

Quantitative trait loci for seedling vigor in rice under field conditions

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Abstract

Previous QTL studies on seedling vigor in rice (*Oryza sativa* L.) were conducted all based on laboratory germination tests. In the current study, a set of recombinant inbred lines derived from a rice cross were assessed for seedling vigor related traits in natural field environments including two treatments (drained soil and flooded soil). Composite interval mapping identified nine QTL for seedling vigor traits that correlated positively with each other. Individual QTL explained 4–14% of the total trait variation. Among the QTL, three and four were specific to the drained and flooded treatments, respectively, while two others were common between the two treatments. Four QTL (*qFV-1-1*, *qFV-3-2*, *qFV-5-1* and *qFV-10*) each simultaneously showed effect on two or more traits with additive effects always in the same direction. The QTL *qFV-5-1* could be further resolved into at least two linked loci, *qFV-5-1a* controlling seedling height and *qFV-5-1b* controlling seedling dry weight while the QTL *qFV-10* could be a single locus with a pleiotropic effect on both seedling height and dry weight. The QTL *qFV-1-1* and *qFV-3-2* expressed specially under the flooded conditions, each pleiotropically controlling both coleoptile and seedling emergence. These two QTL were completely different from that affecting seedling emergence in the drained conditions. Comparison of the QTL indicated that the QTL mapping results based on field assessments could to some extent coincide with those based on lab tests but the discrepancy between the two kinds of experiments could not be overlooked.

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1. Introduction

In cropping practice of rice (*Oryza sativa* L.), many farmers particularly in the tropics are shifting from transplanting to direct sowing because the latter is less labor-intensive (Erguiza et al., 1990). For such cropping system, vigorous modern rice cultivars are increasingly required, which would not only facilitate rapid seedling establishment under a wide range of field conditions but also increase competitive ability against field weeds. Genetic improvement is one of the most efficient approaches to obtain rice cultivars with enhanced seedling vigor. For example, in the southern USA where much of rice is drill-seeded, breeders have developed semidwarf California rice breeding lines with good levels of seedling vigor and semidwarf rice germplasm with long coleoptiles and mesocotyles which promote seedling emergence (McKenzie et al.,

1994). Despite of this, however, difficulty has been experienced in achieving a high level of seedling vigor in modern semidwarf cultivars in California by conventional selection strategies due to the low heritability estimates obtained for seedling vigor traits (McKenzie et al., 1994).

As chromosomal regions or QTL (quantitative trait loci) underlying the expression of agriculturally important traits in many crop species have been identified, marker-assisted selection (MAS) has been suggested as a breeding strategy to introgress a limited number of QTL into elite germplasm (Dudley, 1993). This strategy can minimize linkage drag while expediting the transfer of targeted chromosomal segments from exotic germplasm into desired backgrounds (Hospital and Charcosset, 1997). In contrast to monogenic traits, however, breeders are cautiously optimistic about the advantages of MAS for polygenic traits because of the skepticism that the expression of most QTL is sensitive to environmental conditions (Yousef and Juvik, 2002).

For seedling vigor in rice, several studies have reported the identification of a few QTL (Redoña and Mackill, 1996b; Cui

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et al., 2002a,b; Zhang et al., 2005a). Some of these studies have even demonstrated the involvement of genotype \times environment interactions in the expression of seedling vigor traits (Redoña and Mackill, 1996b; Zhang et al., 2005a). Due to the large environmental effects, it is usually difficult to measure seedling vigor in the field. Therefore, the above studies were all conducted based on laboratory germination tests. Although some researchers have found that seedling vigor evaluated in controlled laboratory tests correlates well with field performance in many crop species (McKenzie et al., 1980; Sthapit and Witsombe, 1998), inconsistencies and difficulties with the prediction of field performance have also been reported (Kolasinska et al., 2000; Clark et al., 2002; Cisse and Ejeta, 2003). Therefore, if possible, the QTL identified for seedling vigor should be validated under field conditions prior to applied utilization in marker-facilitated breeding programs.

In the current study, with a set of recombinant inbred lines (RILs) derived from a *japonica/indica* cross, mapping of QTL for seedling vigor in rice was conducted based on field measurements. The major objective was to evaluate the consistency of the field results presented here with those previously reported based on laboratory tests, especially those reported by Zhang et al. (2005a) with the same set of RILs used in the current study.

