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Association Mapping of Rice Germplasm Accessions for qDTY 1.1 and qDTY 12.1

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ABSTRACT

Keywords

Drought, Candidate gene, Rice, Association mapping, GLM model

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Chhattisgarh state is renowned by the name Rice Bowl of India because rice is cultivated in maximal land area. The research study was carried out by using fifty-eight rice landraces at Research cum Instructional farm of IGKV, Raipur during *Kharif* 2019 under irrigated and rainfed condition in Randomized Block Design (RBD), with two replications. Using the GLM model, for grain yield RM 240 (C#2), RM 3825 (C#1), RM 5753 (C#6) and RM 11 (C#7) exhibited tight association in irrigated condition and in RM 511 (C#12), RM 307 (C#4) and RM 495 (C#1) had tight linkage with grain yield in rainfed condition. Based on two markers i.e., RM 3825 and RM 511 twenty genotypes had both the QTL's that is qDTY1.1 and qDTY 12.1.

Introduction

Rice is a primary staple food in major countries and used widely as a nutritional source. As with increase in demand due to population increment lead to increase in its production, but mainly rainfed condition is present in India, due to which drought leads to loss in yield. The process can be made more efficient and rapid through marker-assisted breeding, a well-known fast-track

approach in crop improvement. QTLs have been identified for grain yield under drought with large effects against drought-susceptible varieties. "A QTL, qDTY12.1, significantly associated with grain yield under reproductive of stage drought stress was identified on chromosome 12. qDTY12.1 is the only QTL reported so far in rice to have shown a large effect against multiple recipient genetic backgrounds as well as under highly diverse upland and lowland rice ecosystems.

qDTY12.1 can be successfully introgressed to improve grain yield under drought of popular high-yielding but drought-susceptible lowland as well as upland adapted varieties following marker-assisted breeding.

Drought is one of the most important abiotic stresses leading threat to agricultural food production especially in rice cultivation hampering rice productivity in rainfed areas. In Asia, more than 23 million ha of rice-growing area are rainfed (Pandey *et al.*, 2007). Eastern India and adjoining areas occupy a large drought-affected area with an estimate of around 17 million ha (Huke and Huke 1997). The green revolution had little impact in rainfed ecosystems (Evenson *et al.*, 2003). Farmers in these areas are growing popular varieties originally bred for irrigated ecosystems (Vikaram *et al.*, 2011). The slow progress in developing rice varieties for drought-prone areas is mainly due to the complex nature of drought-tolerance mechanisms; large genotype $\times$ environment, QTL $\times$ environment and QTL $\times$ recipient genetic background interactions; and the absence of QTLs with a large and consistent effect against high-yielding but drought-susceptible varieties. This becomes even more relevant when we see that qDTY12.1 as well as qDTY2.3 is contributed by IR74371-46-1-1. Recently, candidate gene analysis has been carried out in this QTL region and several genes have been reported as putative candidate genes (Kohli *et al.*, 2010 and Biswal *et al.*, 2012). Swamy *et al.*, 2011 carried out meta-QTL analysis and reported several candidate genes in the same region. qDTY12.1 could be efficiently used in marker-assisted breeding for the improvement of both lowland and upland rice varieties for drought stress." Candidate gene studies have been at the forefront of genetic association studies i.e. identifying risk variants associated with a particular disease. Candidate gene studies are most often selected

as this approach is relatively cheap and quick to perform, and are focused on the selection of genes that have been in some way related to the disease previously and thus come with prior knowledge about gene function. The candidate gene approach begins with selection of a putative candidate gene based on its relevance in the mechanism of the disease (trait) being investigated (Kwon and Goate, 2000 and Patnala *et al.*, 2013).

Materials and Methods

Experimental site

The present research work was regulate at Research cum Instructional farm Department of Genetics and Plant Breeding, College of agriculture, Indira Gandhi Agricultural University, Raipur, Chhattisgarh, during the *Kharif* season of 2019.

Climate and weather

Chhattisgarh is situated between 17°14'N and 24°45'N latitudes and 79°16' E and 84°15' E longitudes. Raipur (C.G.) is lies at 21°16'N latitude and 81°36' E longitude with an altitude of (289.60m). Overhead mean sea level. The maximum mean temperature was 32.30°C & minimum mean temperature was 23.99°C during the crop development time. The overall total rainfall during crop growing period was (1199.2 mm). The highest rainfall received during August month was (316.4 mm).

