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Effectiveness of drought yield QTLs on physiological traits and yield in backcross inbred lines of rice under moisture stress condition

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ABSTRACT

In this study, four Backcross Inbred lines (BIL) with multiple QTL combinations ($qDTY_{2.2}$, $qDTY_{3.1}$ and $qDTY_{8.1}$) were studied to estimate their yielding ability and stability of yield gain as an effect of introgressed drought yield QTL under moisture stress. The four BIL lines namelyCB-193-1 ($qDTY_{2.2}$ and $qDTY_{3.1}$), CB-193-2 ($qDTY_{2.2}$ and $qDTY_{8.1}$), CB-193-3 ($qDTY_{3.1}$ and $qDTY_{8.1}$) and CB- 229 ($qDTY_{2.2}$, $qDTY_{3.1}$ and $qDTY_{8.1}$) were observed for biometrical traits related to yield and physiological parameters under moisture stress. The results showed that the line CB-229 outperformed others under drought, which indicated that, the combination of three QTLs viz., $qDTY_{2.2}$, $qDTY_{3.1}$ and $qDTY_{8.1}$ had a major effect on grain yield under moisture stress than single and 2-QTL lines. Graphical genotyping was carried out using polymorphic SSR markers on these lines and found that they were harbouring many chromosomal segments from Apo, the donor and the maximum recovery of IR64 was found in linkage group 2 and 6. The total protein content, osmotic adjustment and the chlorophyll 'a' were also found to be higher in these lines which conferred tolerance to drought stress. The slow reduction in RWC with higher photosynthetic rate and conductance were found in these lines as of the donor parent Apo.

Key words : *Drought stress, Grain yield, Heritability, Major QTLs, Moisture stress, Physiological parameters, Rice.*

INTRODUCTION

Rice (*Oryza sativa* L.) is basically a water-loving plant and gives good yield under optimum soil moisture regime. But rice yield reduces drastically under soil moisture stress imposed by natural short dry-spells in rainfed upland rice or by withholding water supply under irrigated rice culture. It is of paramount importance to identify the QTLs that affect grain yield under moisture stress. Grain yield in rice represents the multiplicative integration of three main components *i.e.* number of panicles per plant, number of grains per panicle and mean grain weight (Sakamoto and Matsuoka, 2008; Xing and Zhang, 2010). In recent years, attempts have been made to detect and locate QTLs (Quantitative trait loci) or polygenes for grain yield and other important agronomical traits in rice (Venuprasad *et al.,* 2008). In this study, consistent-effect of QTLs associated with grain yield under drought stress were identified using different BILs derived from crossing Apo, a drought-tolerant rice landrace with mega variety IR64 as recipient parents. Four lines with different QTL combinations were compared to find the QTL which has major effect on grain yield during drought by phenotyping for yield and yield-component traits under reproductive-stage drought-stress and non-stress conditions in the *kharif* 2015.

MATERIALS AND METHODS

This present study was conducted at Paddy Breeding Station (PBS), Tamil Nadu Agricultural University, Coimbatore during *kharif* 2015.

Four lines (BILs) of IR64 which were in BC_1F_5generation, developed from the cross combination of IR64 X Apo along with the parents were used in the study. Apo, drought tolerant upland variety, developed at IRRI, recommended for cultivation under aerobic conditions was used as donor parent. Owing to its drought tolerance nature and good performance under aerobic conditions, it served as an important source for mining drought tolerant QTLs. IR64 used as recipient parent is a medium duration and high yielding variety but highly prone to drought.

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BILs from the cross between IR64 X Apo were generated which carried three mega QTL viz., q$DTY_{2.2}$, $qDTY_{3.1}$ and q$DTY_{8.1}$ in different combinations. The four BIL lines of CB 193-1 ($qDTY_{2.2}$ and $qDTY_{3.1}$), CB 193-2 ($qDTY_{2.2}$ and $qDTY_{8.1}$), CB 193-3 ($qDTY_{3.1}$ and $qDTY_{8.1}$), CB 229 ($qDTY_{2.2}$, $qDTY_{3.1}$ and $qDTY_{8.1}$) were raised along with the parents to study the profound expression of QTLs under severe drought condition.

