

Genetic variation and mapping of QTL for kaempferol-3-O-(2'''-O-sinapoyl-β-sophoroside) and other sinapic acid derivatives in the rapeseed DH population SGD14 x Express617

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Background

- **Kaempferol 3-O-(2'''-O-sinapoyl-β-sophoroside)** (kaempferol-3OSS) was recently identified as the key molecule contributing to the bitter taste of rapeseed protein isolates (Hald et al. 2019)
- This finding enables new opportunities to establish rapeseed protein on the vegetable protein market
- In this study the genetic variation and mapping of QTL for kaempferol-3OSS and other sinapic acid derivatives were investigated

Material & Methods

- DH population SGD14 x Exp617 (Behnke et al. 2018) with n = 100 DH lines in n = 4 environments
- Open pollinated seeds were used for the analysis
- RP-HPLC quantification of 9 different kaempferol-glycosids, sinapine, sinapoylglucose and sinapic acid
- Genotyping using Illumina 60K SNP chip
- Genetic framework map consisting of 1764 SNP markers used for QTL mapping

Results

Table 1: Variance components and descriptive statistics for sinapic acid derivatives

	df	Kaempferol-3OSS ^a	Kaempferol-glycosids (sum) ^b	Sinapine ^b	Sinapoylglucose ^b	Sinapic acid ^b
Genotype	99	2.27**	0.06**	0.07**	0.15**	0.002**
Environment	3	0.76**	0.01**	0.01**	0.08**	0.014**
GxE-interaction	253	1.20	0.03	0.52	0.54	0.010
h ²		88	87	36	53	46
Mean ± SD		3.56 ± 1.60	1.18 ± 0.26	7.00 ± 0.45	1.24 ± 0.54	0.22 ± 0.07
Range		1.07 - 8.98	0.58 - 1.71	5.84 - 8.46	0.18 - 3.34	0.11 - 0.50
LSD5%		1.53	0.26	1.01	1.03	0.14
Exp617		1.88 ± 0.75	0.92 ± 0.07	6.67 ± 0.39	2.47 ± 0.75	0.30 ± 0.13
SGDH14		6.10 ± 1.92	1.49 ± 0.11	6.78 ± 0.13	0.48 ± 0.14	0.09 ± 0.04

^a = in µg/g, ^b = in mg/g, df = degrees of freedom, p ≤ 0.01 indicated by **, h² = heritability in %, LSD5% = least significant difference at p ≤ 0.05

Table 2: QTL detected in the SGD14 x Exp617 population using composite interval mapping

QTL	Linkage group	SNP-marker	Position [cM]	Confidence interval 95%	LOD	A ^a	R ² ^b	TR ^c
Kaempferol-3OSS-1	A05	Bn-A05-p3246311	42.0	38.90 - 45.70	5.79	1.10	0.18	44.27
Kaempferol-3OSS-2	A06	Bn-A06-p22278059	143.4	138 - 144	8.28	0.90	0.26	
Kaempferol-glycosids-sum-1	A06	Bn-A06-p21796008	134.6	132.6 - 139.8	16.63	0.18	0.44	
Kaempferol-glycosids-sum-2	A09	Bn-A09-p3257371	126.0	117 - 133.7	4.17	0.08	0.08	66.84
Kaempferol-glycosids-sum-3	C09	Bn-A09-p2730673	2.8	2.1 - 6.9	7.26	0.11	0.15	
Sinapine-1	C09	Bn-scaff_16486_1-p39141	2.11	0.1 - 14.2	4.34	0.18	0.14	14.00
Sinapoylglucose-1	A05	Bn-A05-p14537104	55.9	52.2 - 59.6	3.72	-0.23	0.10	20.32
Sinapoylglucose-2	A07	Bn-A07-p17197152	115.1	114.4 - 117.1	3.61	0.17	0.10	
Sinapic acid-1	A08	Bn-A08-p2715086	6.8	3.4 - 8.1	3.67	-0.02	0.10	19.25
Sinapic acid-2	C05	Bn-scaff_21369_1-p871257	47.4	45.8 - 48.7	3.19	0.02	0.09	

^a = Additive effect; positive additive effect indicating that the alleles increasing the trait were derived from SGD14