Materials and Methods

Fifty-eight genotypes of rice were taken for this research (Table 1). The material was grown under irrigated (transplanted) and rainfed (direct seeded) condition in the wet season of 2019. Nurseries were raised and 21 days old seedlings were eventually transplanted in the field, in RBD with 2

replications. R X R and P X P distance of 25 cm X 15 cm and net plot area was 3m m X 1.5 m. The crop was preserve under irrigated condition. Fertilizer dose @ of 50:40:30 kg per hectare (NPK) was applied.

Before transplanting the whole dose of potassium and phosphorus are applied and half dose of nitrogen are applied as a basal dose. The remaining dose of N was applied in 2 splits, 1st at the period of starting of tillering and 2nd, 1week after it. All the treatment was similar for agronomical practices.

Observations recorded

The observation was recorded on days to 50 % flowering, plant height (cm), flag Leaf length (cm), flag Leaf width (cm), number of effective tiller per plant, panicle length (cm), 1000 grain weight (gm), number of filled grains (NFG), number of unfilled grain (NUFG), total number of grains, biological yield per plant (BYP) (g), harvesting index (HI) (%) and grain yield per plant (GYP) (g) in irrigated and rainfed condition as well.

Statistical analysis

The data was notable in favour to divergent phenotypic and quantitative traits on the 13 yield and panicle related character of rice accessions were subjected to the statistical analysis.

In this calculation mean values were succeed for all character for everyone genotype. These mean data are used to estimate the variability parameters. ANOVA is deliberated by using OPSTAT software.

Molecular study

For molecular characterization, fifty-eight rice germplasm accessions are used. For

estimating the genetic diversity of rice germplasm molecular study was execute, which included “DNA isolation, quantification, dilution of DNA, PCR amplification using microsatellite primers, electrophoresis using polyacrylamide gel, scoring and analysis of data.

Results and Discussion

Total genomic DNA was extracted from 58 lines of rice using CTAB method (Zheng *et al.*, 1995). Fresh and healthy leaves were used for extraction of DNA. The DNA samples were quantified by using Nano Drop Spectroscopy (*NANODROP 2000c*). The quantity of the samples was found in the range from 500-2000 ng/μl. DNA samples were then diluted with sterilized water such that the final concentration of DNA became 50 ng/μl (Table 1–5).

Development of genotypic data based on SSR Markers

Genetic associations among 58 accessions were analyzed, based on phenotypic variation of yield traits with the help of 42 SSR markers covering all the chromosomes. A total of 74 alleles were amplified and the number of alleles per locus generated by each marker ranged from 1 to 4 alleles with an average number of 1.76 alleles per locus. Maximum number of alleles (4) was amplified by marker RM 413, RM 518 and RM 240 marker (Table 5).

Polymorphism Information Content of SSR markers

The PIC value across markers ranged from 0.00 to 0.73 with an average of 0.25. Maximum PIC value was observed on chromosome 4 (RM 518 = 0.73) followed by RM 489 of chromosome 3 (0.70) Table 5 (Fig. 1).

