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QTL Analysis of Agronomic Traits in Rice Using SSR and AFLP Markers

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Abstract

A quantitative trait is a measurable trait that depends on the cumulative action of many genes and their interaction with the environment that can vary among individuals over a given range to produce a continuous distribution of phenotypes. The identification and mapping of QTLs for such traits has great significance for rice breeders. In this study, a genetic analysis of quantitative trait loci (QTLs) affecting 11 agronomical traits was performed using an F_2 population of a cross between two *Oryza sativa* ssp. indica type cultivars, 'Domsiah' and 'IR44', comprising 160 plants. A total of 22 QTLs were detected for 11 traits, including two for plant height (PH), one for full grain per panicle (FG), two for flag leaf width (FLW), three for 1000-grain weight (TGW), two for number of panicles per plant (NP), three for flag leaf length (FL), two for peduncle length (Pd), one for panicle exertion (PE), two for grain yield (GY), two for basal panicle length (BPL) and two for awn length (AL).

Keywords: AFLP, agronomical traits, quantitative trait loci, SSR

Introduction

The rapid progress in the development of polymorphic molecular markers has led to the intensive use of QTL mapping in genetic study for quantitative traits (Wang *et al.*, 2007).

In general, QTLs are identified by correlating genetic variation with trait variation; a significant correlation between genotype and phenotype suggests that DNA status helps determine trait expression (Grisel, 2000). The two general goals of QTL mapping in plants are to (a) increase the biological knowledge of the inheritance and genetic architecture of quantitative traits, both within a species and across related species, and (b) identify markers that can be used as indirect selection tools in breeding (Semagn, 2010).

Numerous genetic studies of quantitative traits have been done in a large number of plant species. With the advent of DNA molecular markers, QTL mapping has become a routine strategy for the discovery of genes involved in complex quantitative traits. Thousands of QTL have been mapped for important agronomical traits in rice (Xing *et al.*, 2008). Several researches have been made about the yield related QTLs. Wang *et al.* (2010) conducted a quantitative trait loci (QTL) analysis of 150 rice recombinant inbred lines (RILs) derived from a cross between two cultivars, *Oryza sativa* ssp. indica cv. '93-11' and *Oryza sativa* ssp. japonica cv. 'Nipponbare' and detected 49 QTL with phenotypic effect ranging from 3.2 to 46.0% for 14 agronomics traits. Five QTL of relatively large effect (14.6-46.0%) were located on small genomic regions, where strong candidate genes were found. Gomez *et al.* (2006) mapped QTLs linked to physio-morphological and plant production traits under drought stress in the field by evaluating 177 F_6 recombinant inbred (RI) lines of 'Bala' × 'Azucena' under rainfed conditions in the target environment (TE). A total of 24 QTLs were identified for various traits under stress, which individually explained 4.6 to 22.3% phenotypic variation. Bei-Bei *et al.* (2003) mapped quantitative trait loci (QTLs) for harvest index, biomass, grain yield, sink capacity and plant height using a DH population containing 81 DH lines from an indica-japonica cross of rice. A total of 21 significant main effect QTLs and 9 pairs of epistatic loci were detected. Of these, three detected QTLs for grain yield collectively accounted for 42% of the phenotypic variation with a LOD of 7110.

Materials and methods

Plant material and field evaluation

The plant material consisted of 160 F_2 individuals derived from a cross between two *Oryza sativa* ssp. indica type cultivars, 'Domsiah' ('DOM') and 'IR44' that differs in all agronomic traits. 'Domsiah' is an Iranian native variety with a long grain. It has a black spot on one end, which gives it the name. It is cultivated mainly in the Guilan province of Iran. 'Domsiah' is especially valued for its aroma (Singh *et al.*, 1996). This Aromatic variety is a high yielding variety too. 'IR44' is an improved rice from IRRI, dwarf and drought and cold resistant. The experiment was carried out in a randomized complete block design, with a spacing of 25×25 cm at the Rice Research Institute of Iran (Rasht). Observations on F_2 plants were taken at the time of flowering and harvesting and the mean values were used

for the QTL analysis. The total of 12 yield related traits were evaluated including full grain per panicle (FG), flag leaf width (FLW), 1000-grain weight (TGW), number of panicles per plant (NP), flag leaf length (FL), peduncle length (Pd), plant height (PH), panicle exertion (PE), total weight of panicle (TWP), grain yield (GY), basal panicle length (BPL) and awn length (AL).

