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RESEARCH ARTICLE

Detection of QTL for panicle architecture in F_2 population of rice

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Abstract. Panicle traits are the most important agronomic characters which directly relate to yield in rice. Panicle length (PL) being one of the major components of rice panicle structure is controlled by quantitative trait loci (QTLs). In our research, conducted at Research Farm of SKUAST-J, crosses of parental lines K 343 and DHMAS were made for generating F_2 mapping population, which were then transplanted into the field using augmented design-I. The F_2 population was used for phenotypic evaluation, development of linkage map and identification of QTLs on the chromosomes by using SSR markers. A total of 450 SSR markers were used for screening both the parents of which 53 highly polymorphic markers were selected and used for genotyping of 233 genotypes of F_2 population. Linkage map was generated using MAPMAKER/EXP3.0 software, seven linkage groups were found distributed on 11 chromosomes of rice. QTLs were detected using QTL Cartographer (v2.5) software. Based on 1000 permutation tests, a logarithm of odds (LOD) threshold value 2.0 and 3.0 was set. Composite interval mapping was used to map QTLs in populations derived from bi-parental crosses. The phenotypic data, genotypic data and the genetic linkage map generated identified total three QTLs of which one was identified for PL *qPL2*, located at 85.01 cM position with 2.1 LOD value and in between the marker intervals RM324–RM208, this QTL explained the phenotype variation by 4.36%. The other two QTLs were identified for spikelet density (SD) *qSD3.1* and *qSD3.2*, located at 28.91 and 39.51 cM, respectively, both with a flanking marker RM6832 on chromosome 3. The LOD value and phenotypic variation explained for *qSD3.1* and *qSD3.2* was 3.00 and 3.25; 9.70 and 12.34% respectively. The reported QTLs identified in the study suggested a less diversity in the parents used and also the rejection of not so useful markers from the used set of markers for PL and SD.

Keywords. quantitativetrait loci; logarithm of odds; simple sequence repeats; composite interval mapping.

Introduction

Enhancing the crop yield is one of the top priorities in crop breeding programmes, and the thrust area of the rice-producing countries is improving and increasing the yield efficiency of various rice varieties. Among various crop breeding efforts, improving plant architecture has been used as a successful strategy. Panicle architecture is a major component of rice yield, which covers several aspects such as panicle length (PL), spikelet density (SD), grain number (GN), primary branch number (PBN) and secondary branch number (SBN), which are inherited as quantitative traits and typically controlled by major and minor QTLs. The advantage of development of molecular markers, rice mapping populations and QTL analysis methods provide a good opportunity for studying and characterizing these traits of panicle architecture. However, the study on QTL analysis majorly has been focussing on traits that are components of grain quality and yield (Hittalmani *et al.* 2003; Fu *et al.* 2010; Hartman *et al.* 2013; Gao *et al.* 2015; Gonzaga *et al.* 2015), while the other traits such as PL and SD have received relatively less attention (Khan *et al.* 2009; Gonzaga *et al.* 2015; Kumar *et al.* 2017). Till date, at least 253 QTLs have been detected and analysed for PL that are distributed on 12 chromosomes of rice. However, only a few QTLs with large effects defined major genes have been cloned and applied in rice plant architecture breeding. PL, together with spikelet number and SD, seed setting rate, determines the grain number per panicle; hence, contributes to yield improvement in rice (Lander *et al.* 1987).

Rice (*Oryza sativa* L.) belongs to the family Poaceae, a monocotyledonous angiosperm and conceivably the oldest and important cereal. Rice is usually considered as a model plant because it has relatively small genome

Table 1. Descriptive statistics, heritability and genetic advance for F_2 population.

Traits	Mean ± SD			Heritability	Genetic advance
	K 343	DHMAS	F_2 plants	F_2 plants	F_2 plants
PL (cm)	26.62 ± 0.40	27.48 ± 0.47	25.65 ± 3.02	0.90	2.62
SD	4.15 ± 0.22	4.72 ± 0.28	4.65 ± 1.15	0.77	1.43

size, vast germplasm collection, good stock of molecular genetic resources and also an efficient transformation system (Ahmadi *et al.* 2008). Rice is the most important crop with regard to human nutrition and caloric intake, providing above one fifth of the total calories consumed worldwide by people (Ando *et al.* 2008). To satisfy the increasing global demand of growing population, a 50% hike in rice production will be required by the year 2050 (Churchill and Doerge 1994), especially in developing countries of Asia and Africa, where populations have been increasing dramatically (Davey *et al.* 2006).

The widespread and comprehensive rice genetic map was published by using simple-sequence repeat (SSR) markers (Lin *et al.* 1996). Rice research have developed and used thousands of SSR markers with their determined chromosomal location and polymorphism levels. Approximately more than 20,000 SSR primers of rice have been developed (Liu *et al.* 2016). These SSR markers are used for linkage maps construction, gene mapping and marker-assisted selection for various traits like panicle architecture (McCouch *et al.* 1997). One important use of SSR markers in agricultural research has been in the development of linkage maps for various diverse rice species and these maps have been easily utilized for identifying chromosomal regions that contain those genes which are controlling quantitative traits using QTL analysis.

