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# Bayesian dissection for genetic architecture of traits associated with nitrogen utilization efficiency in rice

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**Nitrogen is one of the key important nutrients in rice production. High rice grain yield is greatly dependent upon economic nitrogen input and genetic factors. In order to locate quantitative loci for traits associated with nitrogen utilization efficiency in rice, F<sub>9</sub> recombinant inbred lines derived from a Korean tongil type Dasanbyeon and a Chinese japonica variety TR22183 was genetically designed. The six traits of interest were observed on 155 RILs, along with 105 SSR and 103 STS markers. Bayesian model selection technique was used to dissect genetic architecture for traits of interest. A total of 28 main-effect QTLs and 23 pairs of epistatic QTLs were detected for traits associated with nitrogen utilization efficiency. The proportions of phenotypic variation explained by the detected QTLs ranged from 0.09 to 16.90% and from 0.19 to 12.76% for main-effect and epistatic QTLs, respectively. Sixteen of main-effect QTLs interacted with nitrogen level. One pleiotropic QTL was found, governing simultaneously nitrogen dry matter production efficiency and Nitrogen grain production efficiency.**

**Key words:** Rice, nitrogen utilization efficiency, QTL, epistatic, interaction of QTL × nitrogen level.

## INTRODUCTION

Nitrogen is considered as one of the most essential nutrition elements for rice growth in natural ecosystems. In general, continuously increasing nitrogen input may increase rice yield, but long-term and superfluous nitrogen input will result in high production cost, low nitrogen utilization efficiency and even environmental pollution among others. The development of rice variety with high nitrogen utilization efficiency is the most effective, economical and safe approach to overcome these problems. The nitrogen utilization efficiency was considerably sensitive to environmental factors, so that it was difficult to reveal genetic mechanism of these traits only through physiological experiment. Recently, many quantitative trait

loci (QTL) mapping were reported for traits associated with nitrogen utilization efficiency in rice. Fang et al. (2001) found five QTLs contributing to root uptake of NH<sub>4</sub><sup>+</sup>-N, NO<sub>3</sub>-N and nitrogen utilization efficiency traits at seedling stage in a hydroponic experiment. 12 QTLs responsible for nitrogen utilization efficiency traits were detected at seedling stage in a hydroponic experiment by Shan et al. (2005). Tong et al. (2006) have located QTLs for plant height, panicles per hill, chlorophyll content, dry weight of over-ground part and grain yield per hill under different nitrogen levels. However, few researches were about QTL mapping of nitrogen utilization efficiency traits at harvest stage and analysis for interaction between QTL and environment under nitrogen stressed condition (Wang et al., 1999; Yang et al., 2007; Cao et al., 2001).

The dissection of the genetic architecture for quantitative traits involved the estimation of the number, locations, effects of main-effect and epistatic QTLs and

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the analysis for interactions of those QTLs with environments as well. Traditional mapping methods based on the two QTLs model, such as interval mapping and composite interval mapping had been used for detecting epistasis (Carlborg et al., 2005; Fijneman et al., 1996; Boer et al., 2002; Kao and Zeng, 2002), but the detection became increasing difficult as the number of QTLs increases. In contrast, Bayesian mapping is able to simultaneously estimate all unknown parameters in the genetic architecture of quantitative traits by generating posterior samples from the joint posterior distribution for these unknowns. As a kind of Bayesian mapping methodology, Bayesian model selection technique had been developed (Yi et al., 2005; Yi et al., 2007). The mapping method provides an efficient and relatively simple way of identifying epistatic QTL for complex traits.

QTL mapping is not only capable of explaining genetic architecture for quantitative traits, but also is useful for marker-assisted selection. The objective of this study is to use Bayesian model selection to identify the main-effect, epistatic QTLs for nitrogen utilization efficiency traits in F9 recombinant inbred lines of rice and analyze the interactions of these QTLs with nitrogen level.

