

Mapping of QTLs for oil content in an European x Chinese population of winter rapeseed

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ABSTRACT

To investigate whether the European and the Chinese gene pool could contribute different alleles for a further improvement of oil content, a QTL analysis was performed with 282 doubled haploid lines from a cross between the old German cultivar Sollux and the Chinese landrace Gaoyou. In total 18 QTLs with additive effects explaining 40% of the phenotypic variation were detected. Additive x additive epistasis was nearly as important as additive effects. Both the European and the Chinese parent contain favourable alleles, which can be combined.

Key words: Seed quality – QTL – genotype x environment interaction - epistasis

INTRODUCTION

Rapeseed is one of the most important oil crops both in China and in Europe. High seed oil content is one of the most important breeding objectives. The objective of this study was to investigate whether the European and the Chinese gene pools of winter oilseed rape contain different alleles for seed oil which could be combined for further improvement of oil content.

MATERIALS AND METHODS

A QTL analysis was performed with 282 doubled haploid (DH) lines from a cross between the old German cultivar Sollux and the Chinese landrace Gaoyou. Both have high erucic acid and glucosinolate content, and exhibited high seed oil content. The analysis is based on a linkage map including 125 SSR marker loci and phenotypic data from four environments, two in Germany (Reinshof and Weende) and two in China (Xian and Hangzhou). Oil content was determined by near-infrared reflectance spectrophotometry (NIRS) based on 9% moisture of seeds. QTL mapping was done with the software QTLMapper using a mixed model approach (Wang et al. 1999). For experimental details see Zhao (2002).

RESULTS

Phenotypic variation among DH lines: The frequency distributions of the 282 DH lines for oil content at the four test locations (Fig.1) were continuous but with considerable differences between Chinese and German locations. The parents had similar oil content, but a large transgressive segregation was observed in the DH lines. The differences between the lines with the highest and lowest oil content could be up to 19% in Germany and 11% in China. The means of lines between the two regions differed by about 7%.

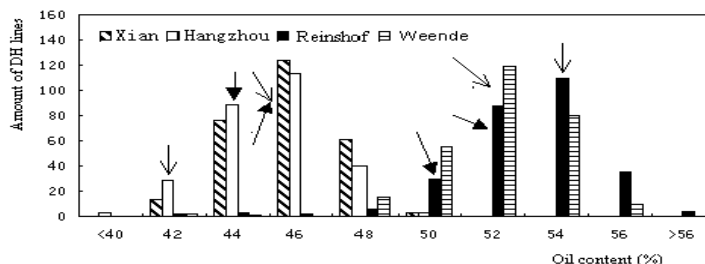


Fig 1. Frequency distribution of oil content of Sollux/Gaoyou (F_1) DH lines at four locations. The two parents are indicated by arrows with \rightarrow for Sollux and \blackrightarrow for Gaoyou.

QTLs and QTL by environment interactions: In total, 18 QTLs were detected showing additive main effects (*a*) and/or additive by environmental interaction effects (*ae*) (Table 1). Results indicated that favourable alleles for oil content were dispersed between the two parents. Of 8 QTLs with additive main effects, Gaoyou alleles increased oil content at three loci while Sollux alleles increased oil content at another five loci. Together, the additive main effects of these 8 QTLs sum up to 5.4% of oil content for homozygous genotypes and explain about 40% of the mean phenotypic variation observed in the DH population. Additive by environment interactions of QTLs were detected in 15 genomic regions, with a prevalence of significant interaction effects in Hangzhou, China and Reinshof, Germany. Furthermore, it was shown that Chinese and European alleles were often more favourable for locations in China and Germany, respectively, but also opposite allelic distributions were identified at some loci.

Table 1. Estimated additive (*a*) and additive by environment interaction (*ae*) effects of QTLs for oil content [%]

Linkage group	Marker interval	Position ^a [cM]	<i>a</i> effect ^b	<i>ae</i> in Xian	<i>ae</i> in Hangzhou	<i>ae</i> in Reinshof	<i>ae</i> in Weende
1	HMR292/HMR327	0.0	0.37**	- 0.29 ^c		0.24*	
2	HMR300a/ HMR066	0.0			- 0.29*	0.32*	
3	HMR449a/MR12	8.0			- 0.34*	0.37*	
7	HMR300c/MR133.2	2.0	- 0.55**		- 0.27*		
9	HMR612a/ HMR612b	0.0		- 0.41 ^c	- 0.56*	0.59*	0.31*
9	HMR438a/HMR310	14.0	0.34**		- 0.48*		
10	HMR643b/HMR615b	2.0		0.31 ^c		- 0.35*	
11-1	MR148/HMR407a	4.0	- 0.26*		- 0.65*	0.40*	
12	HMR299c/HMR403a	2.0	0.27*				
12	HMR353b/HMR364b	2.0		- 0.75 ^c	- 0.34*	0.66*	0.41*
13	HMR067/ MR64	0.0		0.23 ^c	- 0.29*		
14-1	HMR403b/MR229	0.0	0.22**				
14-2	HMR399a/MR155	6.0		0.24 ^c	0.41*	- 0.49*	- 0.19*
15	MR97/ MR54	0.0			0.27*	- 0.31*	
16	HMR348/ MR133	0.0			- 0.33*	0.34*	
17	HMR438b/ HMR344b	0.0			0.30*	- 0.27*	
18	HMR335a/ HMR588	0.0	- 0.52**		0.42*	- 0.23*	- 0.21*
19	HMR615a/ HMR288	0.0	0.22**				