2. Materials and methods

2.1. Rice RIL population

A set of 282 F₁₃ RILs, derived from a cross between Lemont (a *japonica* cultivar) and Teqing (an *indica* cultivar) via single-seed descent, was used in the current study. All plants of the RILs and the two parental lines were planted in the rice-cropping season in Wuhan, China and the seeds harvested at maturation were stored at a temperature lower than 10 °C for use. Prior to field trial, a sample of seeds of the two parents was used to test the germinability at 32 °C and a germination rate of 99.5% at 5 days after incubation was observed, indicating this set of seeds viable and thus suitable for study on seedling vigor.

2.2. Field assessment of seedling vigor related traits

Field assessment of seedling vigor related traits was conducted in the paddy field from July to August of 2004 in Wuhan, China. In order to minimize environmental error, a paper-plate method was newly developed. For each RIL, 40 manually selected filled grains were first treated at 50 °C for 5 days to eliminate residual dormancy, and then surface-sterilized with 0.6% sodium hypochlorite solution for 15 min, rinsed three times with distilled water, pre-germinated by soaking in distilled water at 30 °C for 36 h. The pre-germinated seeds for each RIL were placed equidistantly in a five-row plot in water saturated blotter paper in size of 15 cm \times 20 cm and then covered by 2 layers of soft paper. The soft paper could immediately adhere to the blotter paper to form a so-called paper-plate in which seeds were fixed between the papers. The paper plates of all the RILs and the parental lines were placed

on fine prepared field surface in a randomized complete block with two replicates (the two parental lines were replicated five times in each replicate of the trial) and then covered with sieved dry soil (mesh 6) deep in 2 cm. Because shoots and roots of seedlings could easily penetrate through the papers in the field, the paper plates did not show any influence on seed germination and seedling establishment.

Water condition is one of the most important factors affecting seedling development and growth. Two water treatments (both in two replicates) were therefore designed: (a) drained soil treatment in which water in the drainage ditch circled the seeded bed was maintained 2 cm below the soil surface of the seeded bed and (b) flooded soil treatment in which the 2-cm water depth above the field surface was introduced immediately after completing seeding and was maintained throughout the experimental period. To maintain the water level, water was continuously supplied and the excess water was allowed to overflow.

In the drained treatment, seedling emergence (1st leaf emerged from soil surface) was recorded twice a day at 6:00–7:00 h and 17:00–18:00 h, respectively, at 3–5 days after sowing (DAS). It was expressed as a percentage relative to the number of the sown seeds. According to the frequency distribution of the data, only the data collected at 6:00–7:00 h of 4 DAS showing an approximately normal distribution was further analyzed in the current report. At 7 DAS, 10 seedlings for each RIL were randomly sampled and their seedling heights (from first node to the end of the uppermost leaf, cm) were measured. Following the attached residual seed grains being removed, the seedlings were washed and dried in an oven for 2 days at 70 °C. Seedling dry weight was measured and expressed as mg per seedling.

In the flooded treatment, coleoptile was emerged ahead of the 1st green leaf and therefore coleoptile emergence (coleoptile emerged from soil surface) was firstly recorded twice a day at 6:00–7:00 h and 17:00–18:00 h, respectively, at 3 and 4 DAS. It was expressed as a percentage relative to the number of sown seeds. Seedling emergence was recorded at 6–8 DAS, also twice a day at 6:00–7:00 h and 17:00–18:00 h, respectively. Similar to that in the drained treatment, only the data showing normal distributions (coleoptile emergence at 6:00–7:00 h of 4 DAS and seedling emergence at 17:00–18:00 h of 7 DAS) were further analyzed. At 9 DAS, seedling samples were collected and seedling height and dry weight for each RIL were measured as described in the drained treatment.

2.3. Genotyping of DNA markers and construction of the linkage map

Genotyping of DNA markers (including RFLP and microsatellite markers) was performed and a complete linkage map was constructed as earlier described by Zhang et al. (2005b). The resultant map consists of 198 marker loci including 91 RFLP loci, 106 microsatellite loci, and a single gene locus (*gl-1*), covering all 12 rice chromosomes and spanning 1980.1 cM (Kosambi function) with an average interval of 10.7 cM between markers.