## MATERIALS AND METHODS

### Plant material

A population of 155 recombinant inbred lines (RILs) was derived from the cross of Dasanbyeo × TR22183. The RILs were planted in the Haifeng Farm (Jiangsu Province, China). Physical-chemical properties of control soil were: pH 6.02, organic matter 31.1 g/kg, available nitrogen 143.2 mg/kg, available phosphorus 12.3 mg/kg and available potassium 71.3 mg/kg. All materials were sown on 28 April and transplanted on 28 May. In field trial, these RILs were cultivated in randomized blocks with three nitrogen levels (N0, N-P<sub>2</sub>O<sub>5</sub>-K<sub>2</sub>O = 0 - 150 - 150 kg/ha; N10, N-P<sub>2</sub>O<sub>5</sub>-K<sub>2</sub>O = 150 - 150 - 150 kg/ha and N<sub>20</sub>, N-P<sub>2</sub>O<sub>5</sub>-K<sub>2</sub>O = 300 - 150 - 150 kg/ha). Field management and chemical input for disease and pest control followed the conventional procedures of the experimental farm.

### Field evaluation of traits

A total of six traits, including total nitrogen accumulation (TNA), nitrogen dry matter production efficiency (NDMPE), nitrogen grain production efficiency (NGPE), nitrogen harvest index (NHI) and nitrogen content of grain (NCG) were recorded from randomly chosen twenty plants in the middle of each block at the mature stage.

After the excision of the root, all over-ground part of the plants (straw part and grain) were kept at 105° for 20 min to deactivate enzymes, then dried under 80° for more than 72 h, and finally put into dry chamber at room temperature. By then, dry weight of straw and grain yield per plant could be measured. The nitrogen content was measured by Semimicro Kjeldahl Nitrogen Determination. Calculation of related parameters for nitrogen utilization efficiency was according to Moll et al. (1982).

Total nitrogen accumulation (TNA, g/m<sup>2</sup>) = Total nitrogen accumulation for over-ground part of the plants per unit area.  
Nitrogen dry matter production efficiency (NDMPE, g/g) = the ratio

of plant dry matter per unit area and total nitrogen accumulation.  
Nitrogen grain production efficiency (NGPE, g/g) = the ratio of grain yield per unit area and total nitrogen accumulation.  
Nitrogen harvest index (NHI, %) = the ratio of nitrogen accumulation of grain per unit area and total nitrogen accumulation.  
Nitrogen content of grain (NCG, mg/g) = nitrogen accumulation of grain per unit area.

### Linkage map

Total DNA was extracted from fresh leaf tissue of each selected specimen. Each optimized amplification reaction contained 20 - 40 ng DNA template, 2.0 mmol·l<sup>-1</sup> Mg<sup>2+</sup>, 0.2 mmol·l<sup>-1</sup> of dNTP, 0.4 μmol·l<sup>-1</sup> of each primer and 0.65 U Taq DNA polymerase. The PCR cycles started at 94° (2 min), followed by 35 cycles of 30 s at 94°, 30 s at 50° and 30 s at 68° and finally extended for 8 min at 72°. Amplification products were separated by electrophoresis at a constant power of 60 W for 1.5 - 2 h on 6% polyacrylamide gel in 1×TBE buffer, which were finally proceeded by the procedure of silver-staining.

The segregation data for all the markers were analyzed by chi-square test for goodness of fit to the expected ratio of 1:1. Linkage analysis of the 155 RILs was implemented in the software package mapmaker version 3.0. The linkage map of 1467.5 cM has been constructed by using 105 SSR and 103 STS markers with an average interval of 7.1 cM between adjacent marker loci. If the genetic distance between two adjacent markers exceeded 50 cm, then there will be a splitting of the chromosome segment that the two markers locate on into two linkage groups. Thus, the 12 chromosomes in rice were divided into 17 linkage groups in this study.

