

## Research Article

### Comparative Analyses between Functional Markers Concerning Yield-related Traits of Rapeseed and Sequences of Rice Genome Database

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**Abstract:** *Brassica napus* L. is an important oilseed and fodder crop grown throughout the world. Its yield is the important goal in *B. napus* breeding programs. In this study, comparative analyses were carried out between rapeseed and rice based on the functional markers linked to QTLs of important yield-related traits in rapeseed. The results showed that the level of rapeseed and rice on the sequence homology was extensive and some QTLs controlling the similar traits were found in the region of the homologous genes in rice and rapeseed, simultaneously. This study will be helpful to clone QTL in rapeseed using the information of rice.

**Keywords:** Comparative analysis, functional genes, QTLs, rapeseed, rice

#### INTRODUCTION

Comparative genomics is the study of the relationship of genome structure and function across different biological species or strains using kinds of classification methods and alignment techniques. Sequence alignment is one of the main techniques, which is widely used for researches on bioinformatics, such as database searching, evolutionary and development analysis and protein homology modeling. In higher plants, functional genes among different plants are highly conserved and genes controlling important traits may be located in the same or similar position and be linked with the same molecular markers. The sequence information and genomic resources of the extensively studied model organisms could be used for marker development, map-based gene cloning and candidate gene identification in other plants. Relying on synteny between radish and Arabidopsis, a single radish nuclear gene, Rfo, was cloned by a map-based cloning approach (Brown *et al.*, 2003). In rapeseed (*Brassica napus* L.), the fine mapping of the blackleg R gene was also based on the conserved regions between Arabidopsis and rapeseed (Mayerhofer *et al.*, 2005). Recently, Qin *et al.* (2011) saturated the powdery mildew resistance gene, *Pm6*, in wheat using the collinearity-based markers by extensively exploiting the genomic resources of rice, *Brachypodium distachyon* and the comprehensive Triticeae ESTs (Expressed Sequence Tags).

*B. napus* L. is an important oilseed and fodder crop grown throughout the world. Recently, attention has been given to its potential as a renewable resource for

biofuel production. Yield is the important goal in *B. napus* breeding programs and it is difficult to accurately evaluate and select this trait in conventional breeding programs due to yield complexities arising from both the number of segregating loci of all the traits involved and the influence of genotype×environment interactions. Recent advances in marker technologies have made it possible to discover the Quantitative Trait Loci (QTLs) for the traits and detect the molecular markers linked to them, which will advance selection by marker-assisted methods and facilitate the development of high-yield cultivars (Koeberner *et al.*, 2001).

In a previous publication, we developed 177 functional markers corresponding to 111 differentially expressed genes in hybrid of *B. napus* in an F<sub>2</sub> population resulting from crossing “SI-1300 × Eagle” (Li *et al.*, 2006). Furthermore, QTLs were detected for 12 yield-related traits based on the genetic map containing 177 functional markers. And, 45 functional markers involved in 39 Expressed Sequence Tags (ESTs) were found to be linked with the QTLs of 12 traits (Li *et al.*, 2007). In this study, comparative analyses were carried out between rapeseed and rice based on the functional markers linked to QTLs of important yield-related traits in rapeseed in order to investigate the commonality between different crops on genes controlling the same traits. This study will lay a foundation for cloning the genes of rapeseed using rice genome resources.