Table.1 List of germplasm accessions

Entry number	Name of entry	Entry number	Name of entry
1	IRRI 154	30	Manaw Thukha
2	MINGHUI 63	31	BR28
3	ZHENSHAN 97 B	32	TN1
4	IR 64-21	33	IR6
5	IRBB 66	34	GSR IR2-9-R1-SU3-Y2
6	IR 78222-20-7-148-2-B-B-B-B	35	Zanton::IRGC 31248-1
7	IR 69726-116-1-1	36	URAIBOOL::IRGC 52785-
8	IRRI147	37	Hokkai 188
9	SANHUANGZHAN NO 2	38	IR 126182-1-1-1
10	IR77186-122-2-2-3	39	IR10F360
11	IR77298-14-1-2-10	40	Sahel 108
12	Sambha Mahsuri + Sub1	41	Sahel 134
13	Supa	42	Sahel 177
14	IRRI 104	43	Giza 178
15	N 22::IRGC 19379-1	44	Moroberekan
16	MTU1010	45	DJ123
17	Swarna	46	Oryzica 1
18	Nanhi	47	F50
19	Jasmine 85	48	TEQING
20	Kinandang Patong	49	MG 2::IRGC 79837-1
21	Sadri	50	UPL RI 7::IRTP 9897-C1
22	OM4900	51	CT11891-2-2-7-M
23	IR 95042:13-B-7-11-15-3	52	Oryzica sabana 10
24	IR 93340:14-B-21-17-12-1RGA-2RGA-1-B-B	53	Oryzica sabana 6
25	IR 93354:34-B-5-1-23-1RGA-2RGA-1-B-B	54	Oryzica Llanos 5
26	Khao Hlan On	55	Chhomrong Dhan
27	IR13F167	56	NSIC Rc240
28	IR84984-83-15-481-B	57	Jamir
29	M202	58	IR10M300

Table.2 Significant marker-trait associations based on GLM model ($P>0.05$) in irrigated and rainfed condition during *Kharif* 2019

Trait	Locus	C #	p_	Rs_	Trait	Locus	C #	p_	Rs_
			Marker	Marker				Marker	Marke
Irrigate					Rainfed				
DTF	RM 3825	1	0.0025	0.1536	DTF	RM 3825	1	7.32E-05	0.2478
	RM 11	7	0.0194	0.1379		RM 11	7	5.21E-04	0.2454
	RM 5753	6	0.0246	0.1279		RM 518	4	0.0519	0.1647
PH	RM 6504	1	0.0168	0.1305	PH	RM 240	2	0.0065	0.1802
	RM 28130	12	0.0233	0.0899		RM 413	4	0.0142	0.1844
	RM 240	2	0.0353	0.1249	ET	RM 518	4	0.0252	0.1834
FLL	RM 28160	12	0.0235	0.0975	FLL	RM 240	2	0.0164	0.1474
FLW	OSR 13	1	0.0016	0.2357		OSR 13	1	0.0404	0.1225
	RM 6504	1	0.0141	0.1372		RM 28160	12	0.0431	0.0836
	RM 3825	1	0.045	0.0703		RM 1261	12	0.0479	0.0872
PL	RM 3825	1	0.0085	0.1191	FLW	RM 1261	12	0.0598	0.0818
	OSR 13	1	0.0166	0.1594	PL	OSR 13	1	0.0164	0.1588
	RM 489	3	0.0424	0.1303		RM 240	2	0.0213	0.1393
	RM 5753	6	0.0462	0.1075		RM 489	3	0.0246	0.1538
TGW	RM 236	4	0.0598	0.0731	TGW	RM 1261	12	0.0078	0.118
GY	RM 240	2	0.0075	0.1779		RM 5753	6	0.0385	0.0923
	RM 3825	1	0.0177	0.0978	GY	RM 511	12	0.0397	0.0889
	RM 5753	6	0.0245	0.128		RM 307	4	0.0434	0.0714
	RM 11	7	0.0499	0.1067		RM 495	1	0.0482	0.0726
BY	RM 5753	6	0.0366	0.1152	BY	RM 495	1	0.065	0.0495
	RM 3825	1	0.0529	0.0664	HY	RM 1261	12	0.0138	0.1279
HY	RM 240	2	0.0263	0.1354		RM 236	4	0.0357	0.0848
NFG	RM 11	7	0.0263	0.1283	NFG	RM 125	7	0.0134	0.1543
NUFG	RM 240	2	0.0609	0.0977		RM 489	3	0.0571	0.1179
	RM 28130	12	0.0884	0.0455	NUFG	OSR 13	1	0.0015	0.2404
TNG	RM 11	7	0.0232	0.1319		RM 125	7	0.0277	0.1312
					TNG	RM 125	7	0.0044	0.191
						RM 11	7	0.0273	0.1261
						RM 489	3	0.052	0.1212
						OSR 13	1	0.0659	0.1089
						RM 3520	1	0.071	0.0609