### Bayesian mapping method

In RIL population, there is the assumption that there are  $q$  quantitative trait loci responsible for a trait of interest. The genetic mapping model with main-effects, epistatic effects of QTLs and the interactions between QTL and environment (QE) can be then described by the following linear model:

$$y_{ik} = \mu + \sum_{j=1}^q x_a a_j + x_e e_k + \sum_{j=1}^{q-1} \sum_{j'=j+1}^q x_{aa} (aa)_{jj'} + \sum_{j=1}^{q-1} x_{ae} (ae)_{jk} + \varepsilon_{ik}$$

Where,  $y_{ik}$  = phenotypic value on the  $i$ th individual under the  $k$ th environment;  $\mu$  = population mean;  $a_j$  for  $j = 1, 2, \dots, q$  is the additive effect of the  $j$ th QTL; Variable  $x_a$  = genotype indicator (1 for QQ and -1 for qq);  $e_k$  =  $k$ th environmental effect;  $x_e$  = dummy variable corresponding environmental factor;  $aa$  = epistatic effect between the two QTLs;  $x_{aa}$  = genotype indicator that are determined from the combination of two QTL genotypes through Cockerham's genetic model;  $ae$  = QTL-environment interaction effect;  $x_{ae} = x_a x_e$  and  $\varepsilon_{ik}$  is the residual error.

The linkage map-wide interacting QTL and QTL-environment interaction for all traits on the above model has been analyzed by adopting Bayesian model selection (Yi et al., 2005; Yi et al., 2007) implemented in the package R/qtlbim (www.qtlbim.org) released by Yandell et al. (2007). According to the results by the interval mapping, the expected number is set at 3 for main-effect QTL and 4

**Table 1.** The genetic variation of main traits associated with nitrogen use efficiency in recombinant inbred lines.

Trait	N-level	Parents		RIL population			
		Dasanbyeo	TR22138	Range	Mean	SD	CV (%)
NCS	N0	4.51	8.81	4.02 - 11.06	6.78	1.37	20.14
	N10	5.39	9.39	4.38 - 11.12	7.37	1.42	19.24
	N20	11.65	12.42	4.23 - 13.84	8.45	1.93	22.89
NCG	N0	10.15	11.18	8.98 - 15.16	11.96	1.34	11.23
	N10	8.15	11.50	9.08 - 16.34	12.30	1.46	11.88
	N20	14.61	17.01	9.94 - 18.49	13.61	1.73	12.70
TNA	N0	10.31	5.49	4.31 - 17.87	9.58	2.48	25.88
	N10	10.17	7.85	4.06 - 18.99	11.72	2.57	21.97
	N20	32.56	17.00	7.19 - 37.19	18.99	4.53	23.83
NDMPE	N0	126.90	99.97	60.55 - 156.92	109.74	13.47	12.27
	N10	141.53	96.18	75.79 - 159.77	105.36	13.39	12.71
	N20	75.57	67.46	64.10 - 134.09	93.40	13.73	14.70
NGPE	N0	75.83	50.30	29.46 - 74.86	52.14	8.87	17.02
	N10	85.79	46.07	30.59 - 73.40	48.97	9.20	18.79
	N20	40.45	35.28	26.64 - 70.20	45.57	8.51	18.67
NHI	N0	76.96	56.25	37.39 - 79.12	61.77	7.90	12.79
	N10	69.94	52.96	31.74 - 81.30	59.30	8.92	15.04
	N20	59.08	60.01	36.00 - 85.72	60.84	8.18	13.45

for epistatic QTL, so that upper bound of the number of QTL is  $7 + 3\sqrt{7} = 15$ . The initial values of other parameters were assigned to be defaults. For all analyses, the MCMC sampling ran for  $2 \times 10^5$  rounds after discarding the first  $4 \times 10^4$  rounds as burn-in. To reduce serial correlation in the stored samples, the chain was thinned by the remaining one observation in every 40 rounds, yielding 5000 samples for posterior analysis. In posterior analysis, Bayes factors of main effects per locus, the QTL-environment interaction and epistasis per pair of loci were individually calculated and compared with a BF threshold of 3, or  $2\ln(\text{BF}) = 2.1$ , to claim the significance of each locus and effect (Kass and Raftery, 1995). The genetic effects and the proportions of phenotypic variance explained by the different effects (that is, heritabilities) were also estimated. The heritability of an effect was the estimated variance of the effect divided by the phenotypic variance. All these measurements of individual loci were calculated while adjusting for the effects of all other possible loci.

