

QTL MAPPING FOR YIELD COMPONENTS ACROSS ENVIRONMENTS IN RICE (*ORYZA SATIVA* L.)

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The 123 double haploid lines with their parents IR64 and Azucena were evaluated in the field in two different environments. Among the QTL identified, 15 QTL were significant in Hangzhou and 6 QTL in Hainan but only one QTL controlling total grains was significant in all environments. The results indicate that the genotype by environment was trait dependent. These QTL might be described by their sensibility to environments.

1 Introduction

Since the introduction of molecular markers, RFLP in particular, QTLs mapping in numerous species and for various traits have been well documented (Tanksley 1993; Xiao 1995). Many studies of QTLs mapping have been conducted in a single environment but the variation of gene expression is observed in different environments. Therefore, it is of importance to study the genotype by environment interaction effect of genes which control the performance of the trait. G×E interaction is an important aspect for the assessment of genetic effects as well as the prediction of performance in breeding program, because genotypes values must be inferred from phenotypic responses (Stuber *et al.* 1991). Recently, the effects of environments on QTL was studied by Paterson *et al.* (1991) in F₂ and F₃ populations of tomato in three environments; 29 QTLs were identified but only 4 QTLs were significant in all environments. Stuber *et al.* (1992) used a F₃ lines back crossed to parents in maize, found that there was little evidence for G×E interaction for most QTLs although plant material were grown and measured in six diverse environments. Freye and Douches (1994) studied the environment effects of specific gravity on QTL in potato and found that only 2 out of 10 QTLs were significant in all environments. Lu *et al.* (1996) has reported that only 7 QTLs have been detected in all environment from a total of 22 QTLs mapped for six agronomic traits in a DH population.

The present study describes the QTL mapping for yield components and the investigation of the G×E interaction effect generated in diverse environments.

2 Material and Methods

2.1 Materials

A double haploid population recently developed by Guiderdoni *et al.*(1992) was used in this experiment. This population of 123 lines derived from a cross between the irrigated Indica variety IR64 and the upland Japonica variety Azucena. A total of 175 markers were used in the population for QTLs analysis in this experiment(Huang *et al.*, 1995)

2.2 Field Experiment

The 123 DH lines and their parents IR64 and Azucena were evaluated in the field in two locations Hangzhou and Hainan. The DH lines were grown in the field in Hangzhou from May to October and in Hainan from January to April. Every 10 days observations on 5 plants have been recorded for total grains, fertility rate, full grains, productive tillers, kilogram weight, for each replication until all the lines had headed

2.3 Statistical Analysis

The original values of yield components were used to perform analysis of QTLs linked to the molecular markers by the composite interval mapping (Zeng 1994) with QTL cartography v.1.1b (Basten *et al.*, 1996)

3 Results and Discussion

The results indicate that the maximum phenotypic values of the seven traits scored were higher than both parents. It was indicated that yield components of the DH population segregated continuously and both the skew and the kurt values were less than 1 except for fertility rate. It was suggested that yield components of the DH population fit normal distribution and is suitable for QTLs analysis. Transgressive segregants with yield components higher than the parent IR64 or lower than the parent Azucena were observed.

Total Grains

Five QTLs were mapped for the total grain. Only one QTL Tg4 bordered by the marker RZ163-RG590 was significant in all environments, in contrast the QTLs were significant in at least one environment (table2). The QTL Tg4 located on chromosome 4 and detected in Hangzhou accounted for 22.63 grains increase in total grains.

Fertility Rate

Three QTLs were identified as being significant in at least one environment (Table 2). The QTLs Fr1 and Fr5 had a negative additive effect for about 5% for seed set. In contrast the QTL Fr4 had a positive additive effect and the alleles for increasing fertility rate were from IR64

Full Grains

Four QTLs associated with this trait were found to be significant in at least one environment (Table 2). Three QTLs (Fg3, Fg4-1 and Fg4-2) have been identified in Hangzhou while one QTL Fg4-3 had been mapped in Hainan. All these QTLs had an additive effect for increasing full grain and ranged from 9.84 to 16.65. The QTL Tg4-1 bordered by the marker RZ163-RG590 gave the highest additive effect.