Table 1
Phenotypic analysis of seedling vigor related traits in rice investigated under field conditions

Treatments	Traits ^a	Lemont	Teqing	RIL population			
				Mean ± S.D.	Range	Skewness	Kurtosis
Drained soil	Seedling emergence	46.6	56.8**	40.3 ± 17.2	0–85.0	0.170	–0.633
	Seedling height	7.89	11.93**	8.97 ± 1.50	5.40–14.24	0.464	0.308
	Seedling dry weight	4.63	7.55**	5.38 ± 1.20	2.55–9.15	0.303	0.222
Flooded soil	Coleoptile emergence	62.5	80.8**	46.7 ± 23.0	0–95.0	0.003	–0.883
	Seedling emergence	51.7	85.0**	44.6 ± 23.0	2.5–95.0	0.090	–0.976
	Seedling height	7.25	10.94**	8.27 ± 1.83	3.89–14.62	0.657	0.868
	Seedling dry weight	3.37	5.63**	4.17 ± 1.34	1.50–9.40	0.612	0.901

**indicates differences between the two parents significant at a level of $p < 0.01$.

^a Trait values in the drained treatment cannot be directly compared to the same trait in the flooded treatment because of different incubation durations in both the treatments.

2.4. Data analyses and QTL mapping

The trait data averaged over two replications were used for following analyses. The basic statistics and Pearson phenotypic correlations among the traits were calculated by SAS PROC CORR (SAS Institute, 1996). Differences among the RILs and between the two parents were tested by variance analyses using SAS PROC GLM (SAS Institute, 1996). Main-effect QTL for all the traits assessed were mapped via composite interval mapping by controlling both main and epistatic effects of important markers with the computer program QTLMapper 1.0 based on mixed linear models (Wang et al., 1999). A threshold of LOD score 2.0 was used to declare the significance of a QTL. Such a lower LOD threshold was used since a higher threshold may underestimate putative QTL and show a bias towards genes with larger phenotypic effects (Yano and Sasaki, 1997). Meanwhile, the genetic parameters (effects and test statistics) associated with the QTL were estimated at the positions of respective LOD peaks in individual putative QTL regions. QTL were designated according to the guidelines proposed by McCouch et al. (1997).

3. Results

3.1. Phenotypic analyses

Variance analyses revealed significant differences ($p < 0.01$) between the two parental lines in all the seedling vigor related traits assessed in the current study (Table 1). The

parent Teqing was superior to the parent Lemont in all the traits. It could be therefore expected that the RIL population derived from the cross between the two parents would be suitable for mapping of the QTL for seedling vigor related traits.

In the RIL population, significant differences among the RILs were also revealed by analysis of variance ($p < 0.0001$). Continuous trait variation and obvious transgressive segregations in both high and low directions of the trait values were observed for all the traits. These results implied that both of the parents could possess positive genes at different loci for the traits and more superior genotypes could be obtained from recombination of the positive genes possessed by the two parents.

3.2. Correlation analyses

In the RIL population, all the seedling vigor related traits significantly and positively correlated with each other (Table 2). In the drained treatment, correlation coefficients among the three traits assessed were up to 0.66–0.80 ($p < 0.001$) with the highest correlation coefficient of 0.80 between seedling height and dry weight. In the flooded treatment, the four traits investigated were also highly associated with correlation coefficients of 0.56–0.95 ($p < 0.001$). Of these, the correlation between coleoptile emergence and seedling emergence was up to 0.95. Excepting this, the highest association also occurred between seedling height and dry weight, the same as that in the drained treatment. These results thus suggested that the multiple traits investigated in the current study could be used to comprehensively assess the field performance of seedling

Table 2
Correlation analysis of the seedling vigor related traits in rice investigated under field conditions

Treatments	Traits	1 ^a	2	3	4	5	6	7
Drained soil	1. Seedling emergence							
	2. Seedling height	0.72**						
	3. Seedling dry weight	0.66**	0.80**					
Flooded soil	4. Coleoptile emergence	0.25**	0.14*	0.25**				
	5. Seedling emergence	0.33**	0.20**	0.27**	0.95**			
	6. Seedling height	0.43**	0.50**	0.46**	0.56**	0.62**		
	7. Seedling dry weight	0.36**	0.38**	0.47**	0.65**	0.68**	0.84**	

* and ** indicate significant at the levels of $p < 0.05$ and $p < 0.01$, respectively.

^a The numbers 1–7 denote the traits as showed in the trait column.

