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ESTIMATION OF GAS EXCHANGE PARAMETERS IN BACKCROSS INTROGRESSED LINES OF RICE (*Oryza sativa* L.) WITH DIFFERENT COMBINATIONS OF DROUGHT QTLs

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ABSTRACT

The present investigation was carried out to study the gas exchange parameters in backcross inbred lines of 'Improved White Ponni' (IWP) introgressed with different drought yield QTLs and their parents raised under control and stress conditions. Various gas exchange parameters and single plant yield were observed using portable photosynthetic system (infra red gas analyser - IRGA). Among the genotypes, three combination of QTL line IWP-4-2 recorded significantly higher photosynthetic rate (22.97 µ mol CO_2 m^{-2} s^{-1}), stomatal conductance (0.36 mol H_2O m^{-2} s^{-1}), transpiration rate (6.25 mmol H_2O m^{-2} s^{-1}), internal CO_2 concentration (240.82) ratio between internal and atmospheric CO_2 concentration (0.25) and single plant yield (15.11) which was on par with the tolerant parent Apo (an high yielding *indica* cultivar moderately tolerant to drought stress) under severe moisture stress regime. Overall study clearly revealed that, the performance of introgressed line with three drought QTLs (IWP-4-2) was better than two drought QTL introgressed lines of IWP-1-52 and IWP-1-57. Results from graphical genotyping using three foreground and 36 polymorphic background markers revealed that, the three QTL introgressed line IWP-4-2 had 72.20% genome recovery from Improved White Ponni, 13.89% from APO and 13.89% heterozygous region.

Key words: Drought, graphical genotypes, photosynthetic rate, rice, stomatal conductance, transpiration rate

INTRODUCTION

Rice (*Oryza sativa* L.) is a drought susceptible crop exhibiting serious deleterious effects when exposed to water stress at critical growth stages especially at reproductive stage (Suriyan *et al*., 2010). Global climate change and arithmetically multiplying world populace augmented with drought stress are making the situation more serious; and to cope with the ever growing food, feed and shelter needs of human beings has become more difficult day by day (Honogbo *et al*., 2005, Akram, 2007). Current speculations about increase in drought frequencies along with 1.1-6.4^{o}C increase in global average surface temperature by the end of current century pose serious threat to rice production and the overall food security of Asia. Among the different stresses, drought is the

single largest yield reducing factor in rain-fed areas of South and South East Asia, affecting more than 23 million ha area (Huke and Huke, 1997). In India, drought is a major constraint in rice production and may account for about 15% yield loss (Markandeya *et al.*, 2005). Drought stress is affecting about 50% of rice production in the world (Mostajean and Eichi, 2009).

Understanding the genes that govern rice plant architecture and response to drought stress is urgently needed to enhance chances for developing drought tolerant rice types. Recent progress made in the field of genomics has enabled us to access genes linked with drought tolerance and has enhanced our understanding of this complex phenomenon. In order to identify genes associated with drought stress response and their temporal and spatial regulation, genomic approach is required. Under abiotic stress conditions, expression of many genes is induced, and their products have important roles in stress response and tolerance (Venuprasad *et al.,* 2009a). Exploiting the progenies obtained by hybridizing between such tolerant and susceptible lines are useful to identify important QTL underlying variation in grain yield under drought stress. To date, several QTLs with large and consistent effects on grain yield under drought stress have been identified from drought tolerant rice varieties (Bernier *et al.*, 2007; Venuprasad *et al.*, 2011b).

Drought affects nearly all the plant growth processes; however, the stress response depends upon the intensity, rate duration of exposure and the stages of crop growth. Reduction in photosynthesis of water stressed leaves may be due to stomatal closure (Hsiao, 1973). Farquhar and Sharkey (1982) gave a detailed account of the stomatal functioning in relation to stress condition. Recent studies have indicated that a decrease in photosynthesis under deficit soil moisture may not necessarily be related to stomatal opening; rather non-stomatal control of photosynthesis might have greater influence (Farquhar *et al.*, 1989). This study was undertaken to investigate the gas exchange parameters in introgressed lines of Improved White Ponni with different combination of drought QTLs.