## RESULTS

### Performance of parents and RILs populations

Phenotypic ranges, means, standard deviations, coefficients of variation for six nitrogen using efficiency traits in RILs were listed in Table 1, along with means of their parents. All phenotypic mean of nitrogen utilization efficiency traits in TR22138 was lower than those in Dasanbyeo except for NCS and NCG. In RILs, NCS, NCG and TNA increased with the increase of nitrogen-level, whereas NDMPE, NGPE and NHI decreased. The coefficient of

variation for NCG, NDMPE and NGPE also increased with the increase of nitrogen, but no obvious change existed for the rest. All the investigated traits basically performed a continuous normal distribution and bidirectional transgressive segregation that were suitable for QTL mapping in RI lines and parents.

### Identification of QTLs

A Bayesian model selection was used for mapping QTLs of the observed traits. The analyzed results included HPD (the region of highest posterior density), additive effects, epistatic effects and interactions of QTL×nitrogen level, heritability and  $2\ln\text{BF}$  for main effects and epistatic effects, which were summarized in Tables 2 and 3, respectively.

### Nitrogen content of grain (NCG)

Of all analyzed traits, the number of QTLs detected was the fewest for NCG. Only three QTLs on chromosome 5, 8 and 10 significantly influenced NCG. Two of them interacted with nitrogen level and one pair of main-effect QTLs detected showed epistasis in lower heritability. The main-effect QTL on chromosome 5 explicated the phenotypic variance at the highest level of 16.90%. All main-effect QTLs detected have positive additive effects, suggesting that alleles from the parent 'Dasanbyeo' increased

**Table 2.** Summary of statistics for main-effects and Q×E interactions obtained with Bayesian model selection.

Trait	QTL	LG (Chr.)	HPD	Heritability (%)	Additive	2lnBF	QE
NCG	<i>qNCG-8</i>	8(5)	[20.3, 73.6]	16.90	1.8400	10.6	- 0.3040
	<i>qNCG-12</i>	12(8)	[0.0, 11.3]	1.68	0.2530	11.3	0.0023
	<i>qNCG-14</i>	14(10)	[11.8, 26.6]	1.51	0.2420	7.5	
TNA	<i>qTNA-1</i>	1(1)	[9.5, 19.0]	0.86	0.1450	5.9	0.0058
	<i>qTNA-3</i>	3(1)	[17.9, 80.3]	2.17	0.0128	4.3	
	<i>qTNA-12</i>	12(8)	[22.0, 30.6]	0.09	0.0145	3.8	- 0.0036
	<i>qTNA-14</i>	14(10)	[11.8, 21.5]	5.78	- 0.6886	10.8	- 0.1399
	<i>qTNA-15</i>	15(11)	[15.4, 43.6]	5.88	0.4792	13.9	0.0086
NHI	<i>qNHI-4</i>	4(2)	[0.0, 8.7]	3.66	- 0.2640	4.6	- 0.0081
	<i>qNHI-7</i>	7(4)	[13.1, 21.1]	9.37	- 0.4890	6.0	
	<i>qNHI-8</i>	8(5)	[28.9, 34.6]	11.75	- 0.5370	9.2	
	<i>qNHI-9</i>	9(6)	[22.1, 30.7]	1.75	0.1410	3.4	
	<i>qNHI-12</i>	12(8)	[37.9, 53.1]	5.75	- 0.4560	6.6	- 0.0003
	<i>qNHI-17</i>	17(12)	[72.7, 72.7]	12.44	0.6310	6.8	
NGPE	<i>qNGPE-4</i>	4(2)	[78.5, 83.9]	5.13	- 0.3350	4.5	
	<i>qNGPE-5</i>	5(3)	[30.4, 46.9]	0.30	0.0379	4.3	0.0087
	<i>qNGPE-6</i>	6(3)	[60.2, 69.4]	1.76	- 0.1145	4.5	
	<i>qNGPE-7</i>	7(4)	[0.0, 8.9]	0.33	0.0396	4.5	
	<i>qNGPE-8</i>	8(5)	[81.5, 84.8]	1.31	- 0.1198	7.0	- 0.0088
	<i>qNGPE-9</i>	9(6)	[0.0, 16.4]	5.89	0.3450	4.2	
	<i>qNGPE-12</i>	12(8)	[26.3, 37.9]	2.17	- 0.2331	4.0	
	<i>qNGPE-14</i>	14(10)	[62.9, 71.7]	10.28	- 0.5729	7.0	
	<i>qNGPE-15</i>	15(11)	[30.0, 39.4]	0.75	- 0.0759	4.3	- 0.0081
<i>qNGPE-17</i>	17(12)	[67.2, 67.2]	2.67	0.3252	4.2	- 0.0048	
NDMPE	<i>qNDMPE-5</i>	5(3)	[15.3, 34.5]	0.75	0.0894	5.9	0.1599
	<i>qNDMPE-7</i>	7(4)	[0.0, 8.9]	4.45	0.3482	14.7	0.0049
	<i>qNDMPE-12</i>	12(8)	[0.0, 55.8]	6.55	- 0.4242	19.3	- 0.0076
	<i>qNDMPE-17</i>	17(12)	[8.9, 21.3]	0.37	- 0.0585	5.2	- 0.0167