Table 3
Putative QTL for seedling vigor related traits in rice investigated under field conditions

QTL ^a	Chromosome	Marker intervals	Drained soil treatment				Flooded soil treatment			
			Traits ^b	LOD	A ^c	R ^{2d}	Traits	LOD	A	R ²
<i>qFV-1-1</i>	1	RG140–RM259					CE	2.32	3.50	4.2
<i>qFV-1-2</i>	1	CDO118–RG462					SE	2.07	3.75	3.5
<i>qFV-2</i>	2	RG555–OSR17	SH	3.45	0.325	5.8	SH	2.32	3.59	4.0
<i>qFV-3-1</i>	3	RG341b–RM218	SH	3.79	−0.326	5.8				
<i>qFV-3-2</i>	3	OSR31–RM168					CE	4.94	4.73	7.8
<i>qFV-3-3</i>	3	RM148–RM85	SE	2.18	−3.365	5.7	SE	3.94	5.09	6.5
<i>qFV-5-1</i>	5	RM13–N10150–Y1049	SE	3.92	−3.739	7.0	SH	3.31	−4.747	7.1
			SH	1.92 ^e	−0.239		DW	5.81	−0.438	12.8
			DW	5.58	−3.754	11.6				
<i>qFV-5-2</i>	5	RM161–CDSR49	SH	8.76	−0.506	14.0				
<i>qFV-10</i>	10	C223–RM228	SH	6.91	−0.422	9.8	SH	4.35	−4.731	7.0
			DW	4.99	−3.122	8.0				

^a “FV” in QTL designations was abbreviated from “field vigor”.

^b CE, SE, SH and DW indicate coleoptile emergence, seedling emergence, seedling height and dry weight, respectively.

^c The additive effect is the effect associated with substitution of a Teqing allele by the corresponding Lemont allele.

^d The variance explained by individual QTL.

^e QTL *qFV-5-1* was detected to show an effect on seedling height (SH) in the drained treatment with a LOD score below the threshold of LOD 2.0.

vigor in rice. On the other hand, these correlations implied a genetic basis shared by the multiple seedling vigor related traits, especially between coleoptile emergence and seedling emergence under the flooded conditions, and also between seedling height and dry weight in both the treatments.

Comparatively, correlations of the traits in the drained treatment to the traits in the flooded treatment were greatly reduced to 0.14–0.50 ($p < 0.05$ –0.001; Table 2), which implied presence of significant genotype × treatment interactions in expression of the traits.

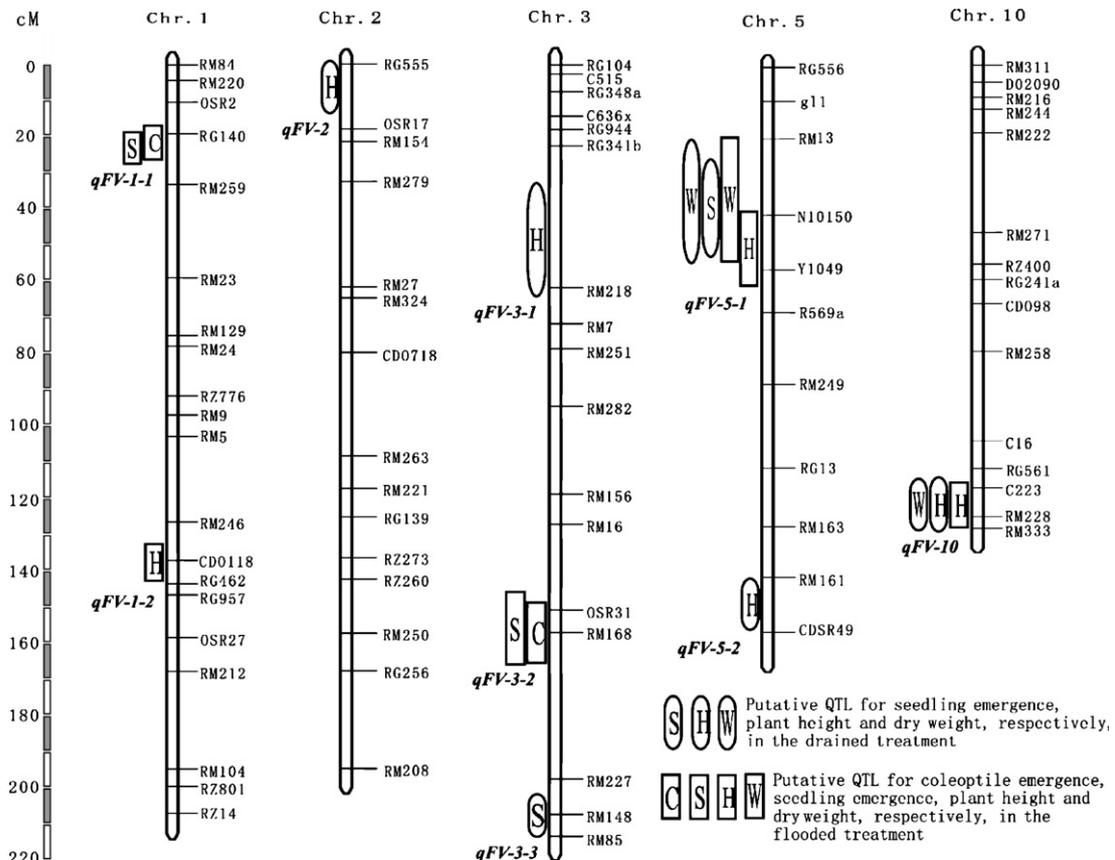


Fig. 1. Molecular genetic map showing locations of putative QTL for seedling vigor related traits in rice investigated under field conditions.