SSR and AFLP analysis

Fresh leaves were used for DNA extraction according to CTAB method (Rogers *et al.*, 1988) with slightly modifications. In this study a set of 105 SSR markers were tested to find the polymorphic markers between the parents (McCouch *et al.*, 2002). The sequences of each of the primer pairs were downloaded from http://www.gramene.org/microsat/ssr.html. Among these, 51 polymorphic markers were chosen. These markers were distributed over all twelve rice chromosomes. PCR reaction was carried out in 10 μl reaction mixture containing 50 ng of template (Genomic DNA), 20 mM MgCl$_2$, 4 mM of dNTPs, 1U of Taq and 2 μM of each primer in 1x reaction buffer. The amplification reaction was performed in the Eppendorf Master cycler with an initial denaturation for 4 minute at 94°C, then 35 cycles: 40 seconds denaturation at 94°C; 40 seconds annealing at 52°C; 2 minute extension at 72°C. Final extension was carried out at 72°C for 5 minutes.

Seven polymorphic AFLP markers were used in this study too. These 7 primer combinations made 63 polymorphic bands. AFLP reactions were performed as described by Vos *et al.* (1995) using EcoRI and MseI primers without a selective base in pre-amplification and with three selective bases in amplification. For this purpose, genomic DNA was digested with a pair of restriction endonucleases (EcoR I and Mse I), and the combination of genomic DNA and restriction enzymes were incubated for 12 hours at 30°C. then double-stranded EcoR I (Eco) and Mse I (Mse) linkers were ligated to the restriction fragments. After that the pre-selective amplification, a subset of all the fragments was amplified, using primers that are complementary to the linker sequences. In the last step, the number of fragments was further reduced by a second round of PCR (selective amplification), in which the PCR primers had an additional three selective bases (Meudt and Clark, 2007). The PCR products were separated on denaturing 6% polyacrylamide gels and the bands were revealed using the silver-staining protocol (Panad *et al.*, 1996). The primers used for AFLP analysis are listed in Tab. 1.

Linkage map construction and QTL analysis

A linkage map was constructed using F$_2$ mapping algorithm with QTXb17 Mapmanager (Manly *et al.*, 2001; http://www.mapmanager.org), based on the segregation data of 51 SSR and 63 AFLP loci in the F$_2$ population. The related genomic distances (cM) were calculated from recombination values using the Kosambi mapping function (Kosambi, 1944). In order to mapping the QTLs, Composite interval mapping was conducted using QTL cartographer version 2.5 (Basten *et al.*, 1997). To determine empirical significance thresholds for declaring a QTL, 1000 permutations were done to calculate LOD thresholds for each trait at $p=0.05$ and $p=0.01$. Permutation testing (using QTL cartographer) indicated that a logarithm of the odds ratio (LOD) score of 2.5 is suitable threshold for this data.

Results

Correlation analysis

According to the results of Duncan's test, a highly significant difference in all traits ($p \le 0.05$), between the two parents Domsiah and IR44 were observed (Tab. 2, Fig 1). Tab. 3 also shows the phenotypic (above diagonal) and genotypic variation among the studied traits. All the studied traits had positive correlation with GY. PE had a negative correlation with BPL, FL, FLW, TGW and AL.

Tab. 1. AFLP primers used for QTL mapping

Primer	Sequence
MseI	5'-GATGAGTCCTGAGTAA-3'
EcoRI	5'-GTAGACTGCGTACCAATTC-3'
MseI adaptor	5'-GACGATGAGTCCTGAG-3'
MseI adaptor	3'-TACTCAGGACTCAT-5'
EcoRI adaptor	5'-CTCGTAGACTGCGTACC-3'
EcoRI adaptor	3'-CATCTGACGCATGGTTAA-5'
E32-M61	Eco-**AAC**+Mse**CTG**
E36-M42	Eco-**ACC**+Mse**AGT**
E39-M39	Eco-**AGA**+Mse**AGA**
E37-M61	Eco-**ACG**+Mse**CTG**
E40-M93	Eco-**AGC**+Mse**TTG**
E35-M90	Eco-**ACA**+Mse**TGT**

Tab. 2. Phenotypic value of parents and F$_2$ population of measured in rice

Trait name	'Domsiah'	'IR44'	F$_2$	T
	m± SD	m± SD	m± SD	m± SD
PH	110.43±11.2	128.22±6.074	132.36±12.063	-60.7**
BPL	25.85±1.87	30.34±2.64	27.30±2.95	-16.8**
PE	5.6±2.1	4.48±1.6	5.41±2.57	-4.30**
NP	31.71±1.73	29.3±3.2	37.39±2.31	-9.05**
Pd	35.6±5.6	40.68±4.6	37.39±7.97	-13.36**
FL	29.7±2.76	38.61±3.8	30.43±4.906	-10.98**
FLW	1±0.2	1.1±0.24	1.18±0.36	-0.8**
AL	3.1±0.87	2.1±0.36	2.98±0.68	0.9**
GY	50.56±4.1	65.43±4.3	55.51±5.098	-24.65**
FG	78.2±4.3	95.5±5.6	81.49±7.59	-45.50**
1000 seed weight	28.23±3.2	34.45±2.2	30.04±3.1	-14.47**