DTF = Days to flowering; PH = plant height (cm); NT = Number of tillers; FLL = Flag leaf Length (cm); FLW = Flag leaf width (cm); PL = Panicle Length (cm); TGW = Thousand grain weight (g); NFG = Number of filled grains; NUFG = Number of unfilled grains; TNG = Total Number of grains; BYP = Biological yield per plant (g); HI = Harvest index (%); GYP = Grain yield per plant (g)

Table.3 Significant marker-trait associations based on MLM model ($P>0.05$) in irrigated and rainfed condition during *Kharif* 2019

Trait	Locus	C #	p_Marke	Rsq_	Trait	Locus	C #	p_Marke	Rsq_
				Marker					Marke
Irrigate					Rainfed				
DTF	RM 3825	1	0.0025	0.1536	DTF	RM 3825	1	7.32E-05	0.2478
	RM 11	7	0.0194	0.1379		RM 11	1	5.21E-04	0.2454
	RM 5753	6	0.0246	0.1279	PH	RM 413	4	0.0109	0.1844
PH	RM 6504	1	0.0165	0.1305		RM 240	2	0.0231	0.1802
	RM 28130	12	0.0233	0.0899	NT	RM 518	4	0.0385	0.1834
	RM 240	2	0.0353	0.1249	FLL	RM 240	2	0.0164	0.1474
NT	RM 6504	1	0.0604	0.0825		OSR 13	1	0.0404	0.1225
FLL	RM 28160	12	0.0235	0.0975	FLW	RM 1261	12	0.0598	0.0818
	OSR 13	1	0.068	0.1019	PL	OSR 13	1	0.0366	0.1588
FLW	OSR 13	1	0.0016	0.2357		RM 240	2	0.039	0.1393
	RM 6504	1	0.0141	0.1372	TGW	RM 1261	12	0.0257	0.118
	RM 3825	1	0.045	0.0703	NFG	RM 125	7	0.0145	0.1543
PL	RM 3825	1	0.0085	0.1191	NUFG	OSR 13	1	0.0015	0.2404
	OSR 13	1	0.0166	0.1594		RM 125	7	0.0277	0.1312
	RM 5753	6	0.056	0.1075	TNG	RM 125	7	0.0049	0.191
TGW	RM 236	2	0.0598	0.0731		RM 11	7	0.0274	0.1261
GY	RM 240	2	0.0075	0.1779		OSR 13	1	0.0539	0.1089
BY	RM 5753	6	0.0522	0.1152					
NFG	RM 11	7	0.0263	0.1283					
TNG	RM 11	7	0.0232	0.1319					

DTF = Days to flowering; PH = plant height (cm); NT = Number of tillers; FLL = Flag leaf Length (cm); FLW = Flag leaf width (cm); PL = Panicle Length (cm); TGW = Thousand grain weight (g); NFG = Number of filled grains; NUGF = Number of unfilled grains; TNG = Total Number of grains; BYP = Biological yield per plant (g); HI = Harvest index (%); GYP = Grain yield per plant (g)

Table.4 List of genotypes having qDTY 1.1 and qDTY 12.1 or both based on markers position