the NCG at three QTLs.

### Total nitrogen accumulation (TNA)

Five main-effect QTLs for TNA were detected on chromosomes 1, 8, 10 and 11. There were two QTLs located on the first chromosome, that is, LG1 and LG3 (Table 2). Each main-effect QTL explained from 0.09 to 5.88% of phenotypic variation. The 'Dasanbyeo' alleles contributed to increased TNA at four QTLs and decreased TNA at a QTL on linkage group 14. All QTLs performed the interactions with nitrogen level, except for *qTNA-3*. Four epistatic interactions were detected between main-effect QTLs. Furthermore two pairs of epistatic interactions were found between main-effect QTLs and minor gene, distributed on LG1 [9.5, 19.0] × LG7 [51.3, 59.9] and LG7 [51.3, 59.9] × LG14 [11.8, 21.5].

### Nitrogen harvest index (NHI)

On chromosome 2, 4, 5, 6, 8 and 12, the main effects of six QTLs were identified to be significant. Among three detected main-effect QTLs and one minor locus, there were four pairs of significant epistatic interactions with higher heritabilities (Table 3). Three large main-effect QTLs were mapped on LG 7, 8 and 17, accounting for about 10% of the phenotypic variance. Only two main-effect QTLs negatively interacted with nitrogen level.

### Nitrogen grain production efficiency (NGPE)

The most number of main-effect QTLs were detected for NGPE. They accounted for between 0.30 and 10.28% of the phenotypic variation for this trait. Interestingly, the QTL located within the HPD [0.0, 8.9] on linkage group 7

**Table 3.** Summary of statistics for epistatic effects obtained with Bayesian model selection.

Trait	Genome position	Heritability (%)	Epistatic effect	2lnBF
<b>NCG</b>	LG12[0.0,11.3]×LG14[11.8,26.5]	1.60	0.3640	3.8
<b>TNA</b>	LG1[9.5,19.0]×LG7[51.3,59.9]	3.49	0.0373	15.2
	LG1[9.5,19.0]×LG12[22.0,30.6]	0.19	0.0391	7.1
	LG1[9.5,19.0]×LG15[15.4,43.6]	3.03	0.7652	16.4
	LG7[51.3,59.9]×LG14[11.8,21.5]	2.22	0.5643	10.8
	LG12[22.0,30.6]×LG14[11.8,21.5]	2.14	0.2465	6.3
	LG12[22.0,30.6]×LG15[15.4,43.6]	7.73	1.1774	19.3
<b>NHI</b>	LG4[0.0,8.7]×LG5[30.4,69.0]	12.76	1.2276	15.8
	LG4[0.0,8.7]×LG12[37.9,53.1]	8.48	1.0887	6.7
	LG5[30.4,69.0]×LG12[37.9,53.1]	9.47	0.6766	16.5
	LG7[13.1,21.1]×LG12[37.9,53.1]	11.77	0.5463	15.8
<b>NGPE</b>	LG5[30.4,46.9]×LG6[60.2,69.4]	3.63	0.6210	6.6
	LG5[30.4,46.9]×LG7[0.0,8.9]	10.15	0.4809	17.2
	LG5[30.4,46.9]×LG8[81.5,84.8]	11.98	1.2407	18.6
	LG5[30.4,46.9]×LG12[26.3,37.9]	9.50	0.0002	15.8
	LG5[30.4,46.9]×LG14[62.9,71.7]	5.63	0.4034	4.4
	LG5[30.4,46.9]×LG15[30.0,39.4]	1.51	0.0000	4.1
	LG6[60.2,69.4]×LG8[81.5,84.8]	3.58	0.6320	9.5
	LG6[60.2,69.4]×LG12[26.3,37.9]	6.72	0.1870	4.9
	LG6[60.2,69.4]×LG14[62.9,71.7]	11.75	1.3964	13.7
	LG12[26.3,37.9]×LG15[30.0,39.4]	4.49	0.6341	7.0
LG14[62.9,71.7]×LG15[30.0,39.4]	4.49	0.7948	7.0	
<b>NDMPE</b>	LG5[15.3,34.5]×LG7[0.0,8.9]	1.88	0.3139	7.7