MATERIALS AND METHODS

The present study was undertaken to study the effect of drought on gas exchange parameters in backcross inbred lines of Improved White Ponni genotypes in severe moisture stress (rain out shelter) and irrigated condition at Paddy Breeding Station, TNAU, Coimbatore (India) located at latitude of 11^{o} N and longitude of 77^{o} E and an altitude of 426.7 m AMSL. The BILs IWP-1-57 and IWP-1-52 were found to possess two QTLs *qDTY* (3.1 + 6.1) and BIL IWP-4-2 possessed three QTLs *qDTY* (2.2 +3.1+6.1). The two and three QTL harbouring lines were selfed to develop BC_1F_4. The selected BC_1F_4 lines were evaluated for their performance under both well-watered and drought conditions (under rain-out shelter) along with their parents. The three SSR markers namely, RM240 (chromosome 2; 31.4 Mb), RM520 (chromosome 3; 30.9 Mb), RM3414 (chromosome 6; 2.8 Mb), exhibiting polymorphism between Improved White Ponni and Apo were used for foreground selection of target drought QTLs *viz.*, *qDTY2.2*, *qDTY3.1* and *qDTY6.1* (QTLs for yield under stress) into IWP.

Five genotypes *viz.*, IWP-4-2, IWP-1-52, IWP-1-57, Improved White Ponni and Apo (a high yielding *indica* cultivar moderately tolerant to drought stress) were raised in a randomized block design in 4 replicates with a plot size of 1.44 m^2. Cultural practices were followed as per Tamil Nadu Agricultural University Crop Production Guide - 2012 (*http://agritech.tnau.ac.in/pdf/2013/CPG%202012.pdf*). Screening for drought tolerance was done at reproductive stage (Garrity and O'Toole, 1994). Regular irrigation was given and drought stress was imposed by withholding the irrigation 25 days before heading. Soil moisture was recorded at 15 and 30 cm depth by gravimetric method at weekly intervals (Reynolds, 1970).

The genotypes were screened across the genome with SSR markers for background analysis to study the genome constitution of the BILs. Around 36 polymorphic SSR primers were used for background analysis and genotypic data generated in this study was subjected to graphical genotyping using GGT ver. 2.0 (acronym for Graphical Genotyping) which gave out a graphical representation of the molecular marker data. The graphical representations and comparisons were made across the BILs as linkage group-wise and also the entire genome level as individual-wise.

Gas exchange parameters like photosynthetic rate, transpiration rate, stomatal conductance, internal CO_2 concentration and Ci/Ca were determined by a portable photosynthesis system (Infra Red Gas Analyser - Model LI-6400 of LICOR inc., Lincoln, Nebraska, USA) equipped with a halogen lamp (6400-02B LED) positioned on the cuvette. Three measurements were taken in the same leaf of each genotype in all five replications. Leaves were inserted in a 3 cm^2 leaf chambers and PPFD at 1200 µmol photons m^{-2} s^{-1} and relative humidity set at 50-55%.

Analysis of variance, mean, variance and standard error deviation were estimated by adopting standard statistical methods (Panse and Sukhatme, 1961). The correlation between gas exchange parameters and yield were worked out as per the methods suggested by Johnson *et al.* (1955).

$$r = Cov._{xy} / (var_x . var_y)^{\wedge 1/2}$$

Where, r = correlation coefficients, $Cov._{xy}$ = covariance between the characters x and y, Vary = variance of x, Var x = variance of y; x = variable x; and y = variable y

The significance of the correlation estimates were tested by using the formula.

$$\text{'t' calculated} = r / (1-r^2/ n-2)^{\wedge 1/2}$$

Where, r = correlation co-efficient; n = Number of observation. By comparing 't' calculated values with 't' table values at 5 and 1% levels at n-2 degrees of freedom, the significance was found.

