

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



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Introduction

The objective was to investigate whether the European and the Chinese gene pools of winter oilseed rape contain different alleles for high oil content which could be combined.

Materials and Methods

- 282 doubled haploid lines from a cross between the old German cultivar Sollux and the Chinese landrace Gaoyou
- Yield tests in two environments in Germany (Göttingen, Weende) and two environments in China (Xian, Hangzhou)
- QTL mapping with QTLMapper
- for details see Zhao (2002)

Results and Discussion

- A large transgressive segregation was observed (Fig. 1)
- 18 QTL with additive (a) and/or additive x environment interaction (ae) effects were detected (Table 1). Favourable alleles for oil content were dispersed between the two parents. The additive effects of 8 QTL sum up to 5.4 % oil content and explain about 40 % of the phenotypic variation. Chinese and European alleles were often (but not always) more favorable for locations in China and Germany, respectively.
- 11 pairs of loci with additive x additive epistatic effects (aa) and/or epistasis x environment interactions (aae) were mapped (Table 2). The effects of 9 pairs with aa effects sum up to 5.0 % oil content, which is almost the same value as the additive effects. Most QTL simultaneously show additive and epistatic effects.

Conclusions

Favorable alleles from Chinese and European oilseed rape can be combined by marker assisted selection. Lines with about 5 % higher oil content than both parents could be identified.

References

Zhao, J., 2002: QTLs for oil content and their relationships to other agronomic traits in an European x Chinese oilseed rape population. Doctoral dissertation, Georg-August-University Göttingen. http://webdoc.sub.gwdg.de/diss/2002/zhao_jianyi/index.html

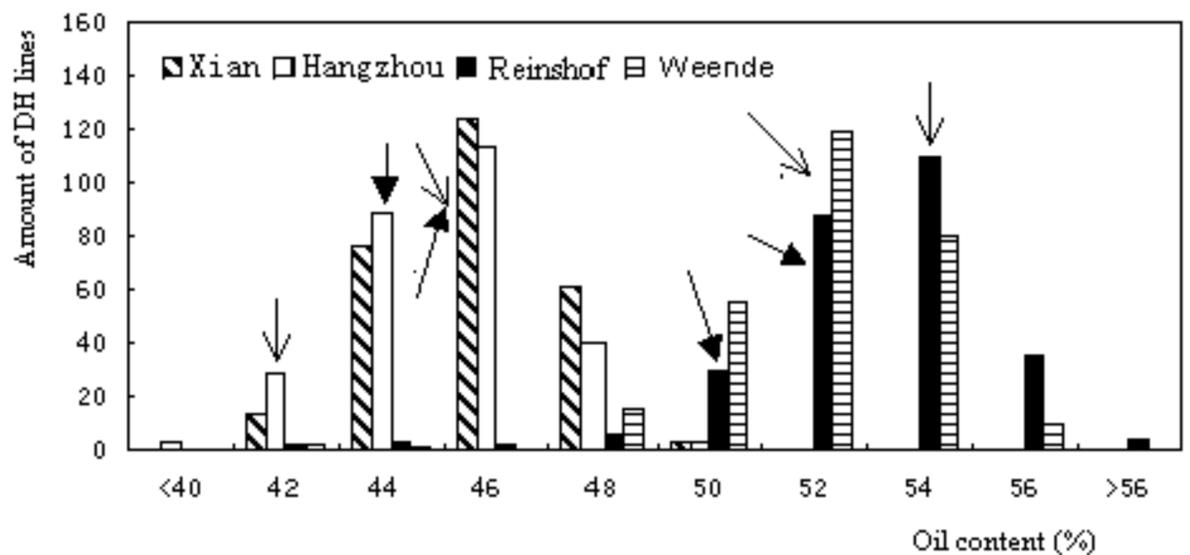


Fig 1. Frequency distribution of oil content of Sollux/Gaoyou (F₁) DH lines at four locations. Two parents are indicated by arrows with → for Sollux → for Gaoyou .

Table 1. Estimated additive (a) and additive x environment interaction (ae) effects of QTL for oil content (%)

Linkage group	Marker interval	QTL Position ^a (cM)	a effect ^b	ae in Xian	ae in Hangzhou	ae in Reinshof	ae in Weende
1	HMR292/HMR327	0.0	0.37**	-0.29**		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**	-0.56**	0.59**	0.31**
9	HMR438a/HMR310	14.0	0.34**		-0.48**		
10	HMR643b/HMR615b	2.0		0.31**		-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**	-0.34**	0.66**	0.41**
13	HMR067/MR64	0.0		0.23**	-0.29**		
14-1	HMR403b/MR229	0.0	0.22**				
14-2	HMR399a/MR155	6.0		0.24**	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. ^a Distance of the QTL from the first marker of the indicated interval. ^b The QTL effect is the phenotypic effect due to the substitution of a 'Gaoyou' allele by an allele of 'Sollux'

Table 2. Estimated epistatic (aa) and epistasis x environment interaction (aae) effects of QTL 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**				-0.25*
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. [†] A positive sign of the epistatic effect indicates that parental allele combinations and a negative sign that recombinant allele combinations increase phenotypic values.

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