

21. Detection of stably-expressed QTL for rice fat content using BIL and CSSL populations

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Rice fat content is one of most important nutritional traits, and its content and composition have a crucial effect on the quality of rice cooking and eating. So far, genetic studies on rice fat content have been carried out on QTL analysis by classical quantitative genetic methods (Hu et al. 2004, Chen et al. 1998, Qi et al. 1983). In most of these studies, a primary mapping population (such as RIL population and DH population) with a single environment was designed for rice fat content QTL detection. The stability of the QTL defined fat content was particularly lacking.

In this study, 85 Backcross inbred lines (BILs) containing 238 RFLP markers and 39 chromosome segment substitution lines (CSSLs) with 166 SSR markers, developed from the cross between Sasanishiki (japonica) and Habataki (indica), were used to detect QTL for rice fat content. We did a chemical analysis of fat content of brown rice flour, using Soxtec-Avanti 2050 total fat system, which had been widely adopted to detect fat content of rice (Matsler et al. 2005). The QTL analysis in BILs was performed using QTL Cartographer 2.5 with composite interval mapping (CIM) method (Basten et al. 1996). LOD value of 2.0 was used as the criterion to detect the significant association between marker and gene loci, after 1,000 permutation tests. In CSSLs, Windows QTL IciMapping v1.4 with inclusive composite interval mapping (ICIM) (Wang et al. 2006, Li et al. 2007) was used to detect QTL based on phenotypic values. In addition, QTL in CSSL population were also determined by the graphical genotype comparison method described by Eshed and Zamir (1995).

The QTL detected in the BIL population are presented in Table 1. Four main-effect QTLs (*qFC-6*, *qFC-7*, *qFC-11-1*, *qFC-11-2*) were identified in BIL population, locating on chromosomes 6, 7 and 11, respectively. Percentages of phenotypic variation explained (PVE) by these QTLs ranged from 0.5% to 19.9%.

Two QTLs (*qFC-3*, *qFC-11-2*) were detected in the CSSL population and mapped on chromosome 3 and 11, with the LOD values of 7.25 and 11.79 and the PVE value of 8.8 and 21.2%, respectively. In the 2 QTLs, the positive allele of *qFC-3* was inherited from Sasanishiki, while *qFC-11-2* was from Habataki.

Interestingly, *qFC-11-2*, identifying in BILs with the highest PVE value, was further detected by QTL analysis in CSSLs. At the same time, the fat content of SH37 harboring a Habataki segment with *qFC-11-2* loci was 3.108%. It was significantly higher than that of the background parent Sasanishiki, which accounted for 2.44%. On the other hand, fat content of SH38, which did not carry the corresponding segment of Habataki, showed a non-significant difference with Sasanishiki (2.384 vs 2.44%, Fig. 1). Therefore, the genetic effect of *qFC-11-2* loci appeared to be stable across the two populations. Comparing with pervious studies (Kang et al. 1998, Hu et al. 2004), we identified *qFC-11-2* as a novel QTL for rice fat content.

Due to the low resolution (10-15cM) of QTL detected in CSSL population, further study will be necessary to develop NILs by backcrossing SH37 with the recurrent parent, Sasanishiki, for accurate genetic analysis. In rice breeding, since *qFC-11-2* is stably-expressed and tagged with well-characterized SSR markers, it will be also useful for marker-assisted selection to improve rice quality.

Table 1 The putative QTLs for rice fat content detected using the BILs and CSSLs

Loci	Marker interval	Population	LOD value	PVE (%)	Additive effect	Positive allele
<i>qFC-3</i>	RM4108-RM3372	CSSL	7.25	8.8	-0.001	S
<i>qFC-6</i>	R2071-R1888	BILs	2.1395	0.5	-0.0016	S
<i>qFC-7</i>	R2394 -R1440	BILs	2.3153	0.38	0.0020	H
<i>qFC-11-1</i>	G257-C1172	BILs	2.4244	18.9	0.0114	H
<i>qFC-11-2</i>	C1172-S723	BILs	3.2457	19.9	0.0122	H
	RM5823-RM1341	CSSLs	11.79	21.2	0.004	H

