QTL ANALYSIS FOR YIELD COMPONENTS IN RICE (ORYZA SATIVA L.) UNDER DIFFERENT ENVIRONMENTS

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ABSTRACT

Quantitative trait loci (QTL) for yield components were identified based on an RFLP map from a double haploid population. The 123 DH lines with their parents IR64 and Azucena were evaluated in the field in two different environments (Hangzhou and Hainan). The study revealed that individual QTLs showed a range of sensibility to environments as some QTLs were detected only in a single environment while others were detected in two environments. The relative rankings of genotypes may well differ in different environments and the relationship may be quite complex. These QTLs might be described with their sensitivity to environment. QTLs associated with total grain (tg3-1, tg3-2, tg4, tg10, tg11) and QTL affecting full grain (fg3, fg4-1, fg4-2) showing the largest effect in one environment were also more likely to be detected in another environment. Therefore identifying QTLs that are consistent across environments would be desirable in a marked selection program.

KEY WORDS: Double Haploid population, QTL, yield components, rice (Oryza sativa), environment

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INTRODUCTION

Most important characters of agricultural crops are inherited quantitatively, influenced by many genes. Yield and its components are quantitatively inherited and controlled by many genes with small effects and subject to the environment affects. The recent advent of molecular markers, RLFP in particular, has greatly facilitated the study of complex quantitative traits and made possible to dissect the polygenes for such traits into individual mendelian factors [7]; [8]. Therefore QTL mapping in numerous species and for various traits has been well documented [7];[8].

Many studies of QTL mapping have been conducted in a single environment but the variation of gene expression is observed in different environments. Paterson et al. (1991) [6] mapped 29 putative QTLs affecting mass per fruit, soluble solid concentration affecting mass per fruit soluble solid concentration and fruit pH. Of these 29 QTLs only 4 markers (14%) were identified in all three environments, 10 markers (34%) in two environments and 15 markers (52%) in a single environment Lu et al.[5] described a study using a double haploid population. They indicated that a total of 22 QTLs for six agronomic traits were detected and were significant in at least one environment, but only 7 were significant in all three environments, 7 were significant in two environments and 8 could be detected in a single environment. Zhang et al. [10] reported in a study on an F_2 and two equivalent F_3 populations that only 17 of the total 44 QTLs were detected in more than one trial indicating that individual QTL seems to be sensitive to the environment. The objective of the present study is to describe the genetic analysis for yield components resistance genes and localise QTL involved in controlling these traits on the molecular map of rice.

MATERIALS AND METHOD

A double haploid population of 123 lines derived from a cross between the irrigated Indica variety IR64 and the upland Japonica Azucena. Six restriction enzymes (DraI, EcoRV, HindIII, ScaI, XbaI, EcoRI) were used for parental polymorphism survey. This map contains 175 markers covering 2005cM with an average distance of 11.5cM between pairs of markers [3]. This new map has been used for QTL analysis in this experiment.

Field experiment

The 123 DH lines and their parents IR64 and Azucena were evaluated in the field using a randomised block design with two replications. The agronomic performance of the DH population was evaluated in the field experiment with two locations, Hangzhou located at 32 N and Hainan located at 18 N. The DH lines were grown in the field in Hangzhou from May to October 2003 and in Hainan from January to June 2003. The germinated seeds were sown in seedling bed and transplanted in the field 30 days later with a single plant hill spaced at 15×30 cm. Observations were taken on 5 central plants of each plot for each replication for the number of grains per panicle (total grain, TG), the percentage of fertile grains (fertility rate, FR), the number of filled grains (full grain, FG), the number of panicles (productive tillers, PT), and the weight of 1000 grains (kilogram weight, KG).