was responsible for both NGPE and NDMPE in positive direction, showing the pleiotropy. Of a total of 10 main-effect QTLs, only 4 main-effect QTLs interacted with nitrogen level. The detected epistatic interactions completely resulted from main-effect QTLs, all performing positive effects.

#### Nitrogen dry matter production efficiency (NDMPE)

Four main-effect QTLs were detected for NDMPE. The proportion of phenotypic variance explained by a single QTL ranged from 0.37 to 6.55%. The 'Dasanbyeol' alleles contributed to increase NDMPE at two QTLs and the R22183' alleles at the other two QTLs also increased the trait. All four QTLs were identified to interact with nitrogen level. The unique epistatic interaction for NDMPE arose between LG5 [15.3, 34.5] and LG7 [0.0, 8.9].

#### DISCUSSION

In many researches on mapping QTL for traits associated with nitrogen use efficiency, few reports focus on those traits at harvest stage, such as nitrogen harvest index,

total nitrogen harvest index, total nitrogen accumulation and physiological nitrogen use efficiency. Under the condition of hydroponic and soil culture with two nitrogen levels, Fang et al. (2001) found one QTL on chromosome 1 and 8 at high nitrogen level but some QTLs on chromosome 2, 3, 4, 5 and 6 at low nitrogen level and the interaction of QTL with low nitrogen level as well. Tong et al. (2006) studied QTLs for plant height and other traits at different nitrogen levels and found most QTLs distributed on chromosomes 2, 3, 7, 11 and 12 under high nitrogen level. Numbers of QTLs detected were different due to the nitrogen level. Cho et al. (2007) identified one QTL for grain nitrogen content on chromosomes 8, 9, 10 and one QTL for straw nitrogen content on chromosome 9 under high nitrogen level; one QTL for grain nitrogen content on chromosome 8, one QTL for straw nitrogen content on chromosome 10 and one QTL for physiological nitrogen use efficiency on chromosome 9 under low nitrogen level. The present study found that 28 main-effect QTLs for traits associated with nitrogen use efficiency were distributed on the 12 linkage groups. Of the 28 main-effect QTLs, none of them are for nitrogen content of straw, but some are for grain nitrogen content distributing on linkage group 8(chromosome 5), 12(chromosome 8) and 14 (chromosome 10), which were similar to the results obtained

by Cho et al. (2007).

The genetic variation underlying quantitative phenotypes results from the segregation of numerous quantitative trait loci, each explaining a portion of the total variation and whose expression is modified by interactions with other genes and by the environment (Mackay, 2001). In this research, 16 of 28 main-effect QTLs detected were identified to be interacted with nitrogen level by using Bayesian model selection. They included one of three main-effect QTLs for nitrogen content of grain, four of five main-effect QTLs for total nitrogen accumulation, two of six main-effect QTLs for nitrogen harvest index, four of ten QTLs for physiological nitrogen use efficiency and all four main-effect QTLs for nitrogen dry matter production efficiency. These results were not consistent with those obtained by Young-II Cho et al. (2007), indicating that the interactions of QTLs with environments existed in wide range and depended on traits of interest and environmental difference. We also found 24 pairs of epistatic QTLs for trait associated with nitrogen utilization efficiency distributing on nine linkage groups. In general, the epistatic interaction includes three types: (1) both QTLs are the main-effect; (2) both QTLs are not the main-effect and the rest are that only one QTL is the main-effect. Only type 1 and 3 were found in this study. Finding of epistatic interactions showed that nitrogen utilization efficiency traits in rice is not only determined by the additive effect, but also by non-additive effects from interaction between non alleles, resulting in the complexity of genetic basis for the traits associated with nitrogen use efficiency.