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Table 1: Functional markers involved in QTLs for agronomic traits in rapeseed

Code	Accession number of rapeseed	Related-traits in rapeseed <sup>d</sup>
ACT2	A1352754	ELMI
ANL2	CD822199	SFB
APL	CD827309	SFB
APRR2	CD821312	SFB, SP
AT103	CB686353	LMI, SDMI, SW, FB
ATH-A	CD831246	SP, SFB
ATH-B	CD837508	YP
ATPS	U68218	FB, YP
AUXDR	CD839494	HPB
AUXR	CD840488	HPB, SDMI, YP, FB, SMI, SP, SFB
BKCOAS	CD813605	PH, SMI
C2H2T	CD827449	SDMI, SW, HPB, SFB
CDKC	CD814110	SP, SFB
CHS	AF076334	SFB
CPS	AF258249	ELMI, LMI, SFB, SP
CYPRT	CD825388	SDMI
DNAPL	CD826774	HPB, PH, SMI, SS
EIF-4F	CD825242	FB, SP, SMI, SFB, SDMI
FERRIT	CD820594	ELMI, LMI
GAPA	CB686102	SMI
GCIPI	CD830043	SW
IRONT	CD832837	YP, SP, SFB
KEMP	CD835629	ELMI, LMI, SDMI, SMI, SFB, HPB, YP
KRCP	CD830343	FB
LADC	CD825067	ELMI, LMI, PH
LD	AF229401	SS
NAM	CD837251	ELMI, LMI, PH
OMET	CD814524	SFB
PTPTP	CB686190	SMI, SW
RabGAP	CD823463	FB, PH, SW, HPB, SDMI, LMI
RPROB	CD815196	YP
RPSaA	CD813694	ELMI, HPB, SFB, YP, LMI, SDMI, SS, SW
RRM	CD820841	ELMI, LMI, SDMI, FB, SW
SCPS	CD813732	SDMI
SCPT	CD815627	ELMI
SUC	AY190281	SFB, ELMI, HPB, LMI, SDMI, SS, SW
THRX	CB686095	LMI
UXS	CD831259	SS
VHSD	CD814345	SFB, ELMI, FB, PH, SMI, SP, YP

a: PH: Plant height; HPB: Height of primary effective branch; LMI: Length of main inflorescence; ELMI: Effective length of main inflorescence; SMI: Number of siliques per plant; SDMI: Siliques density on main inflorescence; FB: Number of first branches; SFB: Number of siliques on main first branch; SS: Number of seeds per silique; SW: 1000-seed weight; SP: Number of siliques per plant; YP: Yield per plant

## MATERIALS AND METHODS

**Functional markers linked to QTLs of agronomic traits in rapeseed:** In total, 45 functional markers involved in 39 different ESTs or genes were found to be linked with the QTLs of agronomic traits (Table 1).

**Databases used for comparative analyses:** NCBI (National Center Biotechnology Information, <http://www.ncbi.nlm.nih.gov>) and Gramene (<http://www.gramene.org/>).

**Software:** Sequence alignment was done by BLASTx in NCBI. The threshold value was set to  $E \leq 10^{-10}$ . The physical positions of the corresponding rice genes were determined in silicon using the software provided by Gramene and the QTLs of related traits in rice were found in Gramene QTL Database.

## RESULTS

**The homologous sequences in rice:** These 39 different ESTs or genes linked with the QTLs of agronomic traits in rapeseed were applied to search homologous sequences

in rice by BLASTx in NCBI. As shown in Table 2, the majority of the sequences in rapeseed found homologous sequences in rice except two genes (AF229401 and CD820841), indicating that the level of rapeseed and rice on the sequence homology is extensive.

**The physical positions of the rice homologous sequences:** It was showed from Table 3 that the physical positions of the corresponding rice genes determined in silicon using the software provided by Gramene. These rice genes dispread in all of 12 chromosomes. Chromosome 1, 4, 7 and 8 had the most corresponding rice genes while Chromosome 6 had the least ones.