Productive Tillers

A total of 5 QTLs controlling this trait were found to be significant in at least one environment (Table 2). All the QTLs identified had a negative additive effect which explain a decrease in productive tillers in both environments.

Kilogram Weight

Five QTLs affecting grain weight were significant in at least one environment (Table 2). Only one QTL Kgwt1-1 located within the interval W1-RG173 was detected in Hainan while QTLs Kgwt1-2, Kgwt2, Kgwt4, Kgwt10 were identified in Hangzhou. Among these QTLs mapped only QTLs Kgwt1-2 and Kgwt2 had a positive additive effect for increasing grain weight

In this study the number of significant QTLs per trait ranged from 3 to 6. A total of 22 QTLs were discovered for five traits of this population in at least one environment. Many of the QTLs had genetic influence on more than one trait. Among the QTLs identified 15 QTL were significant in Hangzhou and 6 QTL were significant in Hainan, but only one QTL detected for total grains was significant in all environments. The results indicate that existence of G×E interaction was trait dependent. These QTLs might be described by their sensibility to the environment factors. Individual QTLs show a range of sensibility to the environments, as some QTLs were detected only in a single environment. The relative rankings of genotypes may well differ in different environments and the relationship may be quite complex (Allard and

Broadshaw 1964). One QTL located on chromosome 4 and bordered by the marker RG163-RG590 had a genetic effect for more than one trait and seems to act as major gene.

Scientists have used this methodology to investigate the G×E but this methodology is not appropriate to distinguish between the genetic main effect and the G×E interaction. Therefore a new complicated methodology should be developed to properly identify the G×E interaction effect.

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Table 1: Detection of QTLs for five agronomic traits in two environments

Locus	Chro	Marker	Env	Likelihood	Additive
Total grain					
Tg3-1	3	RG100-RG191	HN	9.115	-4.553
Tg3-2	3	RZ337A-RZ448	HZ	11.031	8.248
Tg4	4	RZ163-RG590	HN	22.37	7.208
			HZ	49.816	22.63
Tg10	10	G2155-RG134	HN	10.241	-0.757
Tg12	12	RZ816-RG341	HZ	10.013	8.405
Fertility Rate					
Fr1	1	RZ730-RG801	HZ	16.183	-0.047
Fr4	4	RG449-RG788	HN	13.814	0.072
Fr5	5	RZ67-RZ70	HZ	9.583	-0.04
Full Grain					
Fg3	3	RG179-CDO337	HZ	13.653	10.395
Fg4-1	4	RZ163-RG590	HZ	30.621	16.658
Fg4-2	4	RG214-RG143	HZ	24.908	13.235
Fg4-3	4	RG449-RG788	HN	25.79	9.842
Prod. Tillers					
Pt1	1	RZ801-RG810	HZ	29.682	-0.9
Pt4-1	4	RG163-RZ675	HZ	20.804	-0.856
Pt4-2	4	RG214-RG143	HZ	21.863	-0.755
Pt11-1	11	Adh1-RG1094	HN	13.301	-0.711
Pt11-2	11	RZ638-RZ400	HZ	10.403	-0.506
Kgweight					
Kgwt1-1	1	W1-RG173	HN	10.204	-1.26
Kgwt1-2	1	RG690-RZ730	HZ	15.19	1.283
Kgwt2	2	Pall-RZ58	HZ	10.4	0.935
Kgwt4	4	RG190-RG908	HZ	13.928	-1.163
Kgwt10	10	G2155-RG134	HZ	16.792	-1.372

^aQTLs are named by traits abbreviations and chromosome number Tg: total grain, Fr: fertility rate, Fg: full grain, Pt: Prod. Tiller, Kgwt: kilogram weight

^b The environments in which a QTL was detected (HN) Hainan, (HZ) Hangzhou