^b = Percentage of phenotypic variance explained by each QTL

^c = Percentage of phenotypic variance explained by all QTL

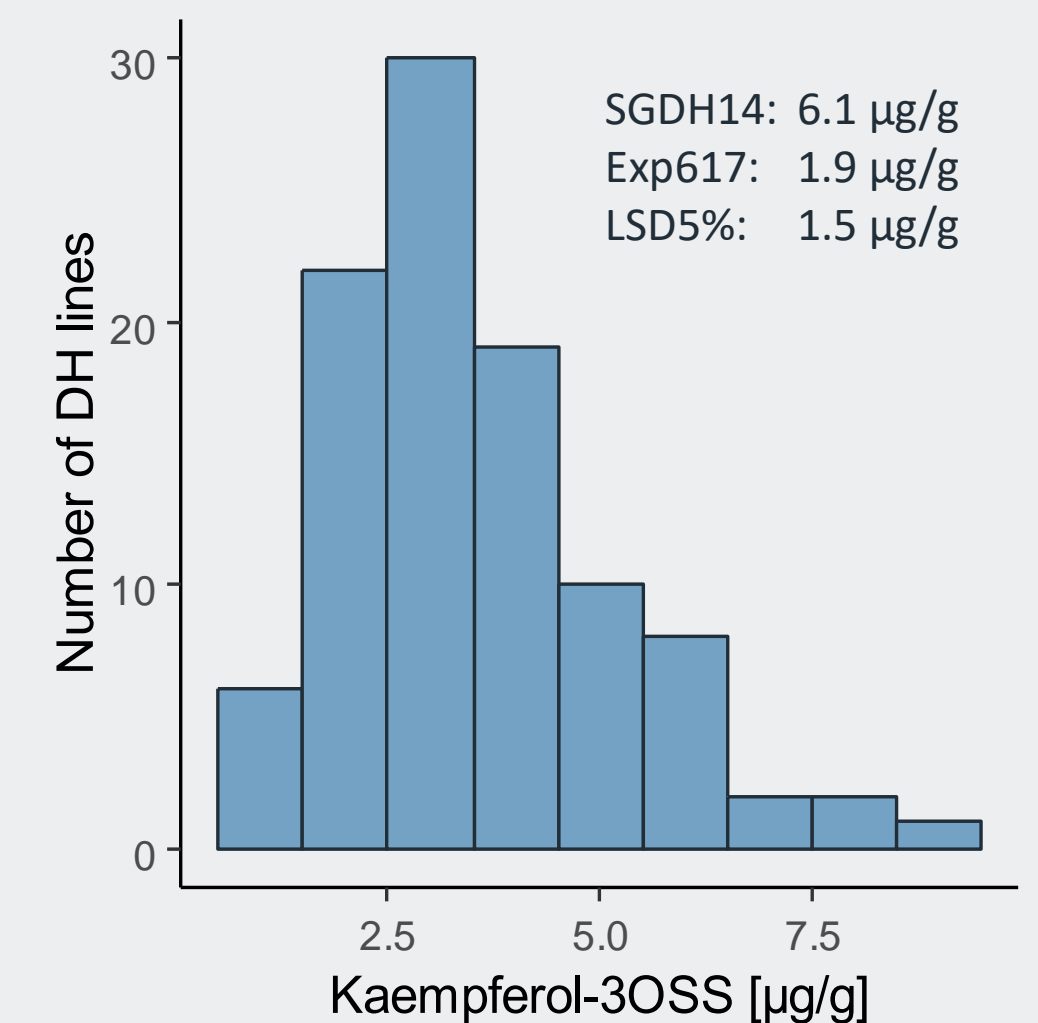


Figure: Kaempferol-3OSS content [µg/g] across 4 environments showing large variation.

Take-home message

- There was high phenotypic variation of kaempferol-3OSS content ranging from 1.1 – 9.0 µg/g
- Genetic variation was significant for all traits and heritabilities were high for kaempferol-3OSS and the sum of kaempferol-glycosids
- For Kaempferol-3OSS and the sum of kaempferol-glycosids the percentage of explained phenotypic variance by all QTL was high
- Identified QTL can be used for marker assisted selection to breed for better protein quality in rapeseed



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References

- Hald, C., Dawid, C., Tressel, R., & Hofmann, T. (2019).** Kaempferol 3-O-(2'''-O-sinapoyl-β-sophoroside) Causes the Undesired Bitter Taste of Canola/Rapeseed Protein Isolates. *Journal of Agricultural and Food Chemistry*, 67(1), 372-378.
- Behnke, N., Suprianto, E., & Möllers, C. (2018).** A major QTL on chromosome C05 significantly reduces acid detergent lignin (ADL) content and increases seed oil and protein content in oilseed rape (*Brassica napus* L.). *Theoretical and Applied Genetics*, 131(11), 2477-2492.

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