**The QTLs for yield related traits around the homologous genes in rice:** The QTLs for yield and related traits were searched in the region where the corresponding rice genes existed in rice genome according to the information provided by the Gramene (Table 4). In the region of homologue rice genes, the QTLs controlling the yield and related traits were found for rice. The similar QTLs controlling the similar traits

Table 2: The homologous sequences in rice compared to the ones located in the QTLs regions of rapeseed

Code	<i>Brassica napus</i> accession number	<i>Oryza sativa</i> accession number	E value
ACT2	AI352754	NP_001051086.1	6.00E-108
ANL2	CD822199	BAD29470.1	3.00E-16
APL	CD827309	AC007858_11	3.00E-17
APRR2	CD821312	NP_001049427.1	2.00E-12
AT103	CB686353	NP_913010.1	1.00E-83
ATA-A	CD831246	NP_001059487.1	1.00E-70
ATA-B	CD837508	NP_001059162.1	1.00E-114
ATPS	U68218	NP_001051234.1	0.00
AUXDR	CD839494	CAJ86257.1	7.00E-83
AUXR	CD840488	XP_479809.1	2.00E-12
BKCOAS	CD813605	NP_001064831.1	9.00E-61
C2H2T	CD827449	AAS98500.1	8.00E-102
CDKC	CD814110	NP_914221.1	9.00E-72
CHS	AF076334	CAA61955.1	0.00
CPS	AF258249	BAD42451.1	4.00E-16
CYPRT	CD825388	BAD38077.1	6.00E-76
DNAPL	CD826774	NP_001059432.1	1.00E-57
EIF-4F	CD825242	XP_473052.1	2.00E-33
FERRIT	CD820594	NP_001065936.1	3.00E-61
GAPA	CB686102	XP_472744.1	5.00E-149
GCIPI	CD830043	BAD54053.1	1.00E-65
IRONT	CD832837	NP_001053450.1	2.00E-68
KEMP	CD835629	ABA99856.1	7.00E-25
KRCP	CD830343	BAD19903.1	1.00E-62
LADC	CD825067	NP_001053450.1	1.00E-13
LD	AF229401	-	-
NAM	CD837251	BAD09612.1	4.00E-57
OMET	CD814524	XP_480185.1	1.00E-32
PTPTP	CB686190	NP_001042544.1	9.00E-107
RabGAP	CD823463	NP_922353.1	2.00E-83
RPROB	CD815196	XP_47993.1	4.00E-116
RPSaA	CD813694	XP_479167.1	1.00E-101
RRM	CD820841	-	-
SCPS	CD813732	AAQ56529.1	6.00E-41
SCPT	CD815627	NP_001067972.1	2.00E-90
SUC	AY190281	ABA99632.1	4.00E-53
THRX	CB686095	NP_001059627.1	5.00E-94
UXS	CD831259	BAB84333.2	2.00E-64
VHSD	CD814345	NP_001046532.1	1.00E-34

Table 3: The physical positions of corresponding rice genes

Code	Accession number of rice	Chromo-some	Clone	Location (Mb)
UXS	BAB84333.2	1	AB079063	36.22
AT103	NP_913010.1	1	AP001072	9.73
LADC	NP_001042674.1	1	AP001080	9.07
PTPTP	NP_001042544.1	1	AP002855	7.71
CDKC	NP_914221.1	1	AP004326	42.46
VHSD	NP_001046532.1	2	AP005007	10.01
ANL2	BAD29470.1	2	AP005885	27.48
ACT2	NP_001051086.1	3	AC091532	29.03
ATPS	NP_001051234.1	3	AC092558	30.48
APRR2	NP_001049427.1	3	AC107226	6.49
EIF-4F	XP_473052.1	4	AL606594	24.72
GAPA	XP_472744.1	4	AL606636	22.72
IRONT	NP_001053450.1	4	AL606695	26.96
CPS	BAD42451.1	4	AL662933	5.31
AUXDR	CAJ86257.1	4	AL732353	34.39
APL	AC007858_11	5	AC120988	28.79
C2H2T	AAS98500.1	5	AC130609	11.64
GCIPI	BAD54053.1	6	AP003634	30.09
ATH-B	NP_001059162.1	7	AP003837	5.85
RPSaA	XP_479167.1	7	AP004988	25.40
ATH-A	NP_001059487.1	7	AP005248	13.74
THRX	NP_001059627.1	7	AP005261	17.26
DNAPL	NP_001059432.1	7	AP005462	12.57
AUXR	XP_479809.1	8	AP003925	1.04
OMET	XP_480185.1	8	AP004460	3.33
RPROB	XP_479931.1	8	AP004591	1.60