3.3. Mapping of QTL for seedling vigor related traits

Due to all the seedling vigor related traits investigated in the current study positively correlated with each other, when the QTL for multiple traits are mapped onto approximately a same interval and produce effects in the same direction, these QTL could be tentatively assumed to be one QTL associated with seedling vigor.

Totally, nine QTL for the seedling vigor related traits were identified in both the drained and flooded treatments (Table 3 and Fig. 1). These QTL were located to chromosomes 1, 2, 3, 5 and 10, respectively. Individual QTL explained only 4–14% of the total trait variation. Among the QTL, three (*qFV-1-1*, *qFV-1-2* and *qFV-3-2*) were detected in only the flooded treatment while the other four (*qFV-2*, *qFV-3-1*, *qFV-3-3* and *qFV-5-2*) in only the drained treatment. Two other QTL (*qFV-5-1* and *qFV-10*) were common between the two treatments. Of the nine QTL, four (*qFV-1-1*, *qFV-1-2*, *qFV-2* and *qFV-3-2*) possessed positive alleles came from the parent Lemont while the others from the parent Teqing, which provided a plausible explanation for the transgressive segregation of all the traits in the RIL population.

3.4. QTL with pleiotropic effects on the seedling vigor related traits

There were four QTL (*qFV-1-1*, *qFV-3-2*, *qFV-5-1* and *qFV-10*), each simultaneously showing effect on two or more traits with the additive effects always in the same direction irrespective of the treatment conditions. This result was in accordance with the positive correlations among the traits. For each of the QTL, comparing the LOD peak location and LOD curve shape for one trait with that for another trait could to

some extent address whether a single locus shows a pleiotropic effect on the traits or a group of tightly linked loci each produces an independent effect on a single trait.

The QTL *qFV-1-1* and *qFV-3-2*, the former located within the interval RG140–RM259 on chromosome 1 and the later within the interval OSR31–RM168 on chromosome 3, each expressed additive effects on both coleoptile and seedling emergence in the flooded treatment (Table 3 and Fig. 1). The positive alleles at the two QTL were all brought by the parent Lemont. For each of the two QTL, both the LOD peak location and LOD curve shape for coleoptile emergence were quite similar to that for seedling emergence (Fig. 2a and b). In combination with the strong correlation between the two traits in the flooded treatment, it was inferred that a single locus at each of the two QTL could simultaneously control both coleoptile and seedling emergence in the flooded conditions.

The QTL *qFV-5-1*, mapped onto the interval RM13–N10150–Y1049 on chromosome 5, was found to show effects on multiple traits, including seedling emergence in the drained treatment, seedling height and dry weight in both the treatments (Table 3 and Fig. 1). For all the traits, the positive genotype came from the parent Teqing. Comparison of the LOD peak locations and LOD curve shapes of the QTL for the above different traits (Fig. 3a) led to a suggestion that within the *qFV-5-1*-containing region, there could be at least two tightly linked loci, one (designated as *qFV-5-1a*) showing a pleiotropic effect on seedling dry weight in the two treatments and seedling emergence in the drained treatment, and the other (designated as *qFV-5-1b*) affecting seedling height in the two treatments (the LOD score was 1.92 in the drained treatment).

The QTL *qFV-10*, mapped onto the interval C223–RM228 on chromosome 10, simultaneously produced effects on seedling height in the two treatments and seedling dry weight

