

Inheritance of oil content in the doubled haploid population SG14 x Express 617

Nina Behnke[✉], Wolfgang Ecke, Heiko C. Becker and Christian Möllers
Georg-August-Universität Göttingen, Department of Crop Sciences, Plant Breeding, Von-Siebold-Str. 8, 37075 Göttingen, Germany. Email: nbehnke@uni-goettingen.de

ABSTRACT

Novel alleles and loci from alien germplasm may help to increase the seed oil content in European winter oilseed rape. The aim of this work is to further increase oil content in European winter oilseed rape by using doubled haploid line SG14, one of the lines with the highest oil content derived from a cross between the German cultivar Sollux and the Chinese cultivar Gaoyou, both having a high oil content. SG14 (++)-quality) was crossed to the German high oil cultivar Express (00-quality), to generate a new doubled haploid population and to study the inheritance of oil content in this population. Following field experiments at nine locations in Germany in 2009/10 several low erucic acid lines with oil contents higher than cultivar Express were identified.

INTRODUCTION

Winter oilseed rape (*Brassica napus* L.) is the most important oil crop in Europe. High seed oil content is therefore one of the most important breeding aims in this crop. Oil content in oilseed rape is a genetically complex trait and a great diversity of favourable alleles might exist when considering different gene pools as is the case in other crop species like sunflower (Leon *et al.* 2003; Al-Chaarani *et al.* 2004), soybean (Hyten *et al.* 2004) or maize (Song *et al.* 2004). Breeding efforts to increase oil content in new cultivars have already been successful by using mainly European breeding material. A new approach was investigated by Zhao *et al.* (2005) using Chinese genetic resources, since these are only distantly related to European material and during the last decades have been bred separately for high yield and oil content. In this previous work, the Chinese cultivar Gaoyou (++)-quality) and the European cultivar Sollux (++)), both known for their high oil contents, were crossed and a doubled haploid (DH) population was developed. After field testing, DH line No.14 (++) turned out to be among those with the highest oil contents and with a combination of all favourable QTL alleles for oil content from both parental cultivars. Subsequently, DH line No.14 (=SG14) was crossed to inbred line 617 of the winter oilseed rape cultivar Express (00-quality). Express 617 has also a high oil content and has been used as a parent in a previous mapping population. From F1 plants (SG14 x Express 617) 251 doubled haploid lines were generated and were tested in 2009/10 in field experiments at nine different locations in Germany. Results about the inheritance of oil, erucic acid (22:1) and glucosinolate (GSL) content in this population and about the ongoing development of a molecular marker map and QTL mapping will be reported.

MATERIAL AND METHODS

Plant material and field experiments: The plant material used for analysis consisted of a DH population of 251 lines developed from F1 plants of a cross between DH line SG14 (++)-quality) and cv. Express, inbred line 617 (00-quality). SG14 is a DH line derived from the cross between the European cultivar Sollux and the Chinese cultivar Gaoyou, both parents of (++)-quality with high oil content. In the DH population of Sollux x Gaoyou SG14 showed superior oil content and a combination of all favourable QTL alleles for oil content. Field experiments with the 251 DH lines, the two parental lines and 8 check cultivars were performed in 2009/10 at nine locations in Germany. At maturity the main racemes of ten open pollinated plants per genotype and location were harvested and bulked for further analysis.

Analytical methods: Oil (%), protein (%), and glucosinolate (GSL; $\mu\text{mol/g}$ seed) content were determined on the basis of 91% seed DM by NIRS. Erucic acid content of the oil (%) was determined by NIRS and for the location Göttingen-Reinshof in addition by gas chromatography (GC).

Statistics: Analysis of variance and calculation of heritabilities were performed by using PLABSTAT software (Utz 2008) considering the locations as random. Mean values of the genotypes across the locations were used to calculate Spearman's rank correlation coefficients between traits. *, ** denotes significant at $P=5\%$ and 1% .

RESULTS

The analysis of variance revealed large and significant differences between the DH lines of the SG14 x Express 617 population for oil content and all other traits (Tab. 1). Variance components for oil content showed a predominant effect of the genotype x location interaction, which, however, also consisted of the experimental error. Heritabilities for oil, erucic acid and glucosinolate content were medium to high and rather low for protein content.