Table 3: Continue

Code	Accession number of rice	Chromo-some	Clone	Location (Mb)
NAM	BAD09612.1	8	AP005544	28.01
SCPS	AAQ56529.1	8	AY360393	12.41
CYPRT	BAD38077.1	9	AP005419	16.40
KRCP	BAD19903.1	9	AP005578	3.73
RabGAP	NP_922353.1	10	AC025296	19.50
BKCOAS	NP_001064831.1	10	AC069145	17.24
SCPT	NP_001067972.1	11	AC133710	18.00
CHS	CAA61955.1	11	AC134256	18.78
KEMP	ABA99856.1	12	BX000457	26.10
FERRIT	NP_001065936.1	12	BX000494	0.32
SUC	ABA99632.1	12	BX664710	27.40

Table 4: Silico-mapping the homologous gene in rice and QTLs for yield-related traits around them

Code	Related-traits in rapeseed	Related-traits in rice <sup>a</sup>
ACT2	ELMI	SW, CT, GN, PH, YP
ANL2	SFB	SW, CT, GN, PNN, PH, SN, SPW
APL	SFB	PBN
APRR2	SFB, SP	YP, PNL, TN
AT103	LMI, SDMI, SW, FB	IL, PNL, PNN, PNW, PH, SBN, SN, TN
ATH-A	SP, SFB	SW, GN, PNL, PH, SN, TN, YP
ATH-B	YP	SW, GN, GW, PNW, TN, YP
ATPS	FB, YP	SW, CT, CL, GN, PH, SBN, SN
AUXDR	HPB	PH, GN, GW, YP, TN, PNN, SN
AUXR	HPB, SDMI, YP, FB, SMI, SP, SFB	IL
BKCOAS	PH, SMI	PH, CT, PNN, SD, PNL
C2H2T	SDMI, SW, HPB, SFB	SW, CL, YP, SDN, SN
CDKC	SP, SFB	BY, PNL, PNN, PH, SDN, SN, TN
CHS	SFB	SW, BY, CT, GN, GW, PNN, PNW, PH, YP, SD, SN, SPW
CPS	ELMI, LMI, SFB, SP	PNL, PNN
CYPRT	SDMI	PNL, PNN, PH, SN, TN
DNAPL	HPB, PH, SMI, SS	SW, GN, SN, TN, YP
EIF-4F	FB, SP, SMI, SFB, SDMI	CT, GN, PNL, PH, SN
FERRIT	ELMI, LMI	SW, SN, YP
GAPA	SMI	CT, GN, PNL, PH, SN, IL
GCIPI	SW	SW, CL, YP, IL, PNL, PNN, PH, SN, TN
IRONT	YP, SP, SFB	CT, GN, PNL, PNN, PH, SN, TN
KEMP	ELMI, LMI, SDMI, SMI, SFB, HPB, YP	SW, GN, PH
KRCP	FB	PNL, SN
LADC	ELMI, LMI, PH	IL, PNL, PNN, PNW
NAM	ELMI, LMI, PH	CT, PNN, TN
OMET	SFB	IL, TN
PTPTP	SMI, SW	IL, PNL, PNN, SBN, SN, TN
RabGAP	FB, PH, SW, HPB, SDMI, LMI	IL, CT, SW, PNN
RPPOB	YP	IL, SW
RPSaA	ELMI, HPB, SFB, LMI, YP, SS, SW, LMI	PH, SN, YP, PNW, PBN
SCPS	SDMI	SW, GN, PNL, PNN, PH, SN, TN
SCPT	ELMI	SW, CT, GN, YP, PNN, SN, SPW
SUC	SFB, ELMI, HPB, LMI, SDMI, SS, SW	PH
THRX	LMI	PNL
UXS	SS	SW, BY, CT, GN, YP, PNN, PH
VHSD	SFB, ELMI, FB, PH, SMI, SP, YP	YP, PNL, PNN, PH, SBN, SD, SN