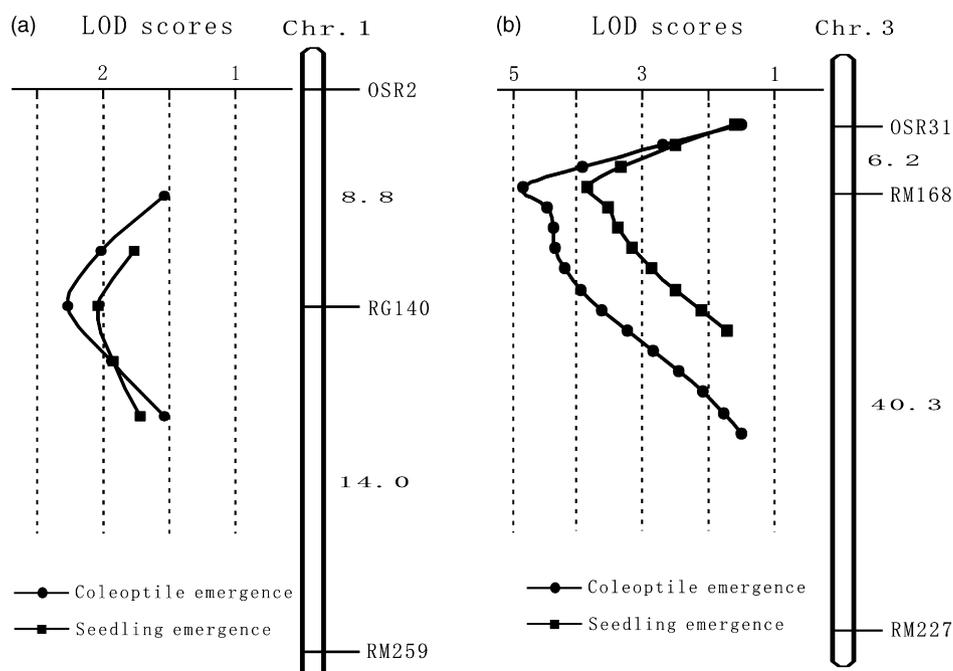


Fig. 2. LOD plots for the QTL *qFV-1-1* (a) and *qFV-3-2* (b) on chromosomes 1 and 3, respectively.

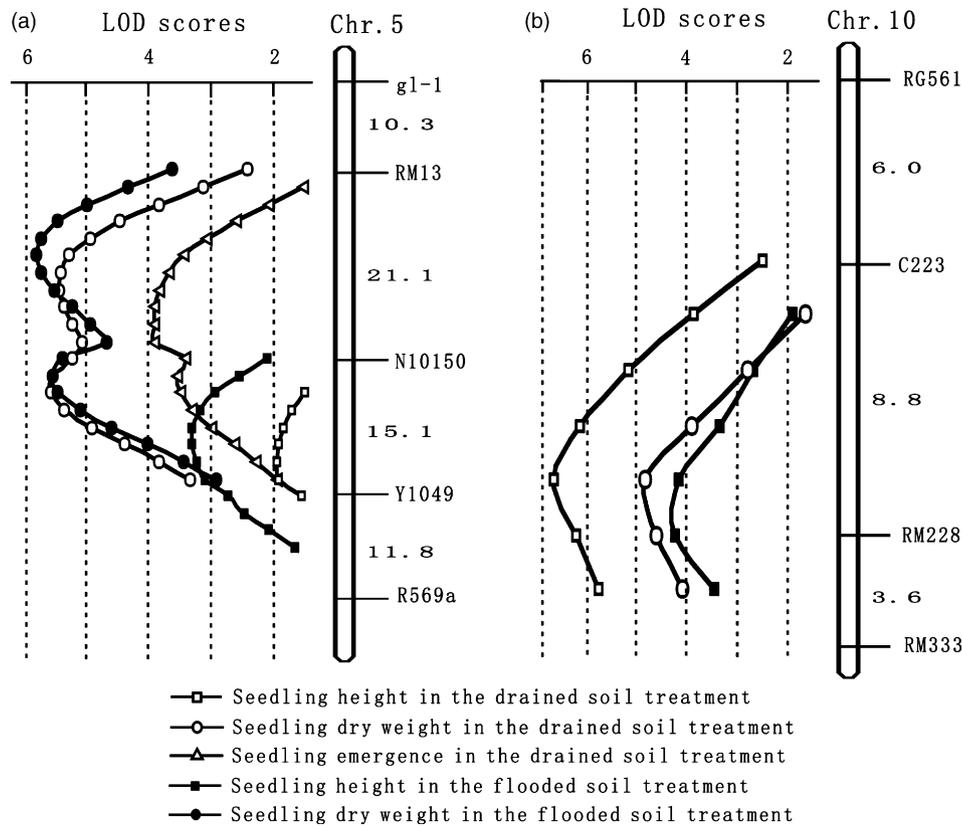


Fig. 3. LOD plots for the QTL *qFV-5-1* (a) and *qFV-10* (b) on chromosomes 5 and 10, respectively.

in the drained treatment (Table 3 and Fig. 1). Also, the trait-increasing genotype came from the parent Teqing. The above two traits showed a very similar LOD peak location and approximately a same LOD curve shape (Fig. 3b). These results provided a support for a possibility that a single locus within the *qFV-10*-containing region could show a pleiotropic effect on both seedling height and dry weight.