Accordingly, in the present study, QTLs for the panicle architecture (PL and SD) were detected in F_2 population of rice developed from the crosses made from the parents, K 343 and DHMAS. Linkage map was constructed using SSR markers of major/minor QTLs for PL and SD. The reported QTLs detected in the present study suggest less diversity in the parents, rejection of not so useful SSR markers among the used set of markers for PL and SD, and will not provide adequate information for gene excavation of panicle components in rice.

Materials and methods

Population development

For a self-pollinating species like rice, populations likely originate from parents that are highly homozygous. In the present study, F_1 seeds were developed by crossing the parents, K 343 and DHMAS. Selfing and crossing are essential criteria in crop improvement process. The F_1 plants were raised during Kharif 2015 along with its parents in pots and successful crossed plants were identified for further selection. During Kharif 2016, two parental lines, i.e. K 343 and DHMAS, F_1 plants along with the generated F_2 population were sown and transplanted in an augmented design-I (unreplicated design) at Experimental Farm of School of Biotechnology, SKUAST, Jammu. The nursery was transplanted in 18×5 m (length×breadth) plot area and with planting density, i.e. an intrarow spacing of 20 cm and interrow spacing of 20 cm were maintained to accommodate 250 F_2 plants of which 233 plants survived and were used for genotypic and phenotypic evaluation.

Phenotypic evaluation

In each row, all the plants were tagged individually in the plot and phenotypic data were recorded for each F_2 plant as per the DUS guidelines of DRR, Hyderabad (McCouch *et al.* 2002) for various traits among which data for PL and SD were the traits of interest in the present study (table 1).

Genetic linkage map and data analysis

A total of 450 SSR markers, well distributed in the whole genome were selected to screen both the parents K 343 and DHMAS for polymorphism. SSRs which showed a good polymorphism in parents were used for genotyping of the 233 F_2 plants. 53 of 450 SSR markers were found to be highly polymorphic and were further used for the PCR amplification of the genomic DNA of F_2 population (see table 2).

Thermal profiles used for DNA amplification was done in five crucial steps: first step initial denaturation was carried out in 1 cycle at a temperature of 94°C for the duration of 5 min. Denaturation of DNA was done at 94°C temperature for the duration of 30 s, annealing of primers to denatured template DNA was done at 55–58°C for the duration of 30 s, followed by extension of primers at 72°C for 30 s, all three steps were carried out in 35 cycles of PCR. Fifth step, final extension was carried out in 1 cycle at 72°C for 7 min.

MAPMAKER/EXP 3.0 software (McCouch *et al.* 2001) was used for constructing the genetic linkage map using the obtained polymorphic SSRs. The results obtained from the agarose gel electrophoresis were converted into scoring data and the software running program was applied

Table 2. Polymorphic SSR markers used for genotyping of the F_2 population.