RESULTS AND DISCUSSION

Various gas exchange parameters were observed during pre-anthesis stage (peak vegetative phase) and after maturation, single plant yield of introgressed lines with different combination of yield QTLs of drought and parents (IWP and Apo) were also recorded under both stress and irrigated condition. Photosynthesis, being the basis of crop growth, development, biomass production and yield, is one of the key physiological processes strongly affected by drought (Chaves, 1991; Lawlor, 1995). The photosynthetic responses to drought are very complex. Generally, during the onset of drought, CO_2 diffusional resistances increase, especially because stomatal aperture can change rapidly (Chaves *et al.*, 2002; Cochard *et al.*, 2002; Lawlor and Cornic, 2002). Because of the primary importance of photosynthesis in determining crop growth, identifying QTLs controlling photosynthesis parameters is an important step in enhancing MAS for improved yield. In the present investigation, IWP-4-2 with three combination of drought yield QTLs *viz.*, *qDTY2.2*, *qDTY3.1* and *qDTY6.1* had registered significantly higher photosynthetic rate (22.97 µ mol CO_2 m^{-2} s^{-1}) in drought condition and this line exhibited minimum reduction in the trait value (42.24%) than other lines on comparing under irrigated condition. It is important to note that all the QTL region increases grain yield under stress condition and did not have any effect on grain yield under non stress condition. Since the potential expression of QTL/ combination of QTL is robust only when the genotypes cultivated in severe stress condition. Whereas in normal irrigated condition, it is very difficult to find out the expression of these QTL.

Among the combination of two QTL lines harbouring *qDTY3.1* and *qDTY6.1*, IWP-1-57 recorded higher photosynthesis (20.05) than IWP-1-52 (16.14) (Table 1). Lawlor and Cornic (2002) has reported that water deficit reduces the rate of photosynthesis in plants. The increase in leaf photosynthetic rate is important to increase the yield potential of rice (Hirasawa *et al.*, 1999) because the photosynthetic rate of individual leaves which form the canopy, affects dry matter

Table 1: Comparison of trait mean values of gas exchange parameters in drought yield QTL introgressed lines of Improved White Ponni under irrigated and water stress conditions (ROS)

Genotypes	Photosynthetic rate (μ mol CO_2 m^{-2} s^{-1})			Stomatal conductance (mol H_2O m^{-2} s^{-1})			Internal CO_2 conc. (Ci)			Transpiration rate (mmol H_2O m^{-2} s^{-1})			Ci/Ca			Single plant yield		
	C	S	ROC	C	S	ROC	C	S	ROC	C	S	ROC	C	S	ROC	C	S	ROC
IWP-4-2	39.8** (a)	22.97** (a)	42.24	6.39** (a)	0.36 (c)	94.37	363.9** (a)	240.8 ** (a)	33.8	20.8** (a)	6.25 (b)	69.95	0.85 (a)	0.45 (b)	47.06	20.15 (a)	15.11 (a)	25.01
IWP-1-52	33.6 (d)	16.14 (c)	51.92	3.57 (c)	0.22 (c)	93.84	347.0 (c)	179.4 (c)	48.3	18.2 (c)	3.97 (d)	78.14	0.79 (c)	0.38 (cd)	51.90	17.53 (c)	11.28 (bc)	35.65
IWP-1-57	36.8 (b)	20.05 (b)	45.53	4.91 (b)	0.29 (c)	94.09	358.5 (b)	209.6 (b)	41.5	19.5** (b)	5.38 (c)	72.42	0.82 (b)	0.41 (bc)	50.00	19.06 (b)	12.99 (ab)	31.85
IWP	32.3 (e)	14.3 (d)	55.70	3.55 (c)	0.22 (b)	93.80	364.8** (a)	195.0 (c)	46.5	13.7 (e)	5.42 (c)	60.35	0.85 (a)	0.34 (d)	60.00	19.64 (ab)	9.61 (c)	51.07
APO	34.4 (c)	22.41** (a)	34.93	6.37** (a)	0.41 (a)	93.56	363.8 ** (a)	246.3** (a)	32.3	16.8 (d)	7.18** (a)	57.36	0.86** (a)	0.53** (a)	38.37	14.04 (d)	10.92 (bc)	22.22
Mean	35.4	19.14		4.96	0.30		359.6	214.2		17.8	5.64		0.83	0.42		18.08	11.98	
SE+	0.18	0.68		0.09	0.07		1.26	0.02		0.24	0.21		0.008	0.01		0.47	1.02	
$CD_{0.05}$	0.41	1.56		0.21	0.16		2.90	0.05		0.56	0.49		0.018	0.05		1.09	2.37	
$CD_{0.01}$	0.59	2.27		0.30	0.23		4.22	0.08		0.81	0.71		0.02	0.06		1.59	3.44	