Tab. 1: Variance components and heritabilities for seed quality traits of the SG14 x Express 617 DH population including the two parental lines and 8 check cultivars; calculated from NIRS data over nine locations (**significant at $P=0.01$; F -Test of ANOVA)

Source of variance	DF	Oil (%)	22:1 (%)	Protein (%)	GSL (%)
Location (L)	8	2.2**	4.1**	1.5**	17.4**
Genotype (G)	264	1.8**	105.8**	0.3**	117.9**
G x L	2055	5.5	209.4	3.5	229.9
Heritability		0.75	0.82	0.46	0.82

Frequency distribution of oil content was continuous, ranging from 42.4 to 50.5% (Fig. 1). The 00-quality cultivar Express 617 had an oil content of 45.5% and the high erucic acid DH line SG14 had an oil content of 49.1%. There were a large number of DH lines with higher oil contents than the cv. Express 617. Frequency distribution of erucic acid content showed as expected (1:2:1 segregation) three groups with low, intermediate and high erucic acid contents (Fig. 2). However, due to partial cross pollination of the open pollinated plants the groups were not clearly separable.

Fig. 1: Distribution of oil content (NIRS, 91% DM; means over nine locations) in the SG14 x Express 617 DH population

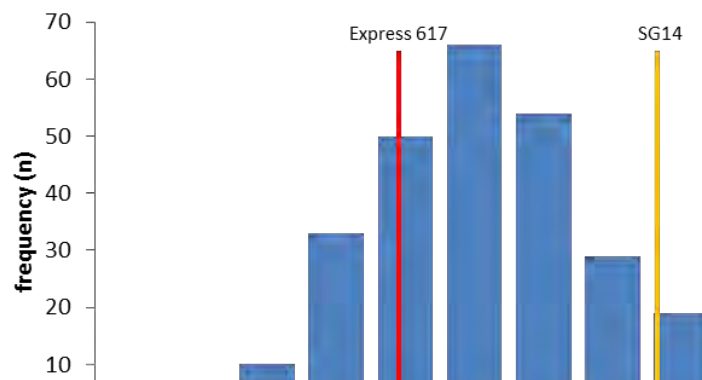
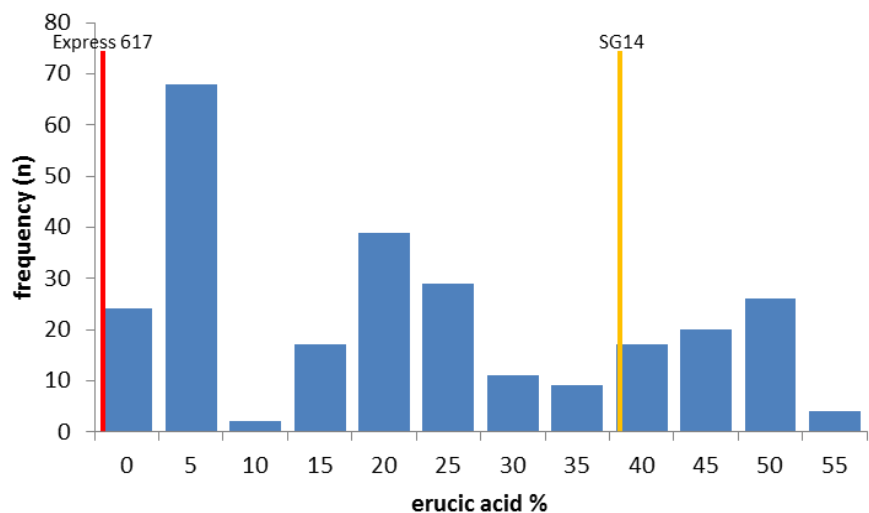
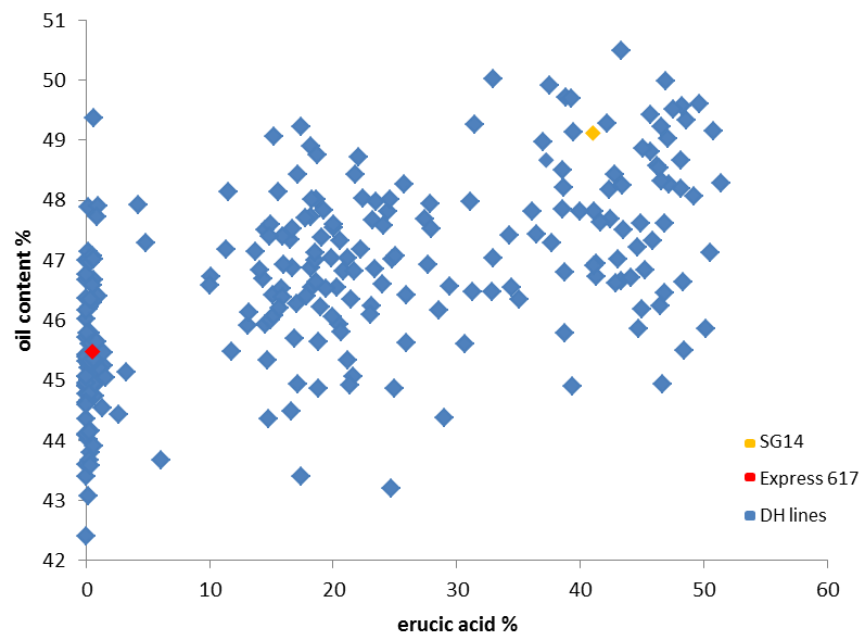