Statistical Analysis

For the present genetic experiments of 123 genotypes with 2 replications in 2 locations (as different environments), QTL mapping was firstly conducted based on phenotypic values at each location by the procedure of composite interval mapping [11]. For CIM analysis between markers i and i+1 using DH population, the statistical model is:

$$\hat{y}_j = \beta_0 + \beta^* X_j^* + \sum_i \beta_i X_j + \varepsilon_j$$

where y_j is the phenotypic value of the jth individual measured; β_0 is the population mean, β^* is the QTL effect ; X_j^* is the coefficient for QTL effect; β_i is the effect for the ith marker; X_i is the coefficient for the ith marker effect; and ε_j is the residual error of the jth individual.

The analysis of QTLs linked to molecular markers [3] was conducted by QTL Cartographer v 1.1b [2] for yield components. A likelihood threshold of 9.49 corresponding to a LOD of 2.4 was equivalent to 5% significance level. Therefore any QTL falling within a given interval with a value equal to 9.49 or greater was considered to be significantly associated with that particular trait.

RESULTS

Detection of QTLs for yield components

Total grains

A total of 4 QTLs were detected in Hangzhou location for the DH population (Table 1, Figure 1) and were located on chromosome 3, 4, 10, and 11, respectively. All these QTLs had a positive additive effect except for QTL Tg11 which was associated with a decrease in additive effect. The QTL tg4 located on chromosome 4 within the markers RZ675-RG163 accounted for an increase of 22.63 grains in total grains.

There were 5 QTLs detected in total from the DH population evaluated in Hainan

Table 1. Estimated genetic effects of QTL for yield components across environments

Trait*	Chr	Locus	Marker interval	Hangzhou	Hainan
	3	tg3-1	RG191-RG678		-4.55
TG		tg3-2	RZ337A-RZ448	8.24	6.9
	4	tg4	RZ675-RG163	22.63	7.20
	10	tg10	RZ257-RG241	-7.65	-9.23
	11	tg11	Adh1-RG1094	7.07	5.70
FR	1	fr1	RG146-RG345	4.16	3.72
	2	Fr2	Amy1A/C-RG95	7.11	
	4	Fr4	RZ449-RZ788	3.50	7.20
	6	Fr6	RZ144-RG667		6.30
FG	3	Fg3	RG179-CDO337	10.39	7.90
	4	fg4-1	RG675-RG163	16.65	9.84
		fg4-2	RG214-RG143		
PT	1	pt1	RG690-RZ730	-0.51	0.71
	2	pt2	Amy1A/C-RG95		0.45
	3	pt3	Pgi-CD087		0.32
	4	pt4	RG675-RG163	0.85	
	8	Pt8	TGMS1.2A10K20	0.51	0.61
KG	1	kg1-1	W1-RG173		-1.26
		kg1-2	RG690-RZ730	1.28	
	2	kg2	Pall-RZ58	0.93	
	3	kg3-1	RZ337A-RZ448		
		kg3-2	CDO87-RG910		
	4	kg4	RG190-RG908	-1.16	
	10	kg10	CDO98-G2155	-1.37	-0.75
	11	kg11	Adh1-RG1094		

• QTLs are named by traits abbreviations and chromosome number, TG: total grains,

FR: fertility rate, FG: full grains, PT: Productive tillers, KG: kilogram weight.

(Table 1, Figure 1) and had the same genetic direction as those found in Hangzhou but with a smaller effect. The QTL tg10 mapped to chromosome 10 between markers RZ257-RG241 had a negative additive effect of -9.23 grains with a high likelihood ratio of 34.22. At this locus, the alleles increasing total grains were from IR64.

A total of four QTLs were detected being common to both environments (table 1) and were located on chromosome 3, 4, 10, and 11 between markers RZ337A-RZ448, RZ675-RG163, RZ257-RG241 and Adh1-RG1094 respectively.

Fertility rate

Three QTLs fr1, fr2 and fr4 were identified as being significant in Hangzhou location (Table 1, Figure 1) and were located on chromosome 1, 2 and 4, respectively. These QTLs had a significant additive effect of about

4% and 7% for seed set. All these QTLs had a positive additive effect and the contributing alleles were from Azucena.