	Marker	Sequence	T_m	Product size
1	RM528	F-5′ GGCATCCAATTTTACCCCTC 3′ R-3′ CCGTAGGTTAAAATGGGGAC 5′	55	232
2	RM13838	F-5′ CCCAACTGCTAGGTTTCTGATCC 3′ R-3′ ACTGTGTTACTGTGTGCCGTTGC 5′	55	129
3	RM262	F-5′CATTCCGTCTCGGCTCAACT 3′ R-3′ CAGAGCAAGGTGGCTTGC 5′	55	154
4	RM227	F-5′ ACCTTTCGTCATAAAGACGAG 3′ R-3′ GATTGGAGAGAAAAGAAGCC 5′	57	106
5	RM6832	F-5′ GTTGTAAATGCCTGAGTGC 3′ R-3′ AAAGAGCTAAACCGCTAGG 5′	55	182
6	RM15838	F-5′ CGATGTCATTCGGTAGAAACAAGC 3′ R-3′ CCTAGTCAAGGCATGGTCAATCC 5′	57	262
7	RM223	F-5′ GAGTGAGCTTGGGCTGAAAC 3′ R-3′ GAAGGCAAGTCTTGGCACTG5′	55	165
8	RM3524	F-5′ CGGAGCTGGTCTAGCCATC 3′ R-3′ GTCTCCGTCTTCCTCACTCG 5′	57	129
9	RM4A	F-5′ TTGACGAGGTCAGCACTGAC 3′ R-3′ AGGGTGTATCCGACTCATCG 5′	55	159
10	RM7492	F-5′ AGATGGTTGCCAAGAGCATG R-3′ GTCACGTGGCGATTTAGGAG	55	145
11	RM517	F-5′ GGCTTACTGGCTTCGATTTG 3′ R-3′ CGTCTCCTTTGGTTAGTGCC 5′	55	266
12	RM5	F-5′ TGCAACTTCTAGCTGCTCGA 3′ R-3′ GCATCCGATCTTGATGGG 5′	55	113
13	RM580	F-5′ GATGAACTCGAATTTGCATCC 3′ R-3′ CACTCCCATGTTTGGCTCC 5′	55	221
14	RM5699	F-5′ ATCGTTTCGCATATGTTT 3′ R-3′ ATCGGTAAAAGATGAGCC 5′	55	167
15	RM447	F-5′ CCCTTGTGCTGTCTCCTCTC 3′ R-3′ ACGGGCTTCTTCTCCTTCTC 5′	55	111
16	RM471	F-5′ ACGCACAAGCAGATGATGAG 3′ R-3′ GGGAGAAGACGAATGTTTGC 5′	55	106
17	RM202	F-5′ CAGATTGGAGATGAAGTCCTCC 3′ R-3′ CCAGCAAGCATGTCAATGTA 5′	55	189
18	RM413	F-5′ GGCGATTCTTGGATGAAGAG 3′ R-3′ TCCCCACCAATCTTGTCTTC 5′	55	79
19	RM169	F-5′ TGGCTGGCTCCGTGGGTAGCTG 3′ R-3′ TCCCGTTGCCGTTCATCCCTCC 5′	55	169
20	RM80	F-5′ TTGAAGGCGCTGAAGGAG 3′ R-3′ CATCAACCTCGTCTTCACCG 5′	55	142
21	RM101	F-5′ GTGAATGGTCAAGTGACTTAGGTG 3′ R-3′ ACACAACATGTTCCCTCCCATGC 5′	55	324
22	RM13840	F-5′ CGGTCTTTAGTAATGGTGCTTTGC 3′ R-3′ GAGGCAGGTGTTTGTCGTCTAGC 5′	55	195
23	RM25003	F-5′ GATTGATCCGAGAGACAAATCC 3′ R-3′ TCGATCAATAGTAGCAGCAGTAGG 5′	55	115
24	RM3295	F-5′ TCGTGTCATGCGATCGAC 3′ R-3′ GCTTCGACTCGACCAAGATC 5′	55	92
25	RM7	F-5′ TTCGCCATGAAGTCTCTCG 3′ R-3′ CCTCCCATCATTTCGTTGTT 5′	55	180
26	RM208	F-5′ TCTGCAAGCCTTGTCTGATG 3′ R-3′ TAAGTCGATCATTGTGTGGACC 5′	55	173
27	RM7102	F-5′ TTGAGAGCGTTTTTAGGATG 3′ R-3′ TCGGTTTACTTGGTTACTCG 5′	55	169
28	RM149	F-5′ GCTGACCAACGAACCTAGGCCG 3′ R-3′ GTTGGAAGCCTTTCCTCGTAACAC 5′	55	233
29	RM240	F-5′ CCTTAATGGGTAGTGTGCAC 3′ R-3′ TGTAACCATTCCTTCCATCC 5′	55	132

Table 2 (*contd*)

	Marker	Sequence	T_m	Product size
30	RM1370	F-5′ AAACGAGAACCAACCGACAC 3′ R-3′ GGAGGGAGGAATGGGTACAC 5′	55	173
31	RM1282	F-5′ AAGCATGACAGCTGCAAGAC 3′ R-3′ GGGGATGAAGGGTAATTTCG 5′	58	157
32	RM3874	F-5′ TGGGTGATCTTAGTTTGGCC 3′ R-3′ AATGTGCCTGCACATGTCAC 5′	55	206
33	RM232	F-5′ CCGGTATCCTTCGATATTGC 3′ R-3′ CCGACTTTTCCTCCTGACG 5′	55	158
34	RM28048	F-5′ TTCAGCCGATCCATTCAATTCC 3′ R-3′ GCTATTGGCCGGAAAGTAGTTAGC 5′	55	93
35	RM7300	F-5′ TCCGTATCCTAGTCGCGATC 3′ R-3′ CGCCGTCATGACTCATACTC 5′	58	102
36	RM3	F-5′ ACACTGTAGCGGCCACTG 3′ R-3′ CCTCCACTGCTCCACATCTT 5′	55	145
37	RM220	F-5′ GGAAGGTAACTGTTTCCAAC 3′ R-3′ GAAATGCTTCCCACATGTCT 5′	55	127
38	RM110	F-5′ TCGAAGCCATCCACCAACGAAG 3′ R-3′ TCCGTACGCCGACGAGGTCGAG 5′	55	156
39	RM231	F-5′ CCAGATTATTTCCTGAGGTC 3′ R-3′ CACTTGCATAGTTCTGCATTG 5′	58	182
40	RM168	F-3′ TGCTGCTTGCCTGCTTCCTTT 3′ R-5′ GAAACGAATCAATCCACGGC 5′	58	116
41	RM545	F-5′ CAATGGCAGAGACCCAAAAG 3′ R-3′ CTGGCATGTAACGACAGTGG 5′	58	226
42	RM204	F-5′ GTGACTGACTTGGTCATAGGG 3′ R-3′ GCTAGCCATGCTCTCGTACC 5′	55	169
43	RM324	F-5′ CTGATTCCACACACTTGTGC 3′ R-3′ GATTCCACGTCAGGATCTTC 5′	55	175
44	RM1211	F-5′ TACAGTGGCGAAAGGAATAC 3′ R-3′ CCATCACGCATGTTAGTTAG 5′	55	213
45	RM218	F-5′ TGGTCAAACCAAGGTCCTTC 3′ R-3′ GACATACATTCTACCCCCGG 5′	55	148
46	RM1178	F-5′ CAGTGGGCGAGCATAGGAG 3′ R-3′ ATCCTTTTCTCCCTCTCTCG 5′	58	112
47	RM315	F-5′ GAGGTACTTCCTCCGTTTCAC 3′ R-3′ AGTCAGCTCACTGTGCAGTG 5′	58	133
48	RM242	F-5′ GGCCAACGTGTGTATGTCTC 3′ R-3′ TATATGCCAAGACGGATGGG 5′	55	225
49	RM167	F-5′ GATCCAGCGTGAGGAACACGT 3′ R-3′ AGTCCGACCACAAGGTGCGTTGTC 5′	55	128
50	RM219	F-5′ CGTCGGATGATGTAAAGCCT 3′ R-3′ CATATCGGCATTCGCCTG 5′	55	202
51	RM144	F-5′ TGCCCTGGCGCAAATTTGATCC 3′ R-3′ GCTAGAGGAGATCAGATGGTAGTG 5′	55	237
52	RM225	F-5′ TGCCCATATGGTCTGGATG 3′ R-3′ GAAAGTGGATCAGGAAGGC 5′	55	140
53	RM216	F-5′ GCATGGCCGATGGTAAAG 3′ R-3′ TGTATAAAACCACACGGCCA 5′	55	146