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## REFERENCES

- Boer MP, Ter Braak CJF, Jansen RC (2002). A penalized likelihood method for mapping epistatic quantitative trait loci with one-dimensional genome searches. *Genetics* 162: 951-960.
- Cao G, Zhu J, He C, Gao Y, Yan J, Wu P (2001). Impact of epistasis and QTL×environment interaction on the developmental behavior of plant height in rice (*Oryza sativa* L.). *Theor. Appl. Genet.* 103: 153-160.
- Carlberg O, Brockmann GA, Haley CS (2005). Simultaneous mapping of epistatic QTL in DU6i x DBA/2 mice. *Mamm Genome* 16: 481-494.
- Cho YI, Jiang WZ, Chin JH, Piao ZZ, Cho YG, McCouch SR, Koh HJ (2007). Identification of QTLs associated with Physiological Nitrogen Use Efficiency in Rice. *Mol. Cells* 23(1): 72-79.
- Fang P, Tao QN, Wu P (2001). QTLs underlying rice root to uptake NH<sub>4</sub>-N and NO<sub>3</sub>-N and rice N use efficiency at seedling stage. *Plant Nutrition and Fertilizer Science* 7 (2): 159-165.
- Fijneman RJ, De Vries SS, Jansen RC, Dermant P (1996). Complex interactions of new quantitative trait loci, Sluc1, Sluc2, Sluc3 and Sluc4, that influence the susceptibility to lung cancer in the mouse. *Nat. Genet* 14: 465-467.
- Kao CH, Zeng ZB (2002). Modeling epistasis of quantitative trait loci using Cockerham's model. *Genetics*, 160: 1243-1261.
- Kass RE, Raftery AE (1995). Bayes factors. *J. Am. Stat. Assoc.* 90: 773-795.
- Mackay TFC (2001). The genetic architecture of quantitative traits. *Annu. Rev. Genet.* 35: 303-339.
- Moll RH, Kamprath EJ, Jackson WA (1982). Analysis and Interpretation of Factors Which Contribute to Efficiency of Nitrogen Utilization. *Agron. J.* 74: 526-564.
- Shan YH, Wang YL, Pan XB (2005). Mapping of QTLs for nitrogen use efficiency and related traits in rice (*Oryza sativa* L.). *Agric. Sci. China* 4(10): 721-727.
- Tong HH, Mei HW, Yu XQ, Xu XY, Li MS, ZHANG SQ, Luo LJ (2006). Identification of Related QTLs at Late Developmental Stage in Rice (*Oryza sativa* L.) Under Two Nitrogen Levels. *Acta Genetica Sinica* 33(5): 458-467.
- Wang DL, Zhu J, Li ZK, Paterson AH (1999). Mapping QTLs with epistatic effects and QTL×environment interactions by mixed linear model approaches. *Theor. Appl. Genet.* 99: 1255-1264.
- Yandell BS, Mehta T, Banerjee S, Shriner D, Venkataraman R, Moon JY, Neely WW, Wu H, VonSmith R, Yi N (2007). R/qtlbim: QTL with Bayesian interval mapping in experimental crosses. *Bioinformatics* 23: 641-634.
- Yang J, Zhu J, Williams RW (2007). Mapping the genetic architecture of complex traits in experimental populations. *Bioinformatics* 23(12): 1527-1536.
- Yi N, Shriner D, Banerjee S, Mehta T, Pomp D, Yandell BS (2007). An efficient Bayesian model selection approach for interacting QTL models with many effects. *Genetics*, 176: 1865-1877.
- Yi N, Yandell BS, Churchill GA, Allison DB, Eisen EJ, Pomp D (2005). Bayesian model selection for genome-wide epistatic quantitative trait loci analysis. *Genetics*, 170: 1333-1344.