PH=plant height; BPL=basal panicle length; PE=panicle exertion; NP=number of panicles per plant; Pd=peduncle length; FL=flag leaf length; FLW=flag leaf width; AL=awn length; GY=grain yield; FG=full grain per panicle

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Tab. 3. Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficients among traits in the 160 F_2 rice individuals

Trait	PH	BPL	PE	NP	Pd	FL	FLW	AL	GY	FG	TGW
PH	1	0.441	0.160	0.234	0.382	0.230	0.150	-0.029	0.376	0.330	0.129
BPL	0.442	1	-0.045	0.090	0.204	0.464	0.079	0.084	0.309	0.318	0.175
PE	0.160	-0.046	1	0.044	0.047	-0.036	-0.086	-0.111	0.209	0.273	-0.035
NP	0.235	0.090	0.043	1	0.234	0.111	-0.049	-0.041	0.218	0.107	0.051
Pd	0.385	0.206	0.047	0.238	1	0.142	0.089	-0.031	0.124	0.074	0.004
FL	0.230	0.463	-0.036	0.111	0.143	1	0.199	0.097	0.253	0.160	0.088
FLW	0.179	0.103	-0.101	-0.051	0.102	0.240	1	0.047	0.029	-0.099	-0.069
AL	-0.030	0.085	-0.113	-0.041	-0.031	0.098	0.056	1	0.010	-0.008	-0.093
GY	0.383	0.314	0.208	0.223	0.127	0.257	0.034	0.005	1	0.720	0.152
FG	0.331	0.320	0.275	0.109	0.074	0.160	-0.119	-0.008	0.734	1	0.217
TGW	0.130	0.179	-0.034	0.050	0.002	0.090	-0.076	-0.093	0.160	0.220	1

PH=plant height; BPL=basal panicle length; PE=panicle exertion; NP=number of panicles per plant; Pd=peduncle length; FL=flag leaf length; FLW=flag leaf width; AL=awn length; GY=grain yield; FG=full grain per panicle; TGW=1000-grain weight

Tab. 4. Putative QTLs for agronomic traits in F_2 population derived from the cross of two rice varieties ('Domsiah' × 'IR44')

Trait	QTL[a]	Flanking markers	Chro	LOD[b]	a[c]	d[d]	d/|a|[e]	PEV[f]
PH	qPH-3	E35-M90-11-E37-M61-11	3	5.71	5.29	-3.52	-0.67	7.62
	qPH-12	E40-M93-2-E39-M39-9	12	3.41	3.53	-4.49	-1.27	2.04
BPL	qBPL-1	E40-M93-5-E36-M42-2	1	2.68	-1.88	0.08	0.04	14.09
	qBPL-11	E32-M62-2-E32-M62-7	11	4.05	1.56	-0.15	-0.09	11.04
FG	qFG-1	RM466-RM8097	1	2.96	5.83	-32.15	-5.51	13.5
PE	qPE-8	RM8264-RM5720	8	3.69	1.13	-1.88	-1.67	18.99
TGW	qGW-3	E40-M93-6-RM6832	3	2.64	5.44	-2.79	-0.51	8.4
	qGW-5	E40-M93-12-E37-M61-6	5	3.03	8.88	-9.31	-1.05	15.45
	qGW-6	RM7179-RM5371	6	5.23	11.12	-1.01	-0.09	28.82
GY	qGY-2	RM221-RM236	2	5.86	-0.57	3.37	5.91	11
	qGY-11	E40-M93-9-E36-M42-3	11	4.36	-0.70	-0.76	-1.09	7.1
Pd	qPd-6	RM7179-RM5371	6	3.06	3.80	0.46	0.12	12.77
	qPd-8	E32-M62-5-RM6208	8	3.01	-2.55	6.10	2.39	3.78
FL	qFL-4	RM261-RM 8212	4	4.40	0.55	-2.54	-4.59	0.04
	qFL-6	RM527-E39-M39-4	6	3.09	-1.17	18.39	15.66	0.23
	qFL-8	E35-M90-10-E32-M62-5	8	2.51	-4.20	4.42	1.05	11.28
FLW	qFLW-1	RM8094-RM466	1	7.30	0.70	6.04	8.66	12.26
	qFLW-2	RM1358-RM300	2	5.04	-0.53	3.14	5.94	10.18
NP	qNP-4	E39-M39-8-RM1359	4	2.97	1.90	-1.35	-0.71	13
	qNP-6	RM7179-RM5371	6	3.85	1.88	-0.98	-0.52	64
AL	qAL-3	E40-M93-6-RM6832	3	3.76	-1.24	1.38	1.12	19.36
	qAL-5	E37-M61-6-RM3148	5	2.99	-0.70	0.89	1.27	8.33