S. No	Markers for qDTY 1.1	Band size (bp)	PIC VALUE	Number of genotypes	Name of genotypes
1	RM 3825	147	0.26	32	IRRI 154, MINGHUI 63, ZHENSHAN 97 B, IR 64-21, IRBB 66, IRRI147, SANHUANGZHA NO 2, IR77186-122-2-2-3, IR77298-14-1-2-10, Supa, IRRI 104, N 22::IRGC 19379-1, MTU1010, Jasmine 85, Sadri, OM4900, IR 95042:13-B-7-11-15-3, IR 93340:14-B-21-17-12-1RGA-2RGA-1-B-B, DJ123, Oryzica 1, F50, TEQING, MG 2::IRGC 79837-1, UPL RI 7::IRTP 9897-C1 CT11891-2-2-7-M, Oryzicasabana 10, Oryzicasabana 6, Oryzica Llanos 5, ChhomrongDhan, NSIC Rc240, Jamir, IR10M300
	Markers for qDTY 12.1	Band size (bp)	PIC VALUE		
2	RM 511	130	0.44	43	MINGHUI 63, ZHENSHAN 97 B, IR 64-21, IRBB 66, IR 69726-116-1-1, SANHUANGZHA NO 2, SambhaMahsuri + Sub1, N 22::IRGC 19379-1, MTU1010, Nanhi, Jasmine 85, KinandangPatong, Sadri, OM4900, IR 95042:13-B-7-11-15-3, IR 93340:14-B-21-17-12-1RGA-2RGA-1-B-B, IR 93354:34-B-5-1-23-1RGA-2RGA-1-B-B, KhaoHlan On, IR13F167, IR84984-83-15-481-B, M202, ManawThukha, BR28, TN1, GSR IR2-9-R1-SU3-Y2, Zanton::IRGC 31248-1, URAIBOOL::IRGC 52785-1, Hokkai 188, IR 126182-1-1-1, IR10F360, Sahel 108, Sahel 134, Sahel 177, Giza 178, Moroberekan, TEQING, CT11891-2-2-7-M, Oryzicasabana 10, Oryzica Llanos 5, ChhomrongDhan, NSIC Rc240, Jamir, IR10M300
Name of common genotype for both QTL (1.1 and 12.1) based on two markers namely, RM 3825 and RM 511					Minghui 63, Zhenshan 97 b, IR 64-21, IRBB 66, Sanhuangzha No 2, N22::IRGC 19379-1, MTU 1010, Jasmine 85, Sadri, OM 4900, IR95042:13-B-7-11-15-3, IR93340:14-B-21-17-12-1RGA-2RGA-1-B-B, Teqing, CT11891-2-2-7-M, Oryzica sabana 10, Oryzica Llanos 5, Chhomrong Dhan, NSCIC Rc240, Jamir, IR10M300

Table.5 List of 42 microsatellite markers with their chromosome locations, number of alleles, allele size and PIC value found among 58 rice accessions.

MARKERS	Forward motif	Reverse motif	C#	Position (cM)	Amplicon Size (bp)	PIC value	No. of Alleles
RM 413	GGCGATTCTTGGATGAAGAG	TCCCCACCAATCTTGTCTTC	5	26.7	71-114	0.48	4
OSR 13	CATTTGTGCGTCACGGAGTA	AGCCACAGCGCCCATCTCTC	3	53.1	85-122	0.51	1
RM 133	TTGGATTGTTTGTCTGGCTCGC	GGAACACGGGGTCGGAAGCGAC	6	0	230	0.00	1
RM 489	ACTTGAGACGATCGGACACC	TCACCCATGGATGTTGTCAG	3	29.2	271	0.70	3
RM 161	TGCAGATGAGAAGCGGCGCCTC	TGTGTCATCAGACGGCGCTCCG	5	96.9	154-187	0.00	1
RM 125	ATCAGCAGCCATGGCAGCGACC	AGGGGATCATGTGCCGAAGGCC	7	24.8	105-147	0.45	3
RM 11	TCTCCTCTTCCCCGATC	ATAGCGGGCGAGGCTTAG	7	47	118-151	0.46	3
RM 307	GTACTACCGACCTACGTTTAC	CTGCTATGCATGAACTGCTC	4	0	116-191	0.51	2
RM 287	TTCCCTGTTAAGAGAGAAATC	GTGTATTTGGTGAAAGCAAC	11	68.6	118	0.68	2
RM 316	CTAGTTGGGCATACGATGGC	ACGCTTATATGTTACGTCAAC	9	1.8	194-216	0.00	1
RM 536	TCTCTCCTCTTGTTTGGCTC	ACACACCAACACGACCACAC	11	55.1	243	0.00	1
RM 520	AGGAGCAAGAAAAGTTCCCC	GCCAATGTGTGACGCAATAG	3	191.6	50-247	0.16	2
RM 236	GCGCTGGTGGAAAATGAG	GGCATCCCTCTTTGATTCCCTC	2	175	105-191	0.44	2
RM 511	CTTCGATCCGGTGACGAC	AACGAAAGCGAAGCTGTCTC	12	59.8	50-130	0.44	2
RM 3739	AGTTGCGCAGCTAATCGATC	AAGATCCAACGGGTCTGTG	12	119.2	110	0.00	1
RM 1261	GTCCATGCCCAAGACACAAC	GTTACATCATGGGTGACCCC	12	61.6	128-167	0.63	2
RM 12010	GGACCGAATCATGAGACAATGG	TTGATGACGTCAAGCGAGAAACC	1	38.91	194-284	0.00	1
RM 3825	AAAGCCCCCAAAGCAGTAC	GTGAAACTCTGGGGTGTTCTG	1	143.7	50-147	0.26	2
RM 28160	AACCACCATCCCCTCCCAACC	CTTATGCCACCACTAACTCCCAAACC	12	17.47	136-249	0.56	2
RM 28199	CGGCTTAGGGAGCGTCTGTAGG	GCATGCTAGTATGGCCACCATATTCC	12	18.15	179	0.00	1
RM 452	CTGATCGAGAGCGTTAAGGG	GGGATCAAACCACGTTTCTG	2	58.4	209	0.00	1
RM 472	CCATGGCCTGAGAGAGAGAG	AGCTAAATGGCCATACGGTG	1	171.6	296	0.00	1
RM 416	GGGAGTTAGGGTTTTGGAGC	TCCAGTTTCACACTGCTTCG	3	191.6	114	0.00	1
RM 518	CTCTTCACTCACTCACCATGG	ATCCATCTGGAGCAAGCAAC	4	25.5	135-171	0.73	4
RM 240	CCTTAATGGGTAGTGTGCAC	TGTAACCATTCCTTCCATCC	2	158	50-132	0.54	4
RM 6504	GAGAGGCGGTAGTATGCTCG	TCTCCAATTTACCGTCACC	1	154.6	50-116	0.59	3
RM 5753	AACATGCTCAACTTCTGGGC	GCTAGGTACGATCCAGCTGC	6	148	201	0.53	3