*, ** indicates the significance level at 0.005 and 0.001, respectively, to declare the putative QTL positions and genetic effects. ^aDistance to the first marker of the indicated interval. ^bThe QTL effect is the phenotypic effect due to substitution of a 'Gaoyou' allele by an allele of 'Sollux'.

Epistasis and epistasis by environment interactions: Eleven pairs of loci with additive x additive epistatic effects (*aa*) and/or epistasis by environmental effects (*aae*) were mapped (Table 2). In total, the effects of nine pairs of epistatic QTLs sum up to 5.0% of oil content for homozygous genotypes, which is almost the same value as the total additive effects of homozygous genotypes. Of nine pairs of epistatic main QTLs, epistatic effects were negative at four pairs of loci, showing that the recombination of parental alleles at the interacting loci resulted in increased oil content, while at another five pairs of loci, the parental combinations were more favourable for oil content. Most identified QTLs simultaneously exhibited additive and epistatic effects (Table 1 and 2).

QTL genotypes of lines with extreme phenotypes: To confirm the potential utilization of mapped QTLs, the 20 lines with the highest oil content over four locations were compared for 16 marker loci (data not shown). Two favourable QTL alleles from Gaoyou with the largest effects were observed in 18 and 19 of the 20 lines, respectively. Of all 16 SSR loci considered, an average fit of 71% for high oil lines was observed. The high oil content of these lines was confirmed in an independent field trial in the following year (data not shown).

Table 2. Estimated epistatic (aa) and epistasis by environment interaction (aae) effects of QTLs for oil content [%]

N [§]	Marker Interval	N	Marker Interval	aa [†] effect	aae in Xian	aae in Hangzhou	aae in Reinshof	aae in Weende
1	HMR407b/HMR292	2	HMR300a/HMR066	- 0.29 [‡]				
1	HMR407b/HMR292	17	HMR318/HMR439		- 0.28		0.20	
1	HMR295c/HMR293	12	HMR353b/HMR364b	0.38 [‡]				
2	HMR300a/HMR066	10	HMR625/HMR643b	0.32 [‡]				
3	HMR449a/MR12	7	HMR300c/MR133.2	- 0.20 [‡]	- 0.26		0.22	
3	HMR449a/MR12	18	HMR335a/HMR588	- 0.20 [‡]				
4	HMR637/MD2.2	12	HMR353b/HMR364b	- 0.29 [‡]				
11-1	MR148/HMR407a	12	HMR299c/HMR403a	0.32 [‡]				- 0.2
11-1	MR148/HMR407a	16	HMR348/MR133	0.21 [‡]				
13	HMR314b/HMR090b	15	MR97/MR54	0.26 [‡]				
14-2	HMR399a/MR155	19	HMR615a/HMR288			- 0.34	0.18	

[§]Linkage group. [†]Sign of epistatic effects: A positive sign of the epistatic effect indicates that parental allele combinations and a negative sign that recombinant allele combinations increase phenotypic values.

DISCUSSION

Three of the eight main QTLs were identified in the same or nearby genomic regions as observed previously (Ecke et al., 1995; Gül, 2002). A close association between the two erucic acid genes and two major QTLs for seed oil content was previously reported, probably due to the increase of molecular mass during the elongation of oleic acid to erucic acid (Ecke et al. 1995). As expected, these two QTLs were not detected in the present material, which did not segregate for erucic acid. The contribution of epistatic effects observed is larger than reported before. This can be explained by the mapping procedure used, which tests all possible digenic combinations for epistasis, whereas conventionally only epistatic effects among QTLs with additive effects are considered. Results from this study revealed several lines with 5% higher oil content than both parents and around 15% and 10% higher oil content than local check varieties in China and in Germany, respectively. These results illustrate that the oil content in elite varieties is still far from the limitation and further increasing the oil content by marker assisted selection is possible.

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