[a]QTLs are named by abbreviations plus chromosomal number; [b]Log10 likelihood; [c]Additive effect; [d]Dominance effect; [e]Degree of dominance; [f]Percentage of total phenotypic variance explained by the QTL

QTL mapping

A total of 23 QTLs were mapped for 11 agronomical traits using CIM. These QTLs were located on chromosomes 1, 2, 3, 4, 5, 6, 8, 11 and 12 (Tab. 4, Fig. 2). TWO QTLs were mapped for plant height. qPH-3 with LOD= 5.71, was identified on chromosome 3 at the position of 89.6 cM (between E35-M90-11 and E37-M61-11) and explained 7.62% of phenotypic variation. The allels from 'DOM' increased plant height for 5.29 cm. the second QTL was located on chromosome 12 at 56.2 cM (between E40-M93-2 and E39-M39-9). qPH-12 with LOD= 3.41 only explained 2.04% of phenotypic variation and had a minor effect on this trait. Like the previous QTL, the alleles from 'DOM' increased the plant height by 3.53 cm. Two QTLs were identified for panicle length. qPL-1 was located on chromosome 1 at 156.7 cM (between E40-M93-5 and E36-M42-2) and with LOD= 2.68 explained 14.09% of phenotypic variation. The allele from 'DOM' increased the PL negatively. The second QTL (qPL-11) with LOD= 4.05 was located on chromosome 11 at 62.4
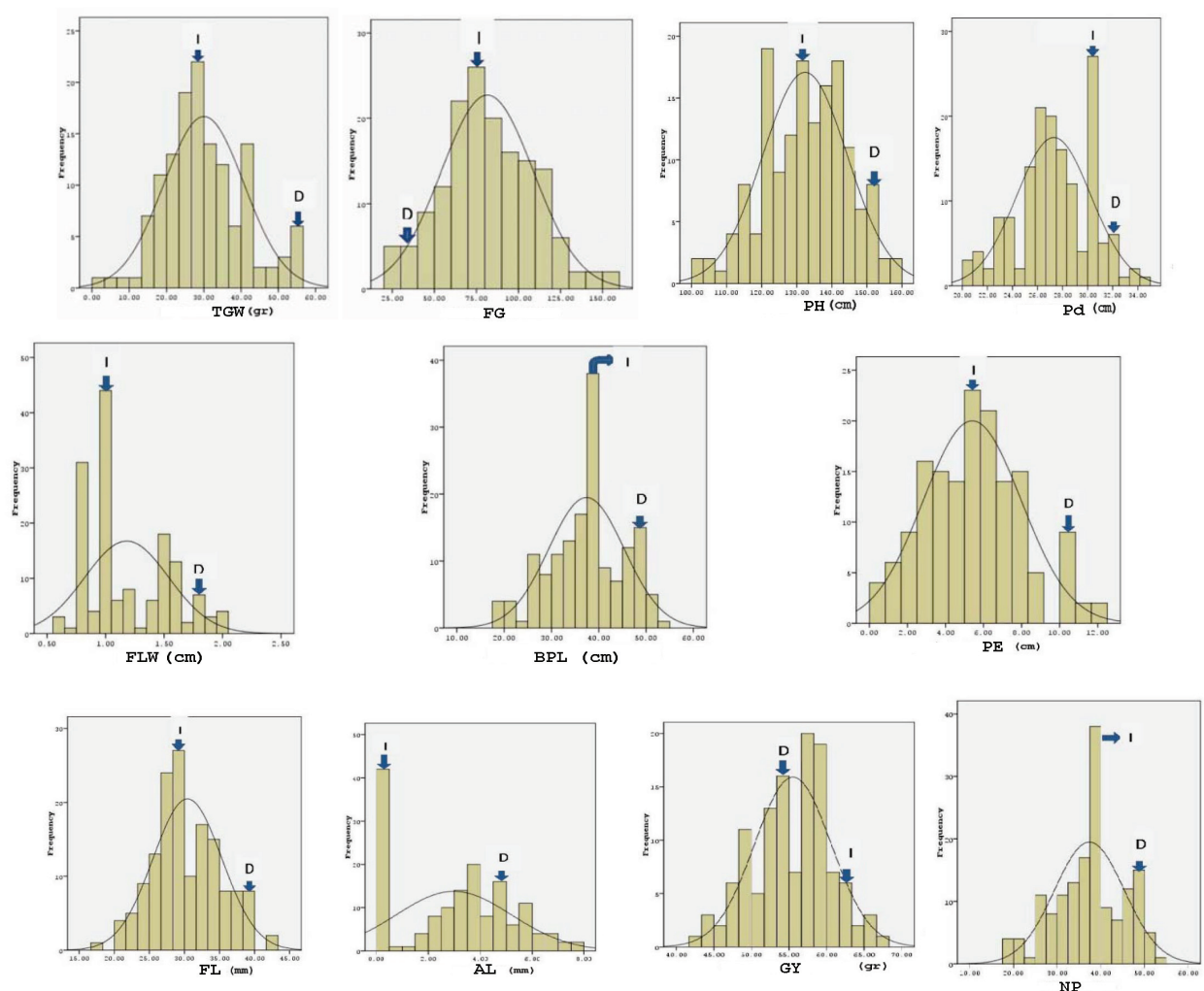
Fig. 1. Frequency distribution of the means of the 160 F$_2$ families for each trait. The parental means of 'IR44' and 'DOM' are indicated by arrows