A total of 3 QTLs (fr1, fr4, fr6) have been detected in Hainan environment (table 1, figure1). The QTL fr1 occupied the same position as the one identified in Hangzhou location. All these QTLs had a positive additive effect and the alleles increasing fertility rate were from Azucena.

Two QTL were detected on chromosome 1 and 4 being common for both environments and were bordered by markers RG146-RG345and RZ449-RZ788 respectively (Table 1).

Full grains

A total of two QTL were found for full grains in Hangzhou (Table 1, figure 1) and were mapped to chromosome

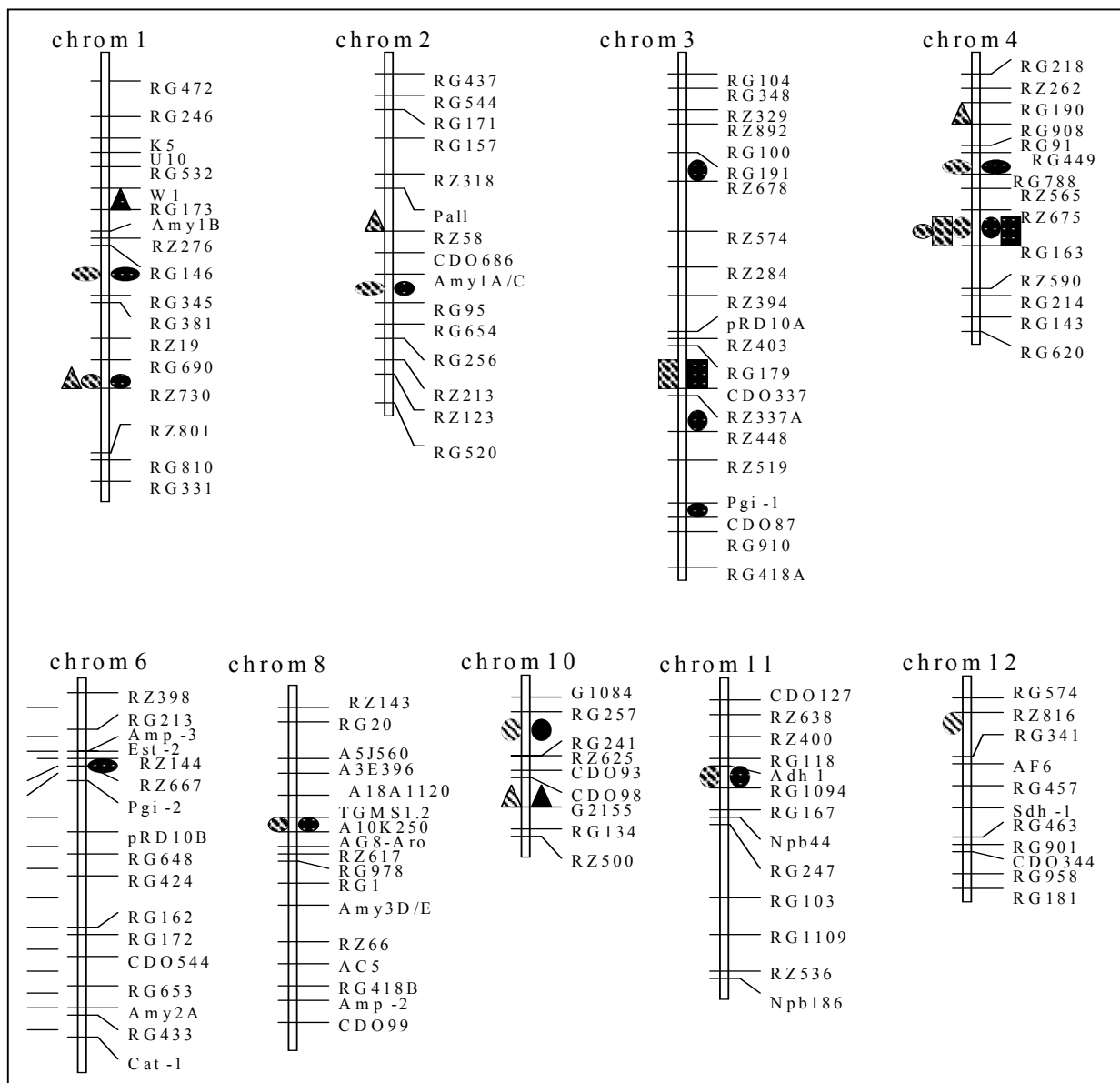J. Cent. Eur. Agric. (2005) 6:3, 317-322

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Figure 1: QTLoci in two environments