according to the instructions given by the manufacturer. Linkage analysis and grouping was carried out using the 'GROUP' command and 'LOD' 3.0. Recombination rate was set at 50cM. The linked markers were optimized using 'COMPARE' command when their number was less than 8. The recombination rate was converted into a genetic map distance (cM) using the 'Kosambi' map function. The located SSR markers (Mohammadi *et al.* 2013) were considered as anchor tags to determine the appropriate linkage groups.

Identification of QTLs

Statistical software, namely, Win QTL Cartographer 2.5 was used for the detection and identification of QTLs associated with panicle architecture (Navea *et al.* 2017). Based

Table 3. Polymorphism as detailed using SSR markers.

Number of SSR primers used	450
Number of polymorphic primers	53
Percentage polymorphism	11.77%

Table 4. Segregation pattern of polymorphic markers in F_2 population.

Total number of segregants	Segregation percentage
Parent-1 type (A)	28.31
Heterozygote type (H)	46.13
Parent-2 type (B)	25.56

on the phenotypic and genotypic observations recorded and the obtained completed linkage map, the panicle architecture trait QTLs were analyzed using composite interval mapping (CIM). For each trait, minimum LOD score of 2.0 and 3.0 was used for the identification of putative QTL in this experiment. The experiment-wise threshold LOD scores for detection of QTL was calculated based on 1000 permutation at $P \leq 0.05$ (Paterson *et al.* 2005). The significance level and walk speed were set at 0.05 and 2 cM, respectively. The values obtained were further plotted in the obtained corresponding genetic linkage map. As mentioned in earlier studies, QTL with LOD scores below the threshold LOD value were considered only as suggestive QTL and those with LOD scores above the threshold value were considered as the definitive QTL (Pinson and Jia 2016).

Results

In this research, two panicle-related traits, PL and SD were investigated in generated F_2 population for phenotypic evaluation, development of linkage map and identification of QTLs on the chromosomes by using SSR markers. The alleles with a variable amplicon length in both the parents were considered as polymorphic leading to a polymorphic percentage of 11.77% (table 3) and banding pattern of few markers with parents can be seen (figure 1).

As the present research utilized F_2 mapping population, so the Mendelian ratio of 1:2:1 had to be followed. A clear segregation pattern of polymorphic markers for F_2 population was calculated. It was seen that the SSR banding pattern of parent-1, parent-2 and heterozygote followed the required Mendelian ratio. Of a total number of 12,207 segregants, 28.31% segregants showed a banding pattern like parent-1 and were denoted as A, 25.56% segregants were like parent-2 and were denoted as B and 46.13% where the heterozygotes were denoted as H (table 4) banding pattern of two markers; RM1282 and RM204 in F_2 population is shown in figures 2 and 3.

Construction of linkage map

A genetic linkage map was constructed at a LOD threshold value >2.0 using Mapmaker/EXP 3.0 software and Kosambi mapping function was used for detection of QTLs based on 53 polymorphic microsatellite markers which resulted in seven linkage groups. The seven linkage