cM (between E32-M62-2 and E32-M62-7) and explained 11.04% of phenotypic variation. The 'DOM' alleles increased the PL for 1.56 for this QTL. Both QTLs for this trait were main effect.

QTL of qPE-8 associated with panicle exertion was detected at chromosome 8 at the position of 37.3 cM (between RM8264 and RM5720) with LOD= 3.69. It contributed to 18.99% of variation and was contributed by 'DOM' with additive effect of 3.69 cm. Two QTLs were associated with number of panicles per plant (NP). The first QTL with LOD= 2.96 was located on chromosome 4 at 215.9 cM (between E39-M39-8 and RM1359) and explained 9.58% of phenotypic variation for this trait. The second QTL with LOD= 3.85 was located on chromosome 6 at 1.5 cM (between RM7179 and RM5371). For both QTLs, the alleles from 'DOM' increased the NP by 1.9 and 1.88 respectively. Two QTL were detected to be associated with peduncle length, qPd-6 and qPd-8. The qPd-6 located at 17.5 cM of chromosome 6 closely linked

to RM7179 contributing 12.77% of variation. The donor for the favorable allele was 'DOM' with the additive effect of 3.80 cm. The qPd-8 located at 159.1 cM of chromosome 8 between E32-M62-5 and RM6208. It was contributed by 'IR44' with the additive effect of 2.55 cm.

Two QTLs for flag leaf width were identified on chromosome 1 and 2. The QTLs qFW-1 and qFW-2 with a LOD scores of 7.30 and 5.04 showed the large effects on the FW and explaining 12.26 and 10.18% of the total phenotypic variance, respectively. In second QTL alleles from 'IR44' decreased FW by 0.53 mm, whereas, for the first QTL that was detected on chromosome 1, allele from 'DOM' increased FW by 0.70 mm. from SPD.

Three QTLs for FL were mapped on chromosomes 4, 6 and 8 respectively. qFL-4 with a LOD score 4.40 on chromosome 4 at 1.5 cM (between RM261 and RM 8212), showed the low effect on the FL. The second QTL (qFL-6) on chromosome 6 at 45 cM (tightly linked with RM527) also showed the low effect on the FL. Whereas qFL-8 on

Chr 1
- RM283
- RM8094
- RM466
- RM8097
- RM8144
- RM8231
- RM5310
- E40-M39-5
- E36-M42-2
- E35-M90-8
- E36-M42-9
- RM3148