a: SW: 1000-seed weight; CT: Culm thickness; GN: Grain number; PH: Plant height; YP: Grain yield; SN: Spikelet number; SPW: Spikelet weight; PBN: Primary branch number; TN: Tiller number; IL: Internode length; SBN: Secondary branch number; BY: Biomass yield; PNL: Panicle length; PNN: Panicle number; PNW: Panicle weight; SDN: Seed number; CL: Culm length

were searched in the region of corresponding genes between rice and rapeseed. For example, RPSaA, encoding a 40S ribosomal protein SA, was found in the region of yield QTL in both rice and rapeseed. RabGAP, RabGAP/TBC domain-containing protein, was found in the region of 1000-seed weight in both rice and rapeseed. VHSD, related to the QTL for YP, PH, FB, SMI and SP in rapeseed. In rice, the homologous gene of VHSD was found also in the

region of QTLs for YP, PNN, PH, SBN and SN. These results showed that some QTLs controlling the similar traits were found in the region of the homologous genes in rice and rapeseed and some have pleiotropy effects.

## CONCLUSION

Rice is a model plant of monocotyledon. And, studies on agronomic traits in rice are carried out in full

swing. A large number of information resources in rice are available. In this research, comparative analyses between rapeseed and rice were carried out based on the functional markers linked to QTLs of important yield-related traits in rapeseed. The results showed that the level of rapeseed and rice on the sequence homology is extensive and some QTLs controlling the similar traits were found in the region of the homologous genes in rice and rapeseed. This study will be helpful for us to understand the genome structure and evolution and clone QTL in rapeseed using the information of rice.

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#### REFERENCES

- Brown, G.G., N. Formanova, H. Jin, R. Wargachuk, C. Dendy, P. Patil, M. Laforest, J. Zhang, W.Y. Cheung and B.S. Landry, 2003. The radish Rfo restorer gene of Ogura cytoplasmic male sterility encodes a protein with multiple pentatricopeptide repeats. *Plant J.*, 35: 262-272.
- Koebner, R.M.D., W. Powell and P. Donini, 2001. The contribution of current and forthcoming DNA molecular marker technologies to wheat and barley genetics and breeding. *Plant Breed. Rev.*, 21: 181-220.
- Li, Y.Y., C.Z. Ma, T.D. Fu, G.S. Yang, J.X. Tu, Q.F. Chen, T.H. Wang, X.G. Zhang and C.Y. Li, 2006. Construction of a molecular functional map of rapeseed (*Brassica napus* L.) using differentially expressed genes between hybrid and its parents. *Euphytica*, 152: 25-39.
- Li, Y., J. Shen, T. Wang, Q. Chen, X. Zhang, T. Fu, J. Meng, J. Tu and C. Ma, 2007. QTL analysis of yield-related traits and their association with functional markers in *Brassica napus* L. *Aust. J. Agr. Res.*, 58: 759-766.
- Mayerhofer, R., K. Wilde, M. Mayerhofer, D. Lydiate, V.K. Bansal, A.G. Good and I.A.P. Parkin, 2005. Complexities of chromosome landing in a highly duplicated genome: Toward map-based cloning of a gene controlling blackleg resistance in *Brassica napus*. *Genetics*, 171: 1977-1988.
- Qin, B., A. Cao, H. Wang, T. Chen, F.M. You, Y. Liu, J. Ji, D. Liu, P. Chen and X.E. Wang, 2011. Collinearity-based marker mining for the fine mapping of Pm6, a powdery mildew resistance gene in wheat. *Theor. Appl. Genet.*, 123: 207-218.