Contd...

MARKERS	Forward motif	Reverse motif	C#	Position (cM)	Amplicon Size (bp)	PIC value	No. of Alleles
RM 1361	ATTCTCTCCGCCTAAACAAC	TTCTCGTGCACAGTTAATACC	1	155.2	214	0.00	1
RM 3520	GAGGCTATATGCTCATGCTC	AAACCTGCAAATGCACAG	1	159.6	150-178	0.39	2
RM 28130	CAGCAGACGTTCCGGTTCTACTCG	AGGACGGTGGTGGTGATCTGG	12	79.7	60-175	0.26	2
RM 28089	GGGAGGACACCTGTGTAAGTAGG	GGTTCAAATGAGACCCAATTCC	12	15.41	150-260	0.19	2
RM 495	AATCCAAGGTGCAGAGATGG	CAACGATGACGAACACAACC	1	2.8	159	0.55	2
RM 486	CCCCCCTCTCTCTCTCTCTC	TAGCCACATCAACAGCTTGC	1	153.5	104	0.00	1
RM 28048	TTCAGCCGATCCATTCAATTCC	GCTATTGGCCGAAAGTAGTTAGC	12	14.10	93	0.00	1
RM 28076	GGGACTTGGGACCAGTTTATGG	TCAGGTCTGTTGGATTCCATGC	12	15.13	289	0.00	1
RM 28086	CCCGCTGCAGCAGTTTATTGAGG	GATCTGGTACCTGCATGGGTTGC	12	15.33	387	0.00	1
RM 283	GTCTACATGTACCCTTGTTGGG	CGGCATGAGAGTCTGTGATG	1	31.4	151	0.00	1
RM 19	CAAAAACAGAGCAGATGAC	CTCAAGATGGACGCCAAGA	12	20.9	226	0.00	1
RM 431	TCCTGCGAACTGAAGAGTTG	AGAGCAAAACCCTGGTTCAC	1	178.3	251	0.00	1
RM 474	AAGATGTACGGGTGGCATTC	TATGAGCTGGTGAGCAATGG	10	0	252	0.00	1

Fig.1 Graphical representation of PIC value of 22 polymorphic SSR markers

Fig.2 Estimation of K and population structure. Changes in ΔK value with the number of subpopulations

Fig.3 Bar plot showing the population structure of 58 rice germplasm accessions based on SSR markers at K=2