Chr 2
- RM221
- RM236
- RM1358
- RM300
- RM5862
- RM262
- RM6318
- E35-M90-9
- E40-M93-11
- E39-M93-1
- RM6733

Chr 3
- RM7000
- RM3441
- RM5955
- E35-M90-11
- E37-M61-11
- E32-M62-6
- E35-M90-3
- E40-M93-6
- RM6832

Chr 4
- RM261
- RM8212
- RM5473
- E35-M90-5
- E37-M61-3
- E35-M90-1
- E32-M62-3
- E37-M61-10
- E39-M93-8
- RM1359

Chr 5
- RM305
- RM5140
- RM188
- RM480
- RM28
- RM335
- E40-M39-12
- E37-M61-6
- RM3345

Chr 6
- RM7179
- RM5371
- RM527
- E39-M93-4
- E37-M61-4
- E37-M61-2
- E35-M90-2
- E39-M39-2
- RM549

Chr 7
- RM420
- RM478
- RM427
- RM11
- E39-M39-5
- E36-M42-5
- E39-M39-3
- E36-M42-4
- E40-M39-8
- RM3608
- RM8006

Chr 8
- RM447
- RM8264
- RM5720
- RM7390
- E35-M90-6
- E35-M90-10
- E32-M62-5
- RM6208

Chr 9
- E35-M90-4
- E37-M61-7
- E40-M93-10
- E37-M61-1
- E36-M42-1
- E32-M62-4
- E37-M61-5
- E32-M62-1
- RM1553

Chr 10
- E39-M39-7
- E40-M93-1
- E40-M93-4
- E40-M93-3
- E32-M62-8
- E40-M93-7
- E36-M42-8
- RM6732

Chr 11
- E37-M61-9
- E39-M39-11
- E32-M62-2
- E32-M62-7
- E37-M61-8
- E40-M93-9
- E36-M42-3
- E35-M90-7
- E36-M42-7
- RM2334

Chr 12
- RM101
- E40-M93-2
- E39-M39-9
- E39-M39-6
- E35-M90-12
- E36-M42-6
- E39-M39-10
- RM7200

Legend:
- PH
- BPL
- PE
- NP
- Pd
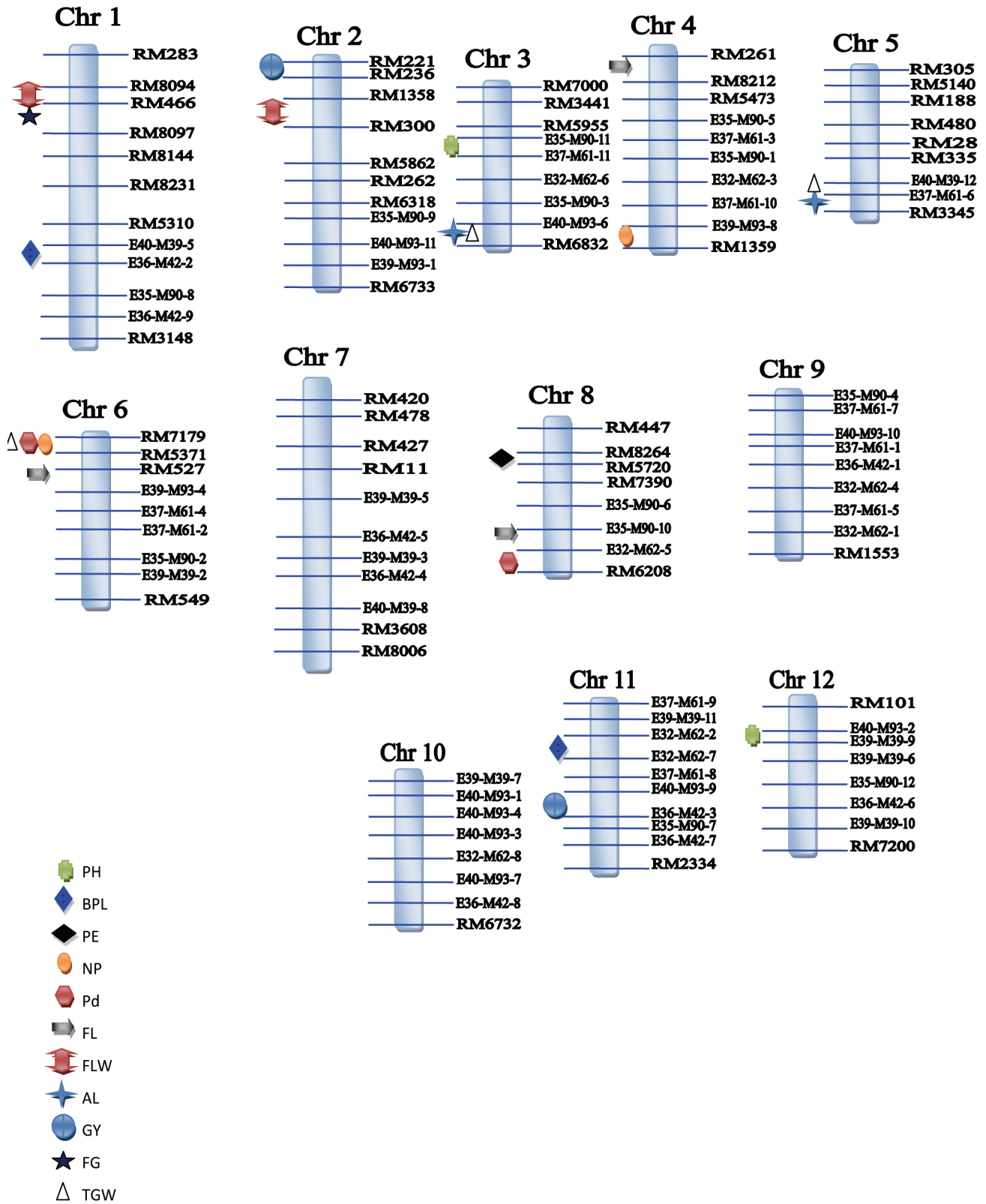- FL
- FLW
- AL
- GY
- FG
- TGW

Fig. 2. QTLs that were mapped for: full grain per panicle (FG), flag leaf width (FLW), 1000-grain weight (TGW), number of panicles per plant (NP), flag leaf length (FL), peduncle length (Pd), plant height (PH), panicle exertion (PE), grain yield (GY), basal panicle length (BPL) and awn length (AL)

chromosome 8 at 144.3 cM (between E35-M90-10 and E32-M62-5) explained 11.28% of the total phenotypic variance. Two QTLs alleles out of all detected QTLs were from 'IR44' and decreased FL. Two QTLs were mapped for AL. the first QTL on chromosome 3 at 207.2 cM (between E40-M93-6 and RM6832) had major effect on this QTL and explained 19.36% of phenotypic variance. The second QTL was mapped on chromosome 5 at 210.1 cM (between E37-M61-6 and RM3148). qAL-5 with LOD score of 2.99, explained 8.33% of phenotypic variance. For both QTLs, alleles from 'IR44' decreased AL by 1.24 and 0.7 mm respectively.

For grain yield, two QTLs were mapped. qGY-2 with LOD= 5.86 on chromosome 2 at 1.5 cM (between RM221 and RM236) explained 19.36% of phenotypic variance for this trait. The alleles from 'DOM' decreased the grain yield by 0.57 gr. The second QTL, qGY-11 at 145.9 cM (between E40-M93-9 and E36-M42-3) on chromosome 12 explained 8.33% of phenotypic variance and had decreasing allele from 'DOM' for grain yield. One QTL was identified for FG. The related QTL was on chromosome 1 at 59.7 cM (between RM466 and RM8097). The alleles from 'IR44' increased the healthy grains by 5.83. Finally three QTLs were identified for 1000 grain weight. These QTLs were mapped on chromosomes 3, 5 and 6 respectively.

qGW-3 was the minor effect QTL for this trait. This QTL with LOD= 2.64 on chromosome 3 at 194.7 cM (between E40-M93-6 and RM6832) only explained 8.5% of phenotypic variance. 'DOM' alleles increased GW for this QTL. The second QTL (qGW-5) on chromosome 5 at 168.8 cM (between E40-M93-12 and E37-M61-6) with LOD= 3.03, explained 15.45% of phenotypic variance. The last QTL was mapped on chromosome 6. This QTL (qGW-6) at 8.5 cM (between RM7179 and RM5371) explained 28.82% of phenotypic variance and was introduced as a major QTL for this trait. For the two last QTLs, alleles from 'DOM' increased the 1000 grain weight by 8.88 and 11.12 gr respectively. Currently, there are still large knowledge gaps on the molecular controls of the basic biological processes related to yield traits. This is especially the case for grain development. With the global development of functional genomic resources, many tools and genetic stocks have now become available for identifying genes underlying these processes (Xing and Zhong, 2010).

Discussion

Since the early 1990s, numerous studies have identified molecular markers linked to QTLs involved in the inheritance of agronomically important traits in a wide range of crop species. Following the discovery of promising QTLs and identification of molecular markers, MAS has been used to transfer single genes or QTL in various species. However, published results in QTL introgressions through MAS are variable, ranging from successful experiments to those with limited success and even a failure (Semagn, 2010). Yield is a complex trait governed by many loci, it is significant that some loci exert a much greater influence on yield. Single genes are known to enhance yield significantly (about 15 to 20% on per plant basis) as also shown in studies using transgenics. It is such genes or major effect QTLs that can be targeted for yield improvement. A combination of more than one major yield QTLs can be pooled together in a genotype for increasing yield (Swamy and Sarla, 2008).

In this study, 22 QTLs were mapped for 11 agronomical traits. These QTLs were distributed on chromosomes 1, 2, 3, 4, 5, 6, 8, 11 and 12. Chromosome 6 had the most QTLs (4 QTLs), and after that, chromosomes 1, 3 and 8 were in the second place (3 QTLs on each chromosomes). 2 QTLs were mapped for PH. The first QTL had partial Dominance effect and the second one had over dominance effect. Sabouri and Biabani (2009) mapped 2 QTLs for PH using an $F_{2:3}$ population derived from a cross between two indica type varieties, Tarommahalli and Khazar. The identified QTLs were mapped on chromosome 3 (2 QTLs). Their study showed that these QTLs have over dominance effect. Zhang *et al.* (2004) mapped QTLs for plant height on the same chromosomes. Two QTLs were mapped for panicle length. Both of them had partial dominance effect and had high effects on the related trait. Xiao *et al.* (1998) mapped QTLs for PL using BC_2 testcross population (V20A/O. *rufipogon*//V20B///V20B////Ce64) consisting of 300 families. They have found seven QTLs for this trait, which two of them were on chromosome 1. Those QTLs explained ~14% of phenotypic variation (same as present study). Sabouri *et al.* (2010) mapped 4 QTLs for panicle length using 236 $F_{2:3}$ families derived from the cross of two rice varieties (Gharib × Sepidroud). They found 1 QTL on chromosome 1 that explained 15.36% of phenotypic variation. Their QTL had over dominance effect.

One QTL was mapped for PE on chromosome 8. This major effect QTL explained 18.99% of phenotypic variance. Yue *et al.* (2008) mapped QTLs related to PE on the same chromosome. They found 1 QTL with LOD= 5.5 on chromosome 8 that explained 15.89% of phenotypic variation. Three QTLs were mapped on chromosomes 3, 5 and 8 respectively. qGW-6 was major effect. Jing *et al.* (2010) mapped 10 agronomical traits using an advanced backcross BC_3 population from a cross between recurrent parent named Yuexiangzhan and donor parent named G52-9. They mapped ten QTLs for the trait of 1000-GWt on chromosomes 3, 4, 5, 6 and 11, explaining the phenotypic variance from 3.77% to 28.67%. Hittalmani *et al.* (2003) mapped QTLs for TGW on the same chromosomes. Two QTLs were mapped for GY. Both of them had partial dominance effect. They explained the phenotypic variation in range of 8-12%. Fu *et al.* (2010) mapped QTLs controlling GY in two generations using 187 SSR

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markers. They mapped 4 QTLs for GY on chromosomes 1, 2, 8 and 12. The QTL on chromosome 2 (qGY-2) was minor effect. Two QTLs were identified on chromosomes 3 and 5. These QTLs had over dominance effect. Rahman *et al.* (2007) mapped QTLs for AL using an $F_{2:3}$ population from the cross between 'IR71033' and 'Junambyeo' (a Korean japonica cultivar) consisting of 146 lines. They found three QTLs on chromosomes 4, 5 and 9. qAL-5 with LOD= 4.09 explained 12% of phenotypic variation.

Two QTLs were detected for NP on chromosomes 4 and 6. Both of these QTLs had partial dominance effect. Mocanda *et al.* (2001) mapped NP related QTLs in a BC2F2 population derived from an inter specific cross between Caiapo, an upland *Oryza sativa* subsp. *japonica* rice variety from Brazil, and an accession of *Oryza rufipogon* from Malaysia. They found two QTLs for NP on chromosomes 6 and 11 respectively. For FL, three QTLs were detected on chromosomes 4, 6 and 8. All three QTLs had over dominance effect. Two of three QTLs were minor effect. The chromosomal regions of these QTL is as same as Rahman *et al.* (2007). For FLW two QTLs were mapped. qFW-1 and qFW-2 had over dominance effect and both of them had major effects on this trait.

In general, the number of QTL detected in this study was relatively lower compared to those of other studies. Susanto *et al.* (2008) believe that It might be due to the size of the population. The larger the mapping population, the more likely to allow detection of more QTL with smaller effect. In most of the cases degree of dominance (d/|a|) were high and there was some cases of over dominance toward increased or decreased a trait of interest which can be associated with observed heterosis in F_1 hybrids (data not shown). Although, additive and dominance genetic effects could be result from the present cross but, one should take into consideration that epistatic effects and linkage may upwardly bias the dominance, and even partial dominance estimation to become pseudo-over dominance (Sabouri *et al.*, 2010).

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