3 between markers RG179-CDO337, chromosome 4 between markers RZ675-RZ163 and markers RG214-RG143. The increase in full grain for these QTL was associated with azucena alleles. The loci tg4-1 mapped to chromosome 4 between markersRZ675-RZ163 had a high additive effect of 16.65 grains and high likelihood ratio and seems to act as major gene.

There were two QTL detected in Hainan (Table 1, Figure 1) and were located on chromosome 3 between markers RG179-CDO337 and chromosome 4 between the markers RG675-RG163. These QTL occupy also the same locus as that identified in Hangzhou but with a minor effect.

Two QTL were found to be common for both environments and were located on chromosome 3 and 4 between markers RG179-CDO337and RG675-RG163 respectively (Table 1).

Productive tillers

Three QTLs were mapped for productive tillers and were significant for Hangzhou environment (Table 1, Figure 1). These QTLs were located on chromosome 1. 2, and 8 respectively. All the alleles increasing productive tillers were from Azucena except for locus pt1 bordered by markers RG690-RZ730 that had a negative additive effect and the alleles contributing for the increase were from IR64. No QTL controlling this trait was identified on chromosome 5, 6, 7, 9, 10, 11 and 12. The QTL located on chromosome 4 gave the highest additive effect of -0.85 with a very high likelihood ratio.

There were 4 QTLs (pt1, pt2, pt3, pt8) identified in Hainan (Table 1, Figure 1). Among these QTL, only one was detected in Hangzhou and having an opposite direction effect.

Two QTLs were found to be common for both environments and were located on chromosome 1 and 8 between markers RG690-RZ730 and TGMS1.2-A10K250 respectively (Table 1).

Kilogram weight

A total of 4 QTLs affecting grain weight were detected (table 1, figure 1) in Hangzhou and were located respectively on chromosome 1, 2, 4, 10. The alleles from Azucena at loci kgwt1-2 and kgwt2 increased grain weight. In contrast the alleles from IR64 were associated with an increase in grain weight at loci kgwt4 and kgwt10 (chromosome 4 and 10). The highest additive effect was obtained by the QTL kgwt10 and was 1.37 g with a likelihood equal to 16.79.

Two QTLs were identified as being significant in Hainan environment (table 1, figure 1). These QTLs had all a negative additive effect. The alleles IR64 increased this parameter at locus kgwt1-1 and kgwt10 (chromosome 1 and 10). Among these QTLs identified only one was the same as that detected in Hangzhou.

Only one QTL has been detected being common for both environments and was located on chromosome 10 between markers CD098-G2155 (table 1).

DISCUSSION

This study reveals that QTL show a range of sensitivity to environments as some QTLs were detected only in single environment while others were detected in all environments. The relative rankings of genotypes may well differ in different environments and the relationship may be quite complex [1]. These QTLs might be described with their sensitivity to environment and this agrees with the results reported by Paterson [6], Zhuang [10], and Lee [4]. QTL associated with total grain (tg3-1, tg3-2, tg4, tg10, tg11) and QTL affecting full grain (fg3, fg4-1, fg4-2) showing the largest effect in one environment were also more likely to be detected in another environment. Therefore, these results tend to support the conclusion made by Tanksley [8] that a substantial proportion of a QTL affecting a quantitative trait in one environment will be active in other environments and that this is especially true for QTLs with major effect. Therefore, identifying QTLs that are consistent across environments would be desirable in a marked selection program [6].

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