Field trials : Trials under reproductive-stage drought-stress (RS) and non-stress (NS) conditions were conducted in completely Randomized block design with four replicates. One seedling was transplanted per hill at 21 days after sowing(DAS) in a two-row plot of 2m length, at a spacing of 0.2×0.2 m under normal condition. After transplanting, 2–5cm of standing water was maintained in the field until maturity under NS condition. Replanting for missing hills was conducted at five days after transplanting (DAT). Under RS condition, direct sowing was taken up, with a plant spacing of 0.2 x 0.2 m in rain out shelter (ROS). The seeds were sown in two row plot of 2m length. Gap filling and thinning to maintain single seedling per hill was done 21 days after sowing. Recommended crop production and protection practices were followed to raise a healthy crop.

Imposition of stress : Under RS condition, irrigation was withheld on 45th day after sowing at the maximum tillering stage to impose severe stress at the reproductive stage. Soil moisture potential was recorded at regular intervals and after the reading reached -70KPa the crop was irrigated thus an intermittent severe stress at the reproductive stage was imposed.

Biometrical observation and analysis : In both the trials, observations were made on days to 50% flowering (DTF), plant height (PH) at maturity, number of productive tillers per plant, panicle length, sterility per cent and grain yield (GY) were recorded. The physiological parameters were recorded when the soil moisture potential was between -60 to -70 KPa. Infrared Gas Analyzer (IRGA), a portable photosynthetic system (LICOR- Model LI 6400 version.5) was used for the measurement of different physiological parameters. Relative water content was estimated by Weatherley Method (1950) and expressed in percentage. The basic principle (Barrs and Weatherley, 1962) of this technique consists essentially in comparing the water content of leaf tissue when fresh leaf sampled with the fully turgid water content and expressing the results on percentage basis. The leaf sap was collected to estimate the osmotic potential and the osmolality (mmol kg^{-1}) of the expressed sap was determined using a vapour pressure osmometer (Vapro, Model 5520 WescorInc., Logan, UT, USA). Osmotic potential (wp) was calculated as $\Psi\pi = -cRT$, where c is concentration, R is the universal gas constant (0.0832) and T is the temperature in degrees Kelvin (310^0 K). Chlorophyll 'a' content was recorded using a portable chlorophyll meter (Minolta SPAD 502) before and after imposing drought (Monje and Bughree,1992). Total soluble protein was estimated from fresh leaf sample as given by Lowry *et al.* (1951).

Genotyping : Fresh leaves for all lines were collected and freeze-dried. DNA was extracted from freeze-dried leaf samples by a modified CTAB method method (Murray and Thompson, 1980). Polymerase chain reaction (PCR) was performed by the method described by Panaud *et al.* (1996). Agrose gel was then used for size separation of the amplified DNA fragments using electrophoresis unit (Genei).The DNA fragments were then visualized using trans-illuminator. Foreground selection was done with RM71, RM520 and RM256 for $qDTY_{2.2}$, $qDTY_{3.1}$ and $qDTY_{8.1}$ respectively. Around 123 polymorphic markers were used for background analysis. Graphical genotyping software GGT 2 (Berloo, 2008) was used for construction of a linkage map thus to study the recurrent parent recovery per cent.

Statistical analysis : Biometrical traits associated with yield and yield contributed traits were subjected to computation of means and standard error of difference (SED) were analyzed using GENERS, as random. For the calculation of variance components, the effect of lines was also considered random. Heritability (h^2) in the broad sense was calculated according to Lush (1940).

$$h^2(\text{B.S.}) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

where,

σ_g^2 = