hybrid performance.

Materials and methods

45 cultivars were chosen from the main rapeseed growing regions in the world to estimate genetic diversity using AFLP with 29 primer combinations. The material can be grouped as follows: 1) 10 new type rapeseed carrying genomic components of Chinese *B. rapa* (N group), including three F_6 lines derived from crosses between Chinese *B. napus* and Chinese *B. rapa*, three BC₁ F_6 lines derived from crosses (Chinese *B. napus* × Chinese *B. rapa*) × Chinese *B. rapa* (Qian *et al.* 2005), four new type F_4 lines derived from crosses Chinese *B. napus* × (*B. carinata* × Chinese *B. rapa*) (Li *et al.* 2005), 2) 9 semi-winter rapeseed from China (C group), including 4 parental *B. napus* of new type rapeseed and 5 elite inbred lines, 3) 9 winter rapeseed from Europe (W group), and 4) 17 spring rapeseed varieties from Europe, Canada and Australia (S group). Among them, 6 spring lines, 2 lines each spring rapeseed growing regions, and 4 winter lines, were crossed with 14 semi-winter rapeseed from China (10 new lines and 4 lines of their parental *B. napus*) to develop F_1 hybrids. The hybrids were evaluated together with their parents and commercial hybrids at different locations during two years. 8 spring rapeseed environments in Europe and Canada for 52combinations between 4 spring and 13 semi-winter lines, 4 winter rapeseed environments in China for all 140 hybrids.

Results

1) Genetic diversity and evolution

Analyses of the 799 polymorphic AFLP fragments revealed that within groups, the new type rapeseed had the highest genetic diversity, followed by the semi-winter normal rapeseed from China. Spring and winter rapeseed had the lowest genetic diversity. Among groups, the new type rapeseed group had the largest average genetic distance to the other three groups

(Table 1). This suggests that the introgression of Chinese B. rapa had increased the genetic variation of rapeseed.

Table 1: Average genetic distances within and among new type rapeseed (N group), Chinese normal rapeseed (C group), spring							
rapeseed (S group) and winter rapeseed (W group) calculated using Nei's method							

Group	Lines analysed –	Average genetic distance (standard deviation)						
		N group	C group	W group	S group			
N group	10	0.427 (0.079)						
C group	9	0.394 (0.081)	0.364 (0.074)					
W group	9	0.424 (0.056)	0.388 (0.040)	0.193 (0.042)				
S group	17	0.430 (0.064)	0.402 (0.042)	0.323 (0.036)	0.226 (0.051)			

2) Rapeseed heterotic patterns

Although the exotic lines were not well adapted to the local environments, with poor seed yield per se, the hybrid combinations exhibited high heterosis for seed yield. In the spring rapeseed growing environments 92% and 68% combinations were above the mean performance of their parents for seed yield and oil content, respectively. Half of the combinations were superior to the local commercial hybrids for seed yield in the 2 winter rapeseed environments in the first year. Regarding the semi-winter growing regions in China, winter by semi-winter combinations exhibited higher heterosis than spring by semi-winter combinations (Figure 1) although the former flowered later and had a shorter time to develop seed. Weak association of parental GD was found with hybrid performance and heteosis, but the correlation between $GCA_{(f+m)}$ and hybrid performance was high and significant, e.g. for spring by semi-winter combinations (Table 2). Additive effects of the genes mainly contributed to hybrid performance as revealed by the predominance of variance of GCA over those of SCA in all of environments. In conclusion, rapeseed heterotic patterns using exotic germplasm can be used in hybrid breeding programs.

Table 2: Correlations between parental genetic distance (GD) and 5 different parameters calculated for seed yield and oil content from a field trial with 52 hybrid combinations in 8 environments (E1 - E8): HP, hybrid performance; MPH, mid-parent heterosis; HPH, high-parent heterosis; GCA (f+m), total general combining ability of both parents; SCA, specific combining ability (*,**

Significant at *p* = 0.05 and 0.01, respectively)