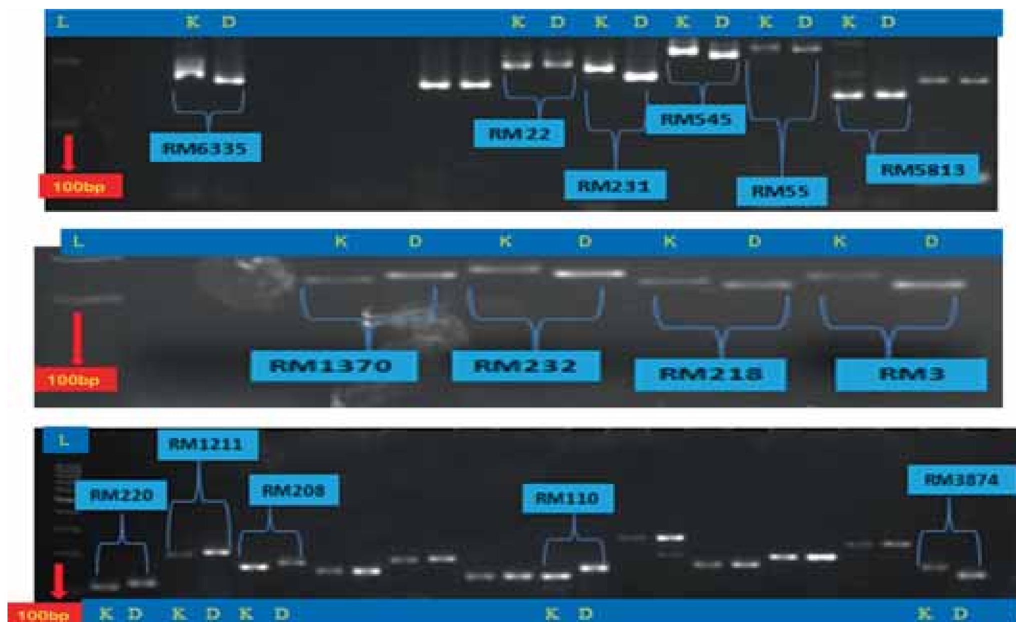

Figure 1. SSR banding pattern in parents using 100 bp ladder, where K is *K*343 and D is *DHMAS*.

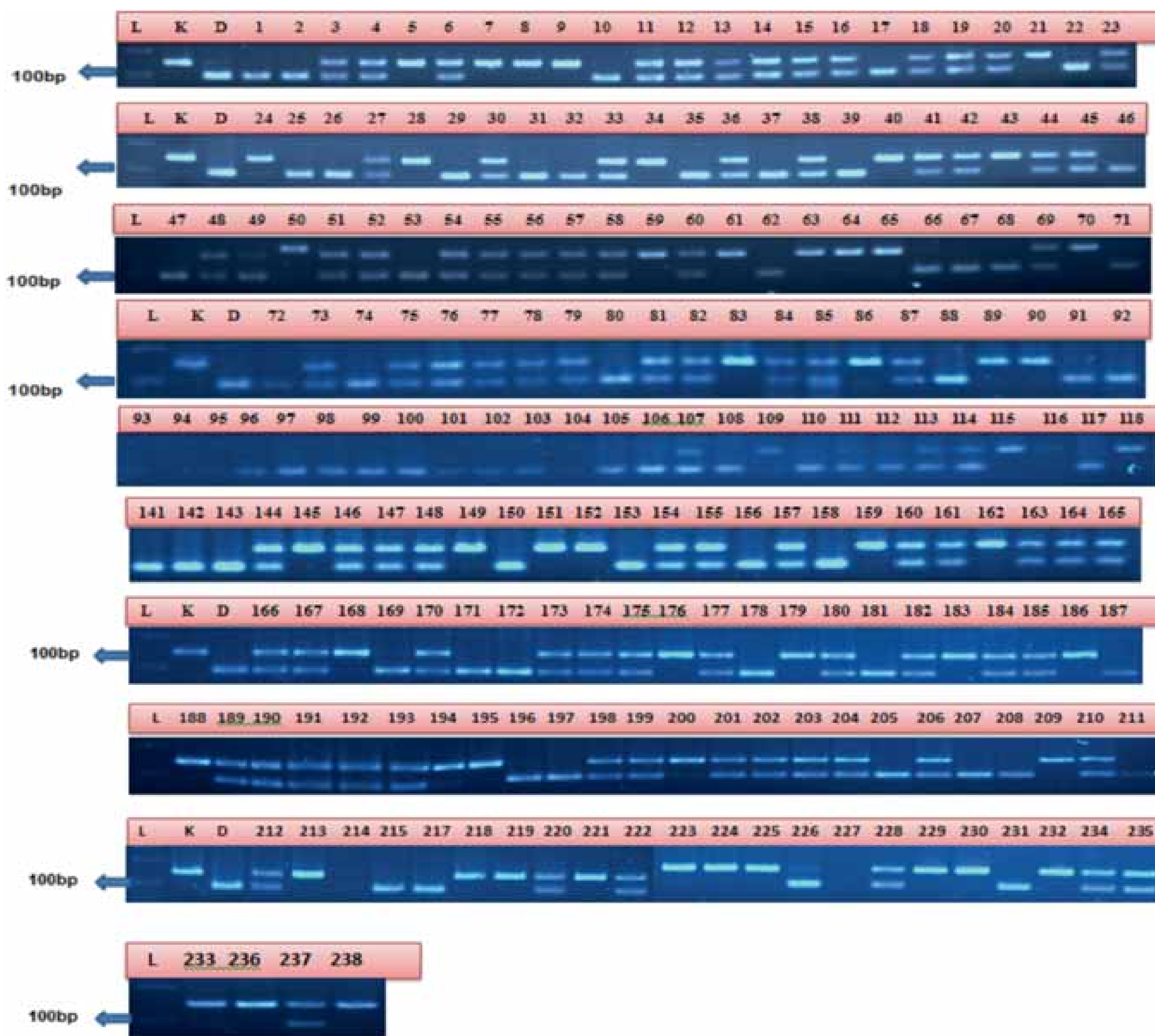

Figure 2. SSR-banding pattern for the marker RM 1282 (157 bp) on F_2 population using 100-bp ladder.