C - Control ; S - Stress; ROC = % Reduction over control; **significant at 1% level; *significant at 5% level; a,b,c,d,e - mean comparison by Least Square Design, a - best performing treatment, e - poorest performing treatment

production. Differences in photosynthetic and leaf gas-exchange capacities of *O. sativa* varieties have been ascribed to genetic variation (Gu *et al.,* 2012). The quantitative trait loci responsible for leaf gas exchange and photosynthetic parameters in *O. sativa* tend to be in the adjacent regions of plant genome; indicative of exertion of selective pressures favouring coordination and high heritability of photosynthetic behaviour (Hu *et al.,* 2009; Gu *et al.,* 2012).

Among the physiological traits studied, GCV was greater in stomatal conductance both under control and stress conditions (Table 2). The lowest GCV was observed for the internal CO_2 concentration in both control and stress conditions. Broad sense heritability was estimated for different traits and computed across two environments. The traits *viz.,* photosynthetic rate, stomatal conductance, transpiration rate, internal CO_2 concentration, single plant yield and Ci/Ca recorded the highest h^2 values of 0.99, 0.99, 0.98, 0.95, 0.94 and 0.88, respectively, under control condition (Table 2). In stress condition, the heritability was higher in photosynthetic rate (0.99), transpiration rate (0.99) followed by stomatal conductance (0.89) and Ci/Ca (0.89). The traits *viz.,* photosynthetic rate, internal CO_2 concentration and Ci/Ca recorded the highest genetic advance in both control and stress conditions. The difference in PCV and GCV varied gradually from control to stress condition. This clearly indicated that, the influence of environment on these traits was enhanced under severe stress condition. These findings were similar to the assumption that traits are much significantly influenced by the environmental factors under moisture stress condition (Fukai and Cooper, 1995).

Under control conditions, photosynthetic rate depicted high and positive correlation with stomatal conductance (0.706) and transpiration rate (0.886) (Table 3). Stomatal conductance recorded high and positive correlation with internal CO_2 concentration (0.536), transpiration rate

Table 2: Variability parameters of physiological traits in both control and stress conditions

	Control				Stress			
Traits	GCV	PCV	h^2	GA(%) of mean	GCV	PCV	h^2	GA(%) of mean
PS	8.37	8.39	0.99	17.19	19.79	20.26	0.95	39.84
SC	28.39	28.48	0.99	58.32	26.88	28.49	0.89	52.25
Ci	2.06	2.10	0.95	4.16	12.99	14.41	0.81	24.12
TR	15.36	15.45	0.98	31.46	20.87	21.37	0.95	42.00
Ci/Ca	3.34	3.55	0.88	6.50	16.60	17.53	0.89	32.37
SPY	13.51	13.89	0.94	27.07	16.64	19.67	0.71	29.01

PR = Photosynthetic rate; SC = Stomatal conductance; Ci = Internal CO_2 concentration; Ca = Atmospheric CO_2 concentration. TR = Transpiration rate; SPY = Single plant yield; GCV = Genotypic variance; PCV = phenotypic variance; h^2 = heritability; GA = Genetic advance

Table 3: Genotypic correlation coefficient for physiological traits under control and stress

Traits	Environment	PR	SC	Ci	TR	Ci/Ca	SPY
PR	C	1.000	0.706**	0.226	0.886**	0.108	0.361
	S	1.000	0.963**	0.925**	0.73**	0.888**	0.751**
SC	C		1.000	0.536*	0.528*	0.572*	-0.307
	S		1.000	1.000**	0.915**	1.000**	0.452*
Ci	C			1.000	-0.233	0.99**	0.08
	S			1.000	0.977**	0.914**	0.479*
TR	C				1.000	-0.322	0.195
	S				1.000	0.82**	0.204
Ci/Ca	C					1.000	-0.13
	S					1.000	0.29
SPY	C						1.000
	S						1.000