Overall, the above analyses revealed that: (a) although the two QTL (*qFV-5-1* and *qFV-10*) simultaneously affected both seedling height and dry weight, it was likely that the QTL *qFV-5-1* could be further resolved into at least two linked loci, *qFV-5-1a* controlling seedling height and *qFV-5-1b* controlling seedling dry weight. In contrast, the QTL *qFV-10* could be a single locus with a pleiotropic effect on both seedling height and dry weight. (b) the QTL *qFV-1-1* and *qFV-3-2* expressed specially in the flooded conditions, each pleiotropically controlling both coleoptile and seedling emergence. These two QTL were completely different from the other two QTL (*qFV-3-3* and *qFV-5-1a*) that affected seedling emergence in the drained conditions.

4. Discussion

One of the most important considerations in studies of quantitative traits is to minimize environmental effects in trial. Generally, seedling vigor related traits in plant crops like rice are quantitatively inherited (Redoña and Mackill, 1996a; Zhang et al., 2005b). Due to the difficulty in the control of field environmental effects, especially with a population of large

sample such as in the current study, previous QTL studies on rice seedling vigor were all based on laboratory tests under controlled conditions, none based on measurements under field environments,

In the current study, a paper-plate method for evaluation of seedling vigor under field conditions has been developed. The success of the paper-plate method in minimizing field experimental effects is primarily due to the following advantages: (a) Allowing seeds to be well-distributed, which is one of the most important factors involved in the control of field experimental effects. In addition, the sowing density can be tuned as it is designed. (b) Making all the sown seeds at an identical depth below the soil surface due to the fixation of the paper-plates, thus resulting in the consistency in water condition and emergence pressure for all the seeds investigated. (c) Making of the paper-plates is in the room instead of in the field outside, which greatly produces labor intensity and shortens the whole sowing time in field experiments.

4.1. Consistency of the QTL for seedling vigor across environments

Previous studies have found that the seedling vigor related traits tended to be positively correlated when they were investigated under a same environment (Yamauchi and Winn, 1996; Redoña and Mackill, 1996a; Zhang et al., 2005a). Similarly, the current study also observed that all the seedling vigor related traits correlated positively with $r=0.66\text{--}0.80$

($p < 0.001$) in the drained soil treatment and $r = 0.56–0.95$ ($p < 0.001$) in the flooded soil condition. In contrast, however, the correlations of the traits in the drained treatment with the traits under the flooded soil condition greatly reduced to 0.5 or less than 0.5. QTL mapping further found that, of the nine QTL identified, three and four QTL were specific to the drained and flooded treatments, respectively, while only two (*qFV-5-1* and *qFV-10*) were common between the two treatments. These results seemed to indicate that some of the genetic factors controlling seedling vigor expressed consistently while the others showed significant genotype \times environment interactions. In fact, several earlier studies have reported the involvement of genotype \times environment interaction in seedling vigor of rice (Redoña and Mackill, 1996b; Zhang et al., 2005a). Through a comparative analysis of seedling vigor QTL identified under different lab temperature conditions in rice, Zhang et al. (2005a) have proposed that significant genotype \times environment interactions for seedling vigor appear to be QTL-specific and some of the QTL do show almost consistent effects across multiple environments. The current study also provided a support to the proposal.

4.2. Identification of QTL for rice seedling emergence specific to flooded environment

The morphogenesis of rice seedling in flooded soil is quite different from that in drained conditions and the differences among rice cultivars existed in seedling establishment in flooded soil (Yamauchi and Biswas, 1997; Yamauchi et al., 1993). Submergence in water has been reported to significantly promote coleoptile elongation (Hoson et al., 1993). Coleoptile emergence above water allows translocation of oxygen and subsequent radical and primary leaf growth (Takahashi, 1978). Thus, coleoptile emerged in advance of 1st leaf in flooded soil in all cultivars (Yamauchi and Biswas, 1997). In contrast, in drained soil, coleoptile and 1st leaf generally emerge simultaneously from soil surface and coleoptile tends to cease elongation when it reaches soil surface (Yamauchi and Biswas, 1997). In the current study, such difference in seedling morphogenesis between the drained and flooded soil environments was also observed. In the flooded treatment, coleoptile emergence was highly correlated with seedling emergence ($r = 0.95$, $p < 0.001$). QTL mapping identified two QTL (*qFV-1-1* and *qFV-3-2*), each simultaneously affecting coleoptile emergence and seedling emergence in the flooded soil and the two QTL were completely different from the other two QTL showing effects on seedling emergence in the drained soil. Further analyses revealed that, at each of the two QTL (*qFV-1-1* and *qFV-3-2*), there could be a single locus to express a pleiotropic effect on both coleoptile emergence and seedling emergence. The Lemont alleles at the two QTL promoted emergence of both coleoptile and seedling. These results suggested that coleoptile emergence and seedling emergence under flooded soil condition could possess a common genetic basis that might be quite different from that in drained soil environment.