groups have been assigned to their respective chromosomes based on the rice chromosome map (Rani *et al.* 2006). Chromosome 1 had six markers with a total map distance of 421.2 cM. Chromosome 2 had seven markers with covering a map distance of 582.1 cM. Chromosome 3 had a map distance of 607.6 cM with nine markers. Chromosome 4 contained two markers covering a map distance of 97.5 cM. Chromosomes 5 and 6 had four markers which covered a map distance of 255.9 and 192.6 cM, respectively. Chromosome 8 had a map distance of 567.9 cM with three markers. Chromosome 9 contained two markers covering a total distance of 18.7 cM. Chromosome 10 had a map distance of 78.8 cM with one marker. Chromosomes 11 and 12 had two and three markers with a map distance of 19.4 and 231.9cM, respectively, making a total of 3971.1 cM (figure 4).

Detection of QTLs

In the present study, CIM was performed using the software Windows QTL cartographer 2.5 (Sasaki *et al.* 2017). Using the phenotypic data, genotypic data and the constructed genetic linkage map, QTL Cartographer detected a total three QTLs of which one QTL named *qPL2* at 85.01cM position on chromosome 2 was found to be associated with PL, this QTL had 2.11 LOD value and was observed to be present in between the marker intervals RM324-RM208. This QTL explained the phenotypic variation by 4.36%.

One significant QTL *qSD3.1* located at 28.91cM with a flanking marker RM6832 was detected on chromosome 3 was found associated with SD. The LOD value for this QTL was 3.00 and explained the phenotypic variability

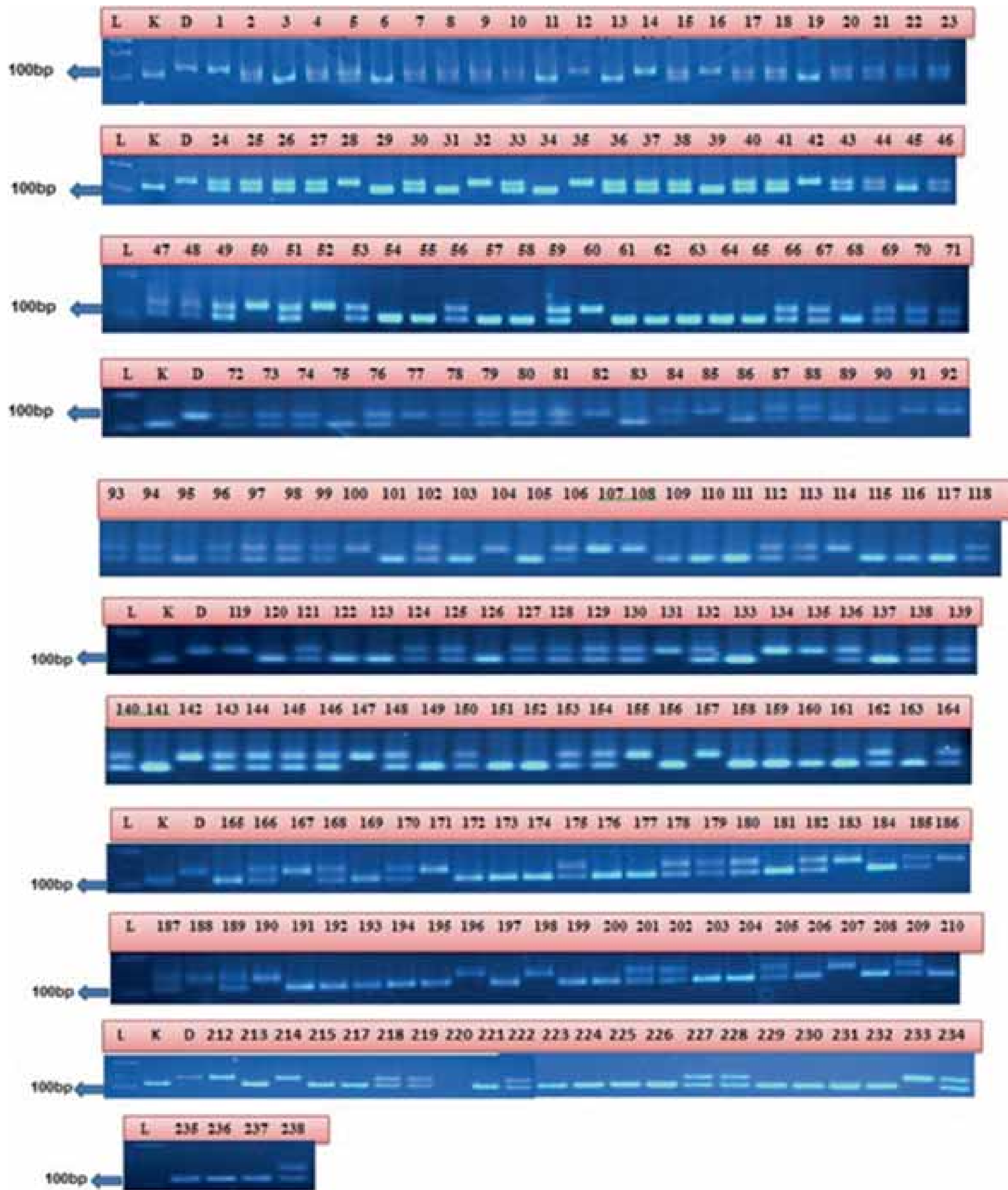

Figure 3. SSR-banding patter for the marker RM 204 (169 bp) on F_2 population using 100-bp ladder.