PR = Photosynthetic rate; SC = Stomatal conductance; Ci = Internal CO_2 concentration; TR = Transpiration rate; SPY = Single plant yield; C = control; S = Stress; * = significant at 1% level; * = significant at 5 % level

(0.528) and Ci/Ca (0.572). Internal CO_2 concentration had significant and positive correlation with Ci/Ca (0.99). Under stress, the physiological traits *viz.*, photosynthetic rate, transpiration rate and stomatal conductance had significant positive correlation with grain yield. Photosynthetic rate had high and positive correlation with stomatal conductance (0.963), internal CO_2 concentration (0.925), transpiration rate (0.73) and Ci/Ca (0.888). Stomatal conductance recorded high and positive correlation with internal CO_2 concentration (1.000), transpiration rate (0.915) and Ci/Ca (1.000). Internal CO_2 concentration had significant and positive correlation with transpiration rate (0.977) and Ci/Ca (0.914). Transpiration rate had significant and positive correlation with Ci/Ca (0.82) (Table 3). Therefore, effective screening and analysis of the photosynthetic and gas exchange characteristics of *O. sativa* varieties under stress conditions has the potential to identify functional traits associated with optimisation of water use efficiency (WUE) and the maintenance of yield attributes under drought (Flexas *et al.*, 2013). Stomata play a paramount role in the control of water loss and gas exchange in leaves. During the onset of drought, stomatal conductivity declines before photosynthesis, and the inhibition of photosynthesis during mild stress is mainly due to the reduction of CO_2 diffusion (Lawlor, 2002). However, the appearance of non-stomatal limitation to photosynthesis was evident in IWP-4-2 as deduced from an increase in Ci/Ca ratio. The traits stomatal conductance and transpiration rate were higher in IWP-4-2 in drought as well as water logged condition which was followed by the genotype IWP-1-57. The adaptive potential of some plant species reducing water losses are achieved by closing of stomata and reduction in the transpiration rate (Tardieu and Davies, 1993). Hence, measurement of transpiration rate is an excellent tool to assess drought tolerant capacity of crop plants. However, reduction of transpiration rate under drought causes increment of leaf temperature is deleterious effect for plants.

Graphical genotyping was carried out for marker data of all the three genotypes and the results provided the pictorial representation of genome recovery (Fig 1a,b,c). The BIL IWP-1-52 registered higher genome recovery of 94.59% from Improved White Ponni than other BILs namely IWP-1-57 (83.78%) and IWP-4-2(72.2%) (Table 4). The genotype IWP-4-2 received genome recovery of 13.89% from the donor parent Apo. The results of GGT ultimately delivered that the genotype IWP-4-2 had 94.59% genome from recipient parent (IWP) and 13.89% from donor parent and 13.89% was heterozygous region. On comparison with phenotyping results, this BIL line had possess all the three yield drought QTLs *qDTY* (2.2 +3.1+6.1) from Apo. In all the three BIL lines, the maximum introgression was observed in chromosome 6. Parida *et al*. (2009) analyzed genomic constitution of rice genotypes based on chromosome-wise physical distribution of variant SNP loci and allele sharing between *indica* and *japonica*. This revealed maximum introgression of *japonica*

Table 4. List of background markers used to determine background recovery in BILs IWP-4-2, IWP-1-52, IWP-1-57