4.3. Comparison of the seedling vigor QTL identified under field conditions with those previously reported by laboratory tests

With the same set of the RILs used in the current study, Zhang et al. (2005a) have reported the identification of seedling vigor QTL under different laboratory temperature conditions, which makes it possible to compare the seedling vigor QTL identified here under field environment with those detected under controlled laboratory conditions. Through such a comparison, it was found that the four QTL (*qFV-3-2* and *qFV-3-3* on chromosome 3, *qFV-5-1* and *qFV-5-2* on chromosome 5) identified under the field environments were also detected under the controlled lab conditions. Although so, however, discrepancy between the field assessments and the lab tests was also found. For example, two QTL (*qFV-1-1* on chromosome 1 and *qFV-10* on chromosome 10) were detected only in the current field study while the other two QTL (*qSV-8-1* and *qSV-8-2* on chromosome 8) appeared to be specific to the lab tests (Zhang et al., 2005a).

Similarly, using another set of RILs in rice, Cui et al. (2002a) identified several seedling vigor QTL under controlled lab conditions. Among these QTL, some (such as QTL marked by markers RG532 and C86, respectively, on chromosome 1, QTL marked by marker RZ403 on chromosome 3) were also detected to show effects under greenhouse environment (Cui et al., 2002b). On the other hand, there were some other QTL specific to lab tests (e.g., a major QTL within the *Waxy*-containing region on chromosome 6) (Cui et al., 2002a) or greenhouse experiment (e.g., QTL marked by C223 on chromosome 10) (Cui et al., 2002b).

The above comparisons seemed to suggest that, for seedling vigor in rice, the QTL mapping results based on lab tests could to some extent coincide with those based on field assessments but the discrepancy between the two kinds of experiments could not be overlooked. Essentially, the above discrepancy was mainly resulted from the differences in experimental conditions. Because the purpose of lab tests is to predict field performance and the climate conditions in the natural field are usually complex and changeable, it is needed to be considered in lab tests that the treatment conditions should be based on a special breeding program oriented toward the target rice cropping areas and, on the other hand, multi-environment testing for the major factors that have significance to seedling vigor, such as temperature and water, would be required, so that the environmental conditions in lab tests could be as close to that in the target field environments as possible.

4.4. Application of the seedling vigor QTL for MAS in rice breeding programs

One of major objectives of QTL mapping is to identify QTL for agriculturally important traits and then put the QTL into application in breeding programs by MAS. Generally, the feasibility of using MAS in breeding programs is dependent on the reproducibility of marker-QTL associations across generations, populations, and environments (Dudley, 1993; Yousef and Juvik, 2002).

For seedling vigor in rice, the QTL *qFV-5-1* not only expressed in the two field treatments of the current study, but also showed effects on multiple seedling vigor related traits measured in the lab tests (Zhang et al., 2005a). Moreover, within the roughly same region on chromosome 5, Redoña and Mackill (1996b) and Cui et al. (2002a) also reported the identification of seedling vigor QTL with their quite different mapping populations although an exact comparison is somewhat difficult due to a lack of markers common between the different maps involved. Another seedling vigor QTL that expressed consistently across environments was *qFV-3-2* within the interval OSR31–RM168 on chromosome 3. This QTL functioned under both the field and lab conditions as described above. Meanwhile, it was also identified by Redoña and Mackill (1996b), Cui et al. (2002a,b) in their different experiments. Such QTL like *qFV-5-1* and *qFV-3-2* are thus noteworthy to be further characterized and used as potential target QTL in improvement of rice seedling vigor by MAS. In contrast to the above QTL, other seedling vigor QTL, such as *qFV-1-1* chromosome 1, appeared to express specially in flooded soil conditions to promote coleoptile and seedling emergence. Such QTL promises to be manipulated by MAS for improvement of rice seedling vigor oriented specially toward the cropping areas where germinated-seeds are directly sown in flooded soil (Yamauchi and Winn, 1996).

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