by 9.70%. Another QTL *qSD3.2* located at 39.51cM with a flanking marker RM6832 was also detected on chromosome 5. The LOD value for this QTL was 3.25 and explained the phenotypic variability by 12.34%. The LOD curve for PL and SD (figure 5) and map position of QTLs of both traits are represented in figure 6. The phenotypic variation explained by the three QTLs was 26.4% of the total variance in the 233 F_2 plants. The identified QTLs were named following McCouch's rule for nomenclature (table 5) (Seck *et al.* 2012).

Discussion

In this study, the linkage groups and the order of markers were determined using MAPMAKER/EXP 3.0 (Stephen *et al.* 1993) based on 53 SSRs to span 3971.1cM. A total of seven linkage groups were obtained from 53 markers whereas 10 markers remained unlinked, i.e. they did not form any linkage group. The seven linkage groups were mapped to 11 chromosomes, i.e. chromosome 1 to chromosome 12, whereas, chromosome 7 did not have any

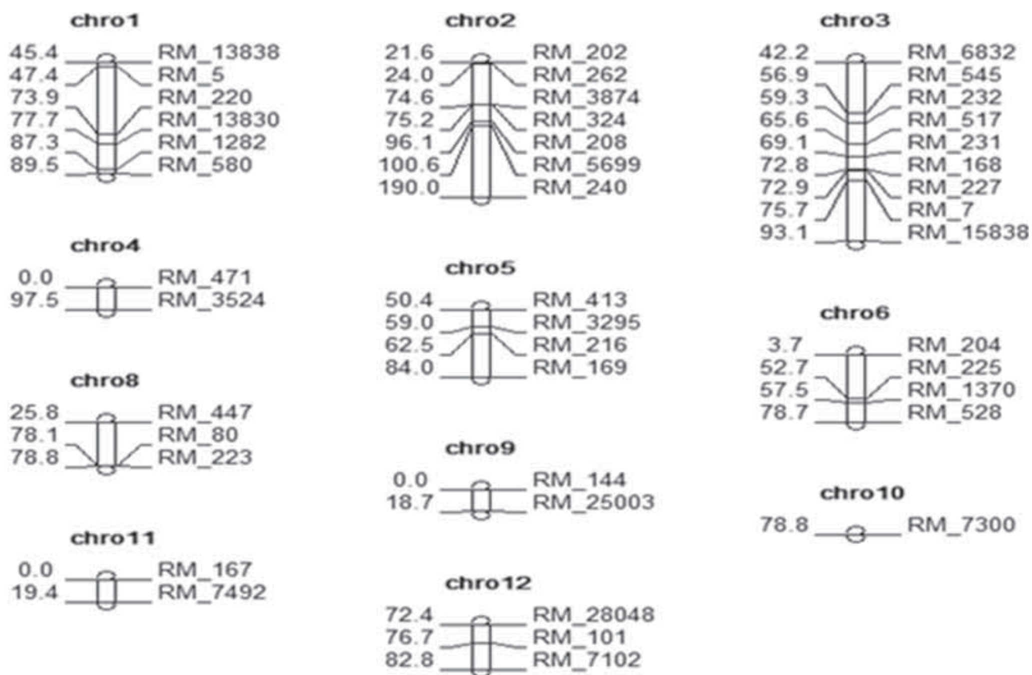

Figure 4. Linkage map for polymorphic SSR markers using MAPMAKER/EXP (v3.0).