Structure and TASSEL analysis Population Structure analysis

The Bayesian model-based STRUCTURE v2.3.4 program was used to infer population structure of rice genotypes. The 58 lines were divided into two sub groups (Fig. 2) based on the result of Structure Harvester, as delta K kinship was highest at K=2. With population inferred ancestry (Q) = 0.80, forty three lines were assigned to subgroup POP1, rest 8 lines were assigned to subgroup POP2 and seven genotypes/ lines namely, IRBB 66 (5), Sadri (21), M 202 (29), Zanton::IRGC 31248-1 (35), DJ123 (45), MG2::IRGC 79837-1(49) and UPLRI7::IRTP9897-C1 (50) were assigned to admixture (AD) which has less than <0.80 inferred ancestry (Fig. 3).

Courtois *et al.*, (2012) has successfully detected two subgroups in their study population and assigned rice varieties into two groups with few admixture lines. Our results are also in conformity with the findings of Borba (2010) suggesting that using structure analysis, the accessions were sub divided into two panels. Likewise, the

association of yield traits with SSR markers was undertaken with GLM model, with markers and sub population as fixed factors, and kinship matrix as random factor.

Marker-trait association

Association analysis between SSR markers and thirteen agronomic and yield attributing traits was carried out using GLM model over the 58 rice germplasm lines. The marker trait associations based on general linear model (GLM) in irrigated and rainfed conditions are presented in Table 2.

The results indicated that 26 and 31 markers were found to be associated with all the traits in irrigated and rainfed conditions respectively. For days to flowering, RM 3825 (C# 1) and RM 11 (C#7) were found to have tight association in irrigated and rainfed condition. However, RM 5753 (C#6; irrigated) and RM 518 (C#4; rainfed) also possessed tight linkage with days to flowering. Taking MLM model into consideration in irrigated condition, RM 240 (C#2) showed tight linkage with grain yield, presented in Table 3.

References

- Borba, T.C., Brondani, R.V., Breseghello, F., Coelho, A.S.G., Mendonça, J.A., Rangel, P.H.N., Brondani, C. 2010. Association mapping for yield and grain quality traits in rice (*Oryza sativa* L.). *Genet Mol Biol* 33(3): 515–524.
- Courtois, B., Audebert, A., Dardou, A., Roques, S. and Ghneim-Herrera., T. 2013. Genome wide association mapping of root traits in a japonica rice panel. *PLoS One* 8(11):7803-7805.
- Evenson, R.E. and Gollin, D. 2003. Assessing the impact of the green revolution, 1960 to 2000. *Science* 300: 758–762.
- Kohli, A., Narciso, J., Oane, R., Popluechai, S. and Kumar, A. 2010. Identification of major candidate genes in a large effect QTL for rice yield under drought stress, Paper presented at International Rice Congress, Hanoi, Vietnam, 9–11.
- Kwon, J.M. and Goate, A.M. 2000. The candidate gene approach. *Alcohol Res Health*. 24(3): 164-168.
- Pandey, S., Bhandari, H.S. and Hardy, B., 2007. Economic costs of drought and rice farmers' coping mechanisms: a cross-country comparative analysis. *Int. Rice Res. Inst.*.
- Patnala, R., Clements, J. and Batra, J. Candidate gene association studies: comprehensive guide to useful *in silico* tools. *BMC Genet* 14, 39 (2013).
- Richharia, R.H. 1979. An aspect of genetic diversity in rice. *Oryza*. 16(1): 1–31.
- Swamy, B.M., Vikram, P., Dixit, S., Ahmed, H.U. and Kumar, A., 2011. Meta-analysis of grain yield QTL identified during agricultural drought in grasses showed consensus. *BMC genomics*, 12(1), p.319.
- Vikram, P., Swamy, B., Dixit, S., Ahmed, H., Cruz, M.T.S., Singh, A. and Kumar, A. 2011. qDTY1.1, a major QTL for rice grain yield under reproductive stage drought stress with a consistent effect in multiple elite genetic backgrounds. *BMC Genet*.12:89. 72-89.
- Zheng, K., Subudhi, P.K., Domingo, J., Magpantay, G. and Huang, N. 1995. Rapid DNA isolation for marker assisted selection in rice breeding. *Rice Genet. Newsletter* 12: 255–258.

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