Primer name	Chr. No.	Chr. position	Primer sequence (forward)	Primer sequence (reverse)	Repeat motifs	IWP -4-2	IWP -1-52	IWP -1-57
RM8077	1	37.4	TGTAAAGTTGTCAAGGGACTACTC	GGGGTATAGTAGACAACATCAAAA	$(GA)_{17}$	-	A	A
RM490	1	51	ATCTGCACACTGCAAACACC	AGCAAGCAGTGCTTTCAGAG	$(CT)_{13}$	A	A	A
RM488	1	101.4	CAGCTAGGGTTTTGAGGCTG	TAGCAACAACCAGCGTATGC	$(GA)_{21}$	A	A	A
RM154	2	4.8	ACCCTCTCCGCCTCGCCTCCTC	CTCCTCCTCCTGCGACCGCTCC	-	A	A	A
RM233	2	16.3	CCAAATGAACCTACATGTTG	GCATTGCAGACAGCTATTGA	$(CT)_{20}$	A	A	H
RM2634	2	80.85	GATTGAAAATTAGAGTTTGCAC	TGCCGAGATTTAGTCAACTA	$(AT)_{31}$	H	A	A
RM3316	2	130.2	TTCGACGATTCTGTACACGC	CATGATCCCAAATGCATGGG	$(CT)_{14}$	B	A	A
RM6283	3	83.3	TGGAGACTGAGCTGATGCC	TCAGGTGGTCGGTTCCTTAC	$(CTG)_{8}$	A	A	A
RM251	3	21.35	GAATGGCAATGGCGCTAG	ATGCGGTTCAAGATTCGATC	$(CT)_{29}$	H	A	H
RM232	3	76.7	CCGGTATCCTTCGATATTGC	CCGACTTTTCCTCCTGACG	$(CT)_{24}$	A	A	A
RM570	3	158.2	GTTCTTCAACTCCCAGTGCG	TGACGATGTGGAAGAGCAAG	$(AG)_{15}$	B	A	A
RM252	4	99	TTCGCTGACGTGATAGGTTG	ATGACTTGATCCCGAGAACG	$(CT)_{19}$	H	A	A
RM255	4	120.8	TGTTGCGTGTGGAGATGTG	CGAAACCGCTCAGTTCAAC	(AGG)5(AG)$_{2}$-$(GA)_{16}$	A	A	A
RM335	4	21.5	GTACACACCCACATCGAGAAG	GCTCTATGCGAGTATCCATGG	$(CTT)_{25}$	A	A	A
RM122	5	2.3	GAGTCGATGTAATGTCATCAGTGC	GAAGGAGGTATCGCTTTGTTGGAC	(GA)7A(GA)$_{2}$A$(GA)_{11}$	A	A	A
RM440	5	92.7	CATGCAACAACGTCACCTTC	ATGGTTGGTAGGCACCAAAG	$(CTT)_{22}$	A	A	A
RM169	5	57.9	TGGCTGGCTCCGTGGGTAGCTG	TCCCGTTGCCGTTCATCCCTCC	$(GA)_{12}$	A	A	A
RM574	5	41	GGCGAATTCTTTGCACTTGG	ACGGTTTGGTAGGGTGTCAC	$(GA)_{11}$	A	A	A