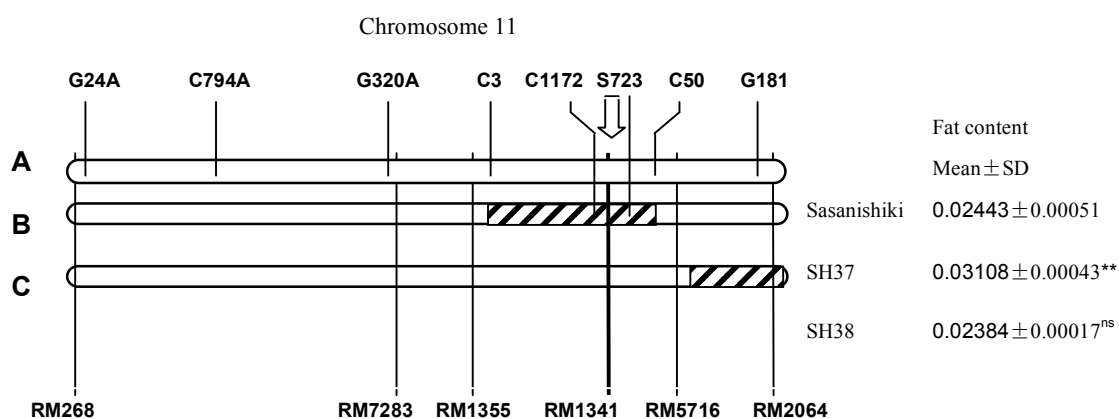




Fig.1. Stable QTL, *qFC-11-2*, for fat content using two mapping populations and differences of fat content between genetic background parent Sasanishiki and target CSSLs with or without carrying fat content QTL alleles

A: Sasanishiki/Habataki/Sasanishiki BILs map ; ∇ putative QTL (*qFC-11-2*);

B: Sasanishiki/Habataki CSSL SH37,  Habataki segment harboring QTL for fat content;

C: Sasanishiki/Habataki CSSL SH38,  Habataki segment which does not harbor QTL for fat content;

Note: ** mean the level of 1% of significant difference between fat content of Sasanishiki and target CSSLs with or without carrying QTL alleles, ^{ns} represents non-significant differences between fat content of Sasanishiki and target CSSLs with or without carrying QTL alleles.

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References

- Basten C. J., B. S. Weir and Z. B. Zeng, 1996. QTL catogrepher. North Carolina State University, NC.
- Chen J. G. and J. Zhu, 1998. Genetic analysis of fat content in indica-japonica intersubspecific hybrid rice. *J. Trop Subtrop Bot.* 6: 347-351.
- Eshed Y. and D. Zamir, 1995. An introgression line population of *Lycopersicon pernellii* in the cultivated tomato enables the identification and fine mapping of yield-associated QTL. *Genetics*, 141: 1147-1116.
- Hu Z. L., P. Li, M. Q. Zhou, Z. H. Zhang, L. X. Wang, L. H. Zhu and Y. G. Zhu, 2004. Mapping of quantitative trait loci (QTLs) for rice protein and fat content using doubled haploid lines. *Euphytica* 135: 47-54.
- Kang H. J., Y. G. Cho, Y. T. Lee, Y. D. Kim, M. Y. Eun and J. U. Shim, 1998. QTL mapping of gene chemical properties based on molecular map of rice. *Korean J. Crop Sci.* 44: 199-204.
- Li H., G. Ye and J. Wang, 2007. A modified algorithm for the improvement of composite interval mapping. *Genetics*. 175: 361-374.
- Matsler A. L. and T. J. Siehenmorgen, 2005. Evaluation of operating conditions for surface lipid extraction from rice using a Soxtec system. *Cereal Chem.* 82: 282-286.
- Qi Z. B., Li B. J., Yang W. G., Wu X. F., 1983. A study on the genetic of exterior quality and fat of the rice grains. *Acta Genetica Sinica*, 10: 452-458.
- Wang J., X. Wan, J. Crossa, J. Crouch, J. Weng, H. Zhai and J. Wan, 2006. QTL mapping of grain length in rice (*Oryza sativa* L.) using chromosome segment substitution lines. *Genetical Res.* 88: 93-104.