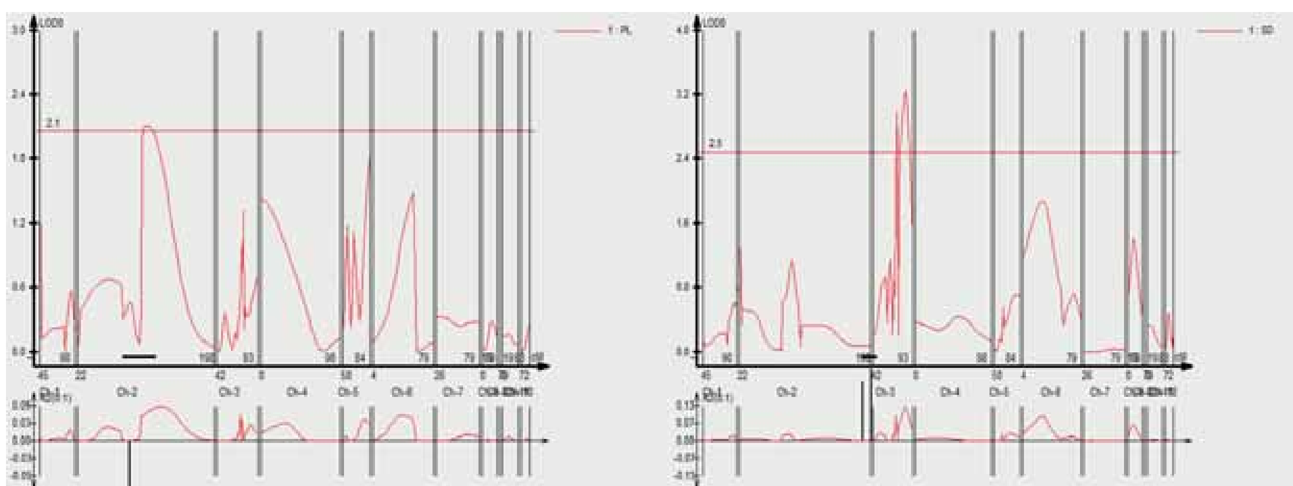

Figure 5. LOD curve for PL and SD.

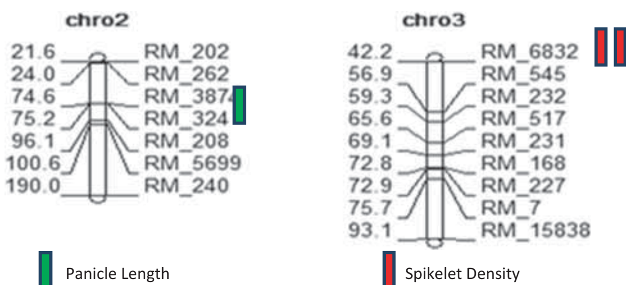

Figure 6. Pictorial representation of map position of QTLs of PL and SD.

marker; similar reports were published by Temnykh *et al.* (2001) and Ando *et al.* (2008). The amount of phenotypic variation explained by a QTL was used to characterize it as major or minor QTL. A QTL that explains less than 10% of the total variation has been categorized as minor QTL whereas a QTL with more than 10% of total phenotypic variation has been assigned as major QTL. This criterion of phenotypic variation has been used in several QTL studies in rice and other crops (Wang *et al.* 2004, 2007). However, in various studies, a category of 20% of phenotypic variation has been used for classifying major and minor QTLs (Xing *et al.* 2002). Therefore, threshold level for classification of minor and major QTL has been

Table 5. QTL identified for PL and SD from F_2 population.

Trait	Chr. no.	No. of QTLs	QTL	LOD value	Marker Interval	Position (cM)	Additive effect	PVE % (R^2)
PL	2	1	*qPL2*	2.11	RM324-RM208	85.01	0.88	4.36
SD	3	1	*qSD3.1*	3.11	RM6832	28.91	−0.52	9.70
	3	1	*qSD3.2*	3.25	RM6832	39.51	−0.55	12.34

Total variation explained by three QTLs.

varying from one study to another. During QTL analysis, recognized 'stable' QTLs are few whereas minor and environment-specific QTLs are usually ignored (Yonemaru *et al.* 2010). Most recently, Takai *et al.* (2018) identified novel QTLs for spikelet per panicle in F_2 population generated from *indica* × *japonica* combinations, also Zhu *et al.* (2018) have identified a novel QTL for PL.

Traits of panicle architecture, PL, one QTL, named as *qPL2* at 85.01cM position on chromosome 2 with 2.11 LOD value was detected. This QTL explained the phenotypic variation by 4.36%, hence making it a minor QTL, Ahmadi *et al.* (2008) also obtained similar results. QTL, namely *qPL2a*, at chromosome 2 with 5% PVE and LOD score of 2.1 was reported by Pinson and Jia (2016). Another target trait for SD, a minor QTL *qSD3.1* located at 28.91 cM position with PVE% 4.36 and a major QTL *qSD3.2* with PVE % 12.34 were detected on chromosome 3, a similar LOD value for SD was reported by Ahmadi *et al.* (2008) and Mohammadi *et al.* (2013) also explained the phenotypic variability less than 10% for SD making it a minor QTL whereas Navea *et al.* (2017), reported a major QTL *qSPP2.1* for SD with 12.93% PVE similar to the results in the present study. Although heritability for PL and SD was observed to be high 0.9 and 0.68, respectively, still detection of minor QTLs may be due to the set of markers used or the phenotypic expression of these traits may be affected by both environmental effects and pleiotropic effects of genes given for nontarget traits, such as days to flowering or culm length.

Thus, the parameters of detected QTLs, such as their chromosomal positions, additive effect and percentage of phenotypic variance explained are not always evaluated correctly (Temnykh *et al.* 2001). While 450 SSR markers were used in screening, still polymorphic rate was seen as 11.77% for panicle architecture in the F_2 population of K 343/DHMAS, this concludes that there is no good amount of variation among the two types of parents used and also set of markers used were not so useful for the identification of QTLs for given traits on the given F_2 population, hence, can be used as rejected markers in further studies for PL and SD. Also, selfing of the developed F_2 population every season can be done for next few generations for development of recombinant inbred lines (RILs) or near isogenic lines (NILs) along with the detected QTLs in F_2 population which can be useful for the validation and stability of the QTLs found in the population.

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