RM39	5	78.7	GCCTCTCTCGTCTCCTTCCT	AATTCAAACTGCGGTGGC	$(CT)_{17}$CCA$(TC)_{3}$	A	A	A
RM430	5	78.7	AAACAACGACGTCCCTGATC	GTGCCTCCGTGGTTATGAAC	$(GA)_{25}$	A	A	A
RM508	6	2.25	GGATAGATCATGTGTGGGGG	ACCCGTGAACCACAAAGAAC	$(AG)_{17}$	B	A	B
RM585	6	25.1	CAGTCTTGCTCCGTTTGTTG	CTGTGACTGACTTGGTCATAGG	$(TC)_{45}$	B	H	B
RM400	6	134.5	ACACCAGGCTACCCAAACTC	CGGAGAGATCTGACATGTGG	$(ATA)_{63}$	A	A	A
RM11	7	47	TCTCCTCTTCCCCCGATC	ATAGCGGGCGAGGCTTAG	$(GA)_{17}$	H	A	A
RM336	7	61	CTTACAGAGAAACGGCATCG	GCTGGTTTGTTTCAGGTTCG	$(CTT)_{18}$	H	A	H
RM447	8	124.6	CCCTTGTGCTGTCTCCTCTC	ACGGGCTTCTTCTCCTTCTC	$(CTT)_{8}$	A	A	A
RM6999	8	32.7	TTATCTGGGATCCATCGAGC	GTGAATTTCCTTGGAGGGAC	$(TTG)_{15}$	A	A	A
RM245	9	112.3	ATGCCGCCAGTGAATAGC	CTGAGAATCCAATTATCTGGGG	$(CT)_{14}$	A	A	A
RM242	9	73.3	GGCCAACGTGTGTATGTCTC	TATATGCCAAGACGGATGGG	$(CT)_{26}$	A	A	A
RM5841	10	72.77	CCTCTCTCTCTCTCTCCCCC	TGTTATTGGCACGTGGTGTG	$(ATA)_{19}$	A	A	H
RM3773	10	59.9	CTGGATGAAAGGATACAACA	CACATTATCTGTCAAGGTCC	$(GA)_{18}$	A	H	A
RM228	10	81.2	CTGGCCATTAGTCCTTGG	GCTTGCGGCTCTGCTTAC	(CA)6$(GA)_{36}$	A	A	A
RM222	10	11.3	CTTAAATGGGCCACATGCG	CAAAGCTTCCGGCCAAAAG	$(CT)_{18}$	A	A	A
RM286	11	2.2	GGCTTCATCTTTGGCGAC	CCGGATTCACGAGATAAACTC	$(GA)_{16}$	A	A	A
RM287	11	68.6	TTCCCTGTTAAGAGAGAAATC	GTGTATTTGGTGAAAGCAAC	$(GA)_{21}$	B	A	A
RM332	11	27.9	GCGAAGGCGAAGGTGAAG	CATGAGTGATCTCACTCACCC	$(CTT)_{5\text{-}12\text{-}(}CTT)_{14}$	A	A	A
RM235	12	21.8	AGAAGCTAGGGCTAACGAAC	TCACCTGGTCAGCCTCTTTC	$(CT)_{24}$	A	A	A
Recurrent parent genome recovery (%)						72.2	94.5	83.7