Environments	GD					HP			
	HP	MPH	HPH	GCA (f + m)	SCA	MPH	HPH	GCA _(f+m)	SCA
Seed yield									
E1	-0.02	0.27	0.03	0	-0.03	0.65**	0.91**	0.78**	0.63**
E2	0.2	0.21	0.36	0.17	0.12	0.64**	0.90**	0.93**	0.37
E3	0.14	0.35	0.15	0.27	-0.13	0.58**	0.87**	0.82**	0.57*
E4	0.11	0.38**	0.32	0.13	0.01	0.61**	0.38**	0.78**	0.63**
E5	-0.07	0.44*	0.18	-0.02	-0.09	0.33	0.16	0.86**	0.50**
E6	0.42*	0.36	0.29	0.42*	0.14	0.02	0.06	0.73**	0.43**
E7	0.1	0.33*	0.15	0.13	0.02	0.69**	0.77**	0.72**	0.69**
E8	-0.13	0.47**	-0.11	-0.13	-0.03	0.46**	0.84**	0.88**	0.47**
Mean	0.09	0.35	0.17	0.12	0.01	0.50	0.61	0.81	0.54
Oil content									
E1	0.22	0.56**	0.34	0.23	0.05	0.63**	0.60**	0.86**	0.51**
E2	-0.18	0.19	0.11	-0.29	0.07	0.53**	0.60**	0.78**	0.62**
E3	-0.23	0.43*	-0.18	-0.31	0.10	0.36	0.88**	0.87**	0.49*
E4	-0.41**	0.16	-0.23	-0.47**	-0.02	0.59**	0.84**	0.86**	0.52**
E5	-0.07	0.37	0.06	-0.09	0	0.36	0.49**	0.79**	0.61**
E6	-0.28	0.38	-0.08	-0.26	-0.10	0.43*	0.67**	0.90**	0.43*
E7	-0.12	0.35**	-0.20	-0.25	0.10	0.66**	0.80**	0.76**	0.65**
E8	-0.37	0.49**	-0.16	-0.44**	0.01	0.11	0.71**	0.86**	0.52**
Mean	-0.18	0.4	-0.04	-0.24	0.03	0.46	0.70	0.84	0.54

Discussion

The germplasm of rapeseed is narrower in comparison with its two parental species partly due to its short history of domestication. Our results suggest that introgressions into *B. napus* from Chinese *B. rapa* significantly increased the genetic diversity, and that this introgression played an important role in Chinese rapeseed evolution in respect of the procedure of rapeseed domestication in China (Qian et al. 2006). The possible explanations are easy crosses between *B. rapa* and *B. napus*, and clear difference between Asian and European *B. rapa* since current rapeseed originated from a spontaneous hybridization between *B. rapa* and *B. oleracea* in Europe. The study of heterotic patterns also shows that Chinese semi-winter rapeseed exhibited favourable alleles for seed yield and other agronomic traits different from winter and spring rapeseed.

Interestingly, we found that some lines with high GCA in one environment or growing region generally exhibited the same tendency in other environments or regions. This is in accordance with the role of additive effects mainly contributing to hybrid performance detected in this study. It is useful to shuttle breeding by exchanging elite germplasm among different rapeseed growing regions.

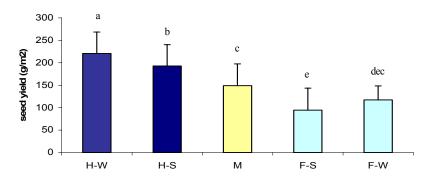


Figure 1: Comparison among parents and hybrids (M, semi-winter rapeseed lines; F-W and F-S, winter and spring rapeseed lines; H-W, hybrids derived from winter × semi-winter lines; and H-S, hybrids derived from spring rapeseed and semi-winter rapeseed) for seed yield (g/m²) (column) and half standard deviation (bar) over 3 environments in China in 2005 and 2006 (Columns with the same letter do not differ significantly)

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References

Li M, Li Z, Zhang C, Qian W, Meng J (2005) TAG 110: 1284-1289 Qian W, Chen X, Fu D, Zou J, Meng J (2005) TAG 110: 1187-1194 Qian W, Meng J, Li M, Frauen M, Sass O, Noack J, Jung C (2006) TAG 113: 49-54 Qian W, Liu R, Meng J (2003) Euphytic 134: 9-15 Udall J, Quijada P, Lambert B, Osborn T (2006) TAG 113: 597-609