Fig. 2: Distribution of the erucic acid content (GC) in the DH population SG14 x Express 617 at the location Göttingen-Reinshof



In the population there was a significant positive correlation between oil and erucic acid content (Spearman's rank correlation coefficient = 0.716**; NIRS; means over nine locations) and a significant negative correlation between oil and protein content (-0.423**). There was no close correlation between oil and glucosinolate content (-0.121). Although the low erucic acid lines had on the average lower oil contents, there were some lines with oil contents higher than cv. Express 617 (Fig. 3).

Fig. 3: Correlation between oil (means over nine locations) and erucic acid content (GC; only Göttingen-Reinshof) in the SG14 x Express 617 DH population



DISCUSSION AND PROSPECTS

A considerable variation for oil content was observed in the doubled haploid population derived from the cross SG14 x Express 617. The population was segregating for erucic acid content. Considering the GC values for erucic acid content of the seeds of the location Göttingen-Reinshof (Fig. 3) a 1:2:1 segregation can be assumed. From n=251 DH lines 89, 105 and 67 had an erucic acid content of <10%, 10 to 35% and >35%, respectively.

As expected there was a close positive correlation between erucic acid and oil content which makes comparison of oil contents between genotypes difficult. Regression analysis will be applied to correct the oil contents of the erucic acid containing genotypes. Nevertheless, there were a number of doubled haploid lines with low erucic acid contents which had oil contents higher than cv. Express 617. Currently the DH population is tested a second year in field experiments at nine locations. Work is also in progress to develop a molecular marker map which will be used to map QTL for oil content and other traits in this population. Results will be compared with results from earlier studies (Zhao *et al.* 2005, Zhao *et al.* 2006, Radoev *et al.* 2008).

ACKNOWLEDGEMENTS

The authors gratefully acknowledge the Fachagentur für Nachwachsende Rohstoffe (FNR e.V.) and the Gemeinschaft zur Förderung der privaten deutschen Pflanzenzüchtung (GFP e.V.) for funding this research project (ÖE 135/10 NR) as well as the participating breeders for performing field experiments.

REFERENCES

- Al-Chaarani GR, L Gentsbittel, XQ Huang, A Sarrafi (2004) Genotypic variation and identification of QTLs for agronomic traits, using AFLP and SSR markers in RILs of sunflower (*Helianthus annuus* L.). *Theor Appl Genet* 109:1353–1360
- Hyten DL, CE Pantalone, AM Sams, D Saxton, TR Landau-Ellis, TR Stefaniak, ME Schmidt (2004) Seed quality QTL in a prominent soybean population. *Theor Appl Genet* 109:552–561
- Leon AJ, FH Andrade, M Lee (2003) Genetic analysis of seed oil concentration across generations and environments in sunflower. *Crop Sci* 43:135–140
- Radoev M, HC Becker, W Ecke (2008) Genetic analysis of heterosis for yield and yield components in rapeseed (*Brassica napus* L.) by QTL mapping. *Genetics* 179:1547-1558
- Song XF, TM Song, JR Dai, T Rochefort, JS Li (2004) QTL mapping of kernel oil concentration with high-oil maize by SSR markers. *Maydica* 49:41–48
- Zhao J, HC Becker, D Zhang, Y Zhang, W Ecke (2005) Oil content in a European · Chinese rapeseed population: QTL with additive and epistatic effects and their genotype-environment interactions. *Crop Sci* 45:51–59
- Zhao J, HC Becker, D Zhang, Y Zhang, W Ecke (2006) Conditional QTL mapping of oil content in rapeseed with respect to protein content and traits related to plant development and grain yield. *Theor Appl Genet* 113:33–38