A = Recurrent parent (Improved White Ponni); B = Donor parent (Apo); H = Heterozygote; Chr = chromosome

in chromosome 12 (average 63%) followed by chromosomes 7 (59%) and 1 (57%). In contrast chromosome 6 contained maximum introgression (68%) of *indica* genome. Parida *et al*. (2012) also reported that, SNP alleles for each locus were marked in different colors and incorporated in ascending order of physical location (bp) beginning from the short arm telomere to the long arm telomere of each rice chromosome to generate allele sharing maps of individual rice genotypes and determine the extent of recombination and introgression across chromosomes. Guo *et al*. (2013) reported that, the *O. minuta* chromosomal segments harbored chromosomal fragments of *O. sativa* ranging from 1.15 to 27.6%, with an overall average of 8.57%. At each locus, the ratio of substitution of *O. minuta* alleles had a range of 1.5−25.2%, with an average of 8.3%. Therefore, graphical genotypes provides insight of selection of introgressed lines with maximum recurrent parent recovery and hastens the process of selection in advanced backcross populations in any plant species.

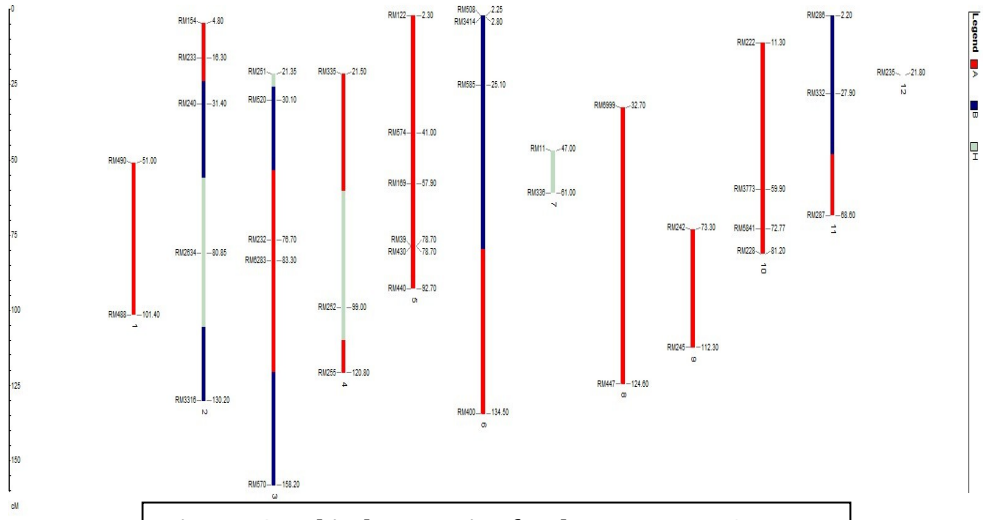

Fig. 1a: Graphical genotyping for the BIL IWP-4-2

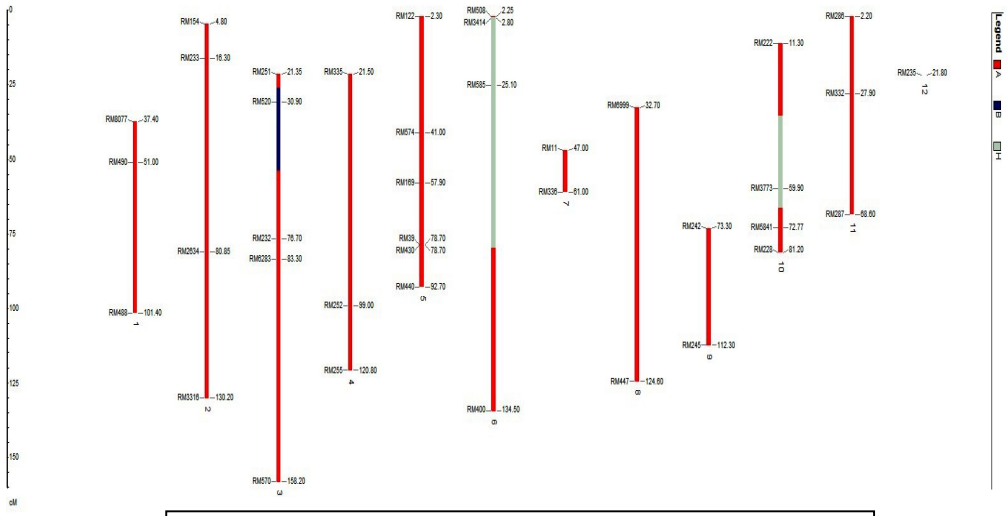

Fig. 1b: Graphical genotyping for the BIL IWP-1-52

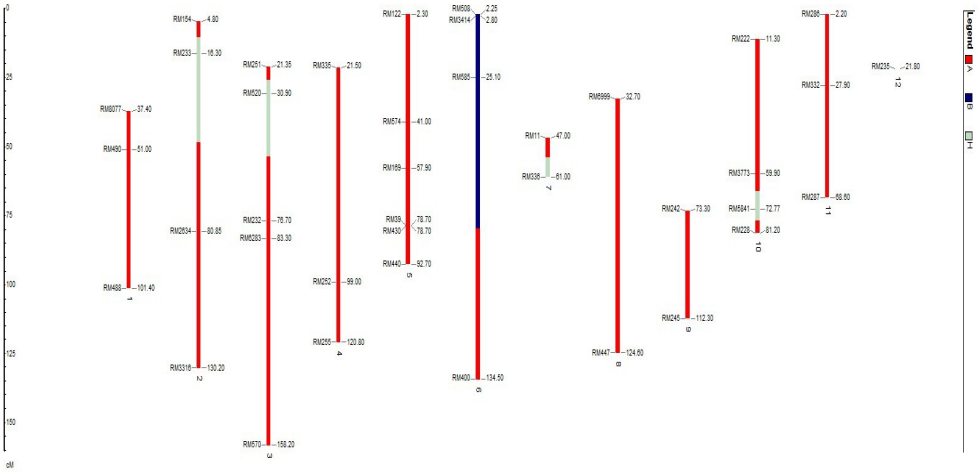

Fig. 1c: Graphical genotyping for the BIL IWP-1-57

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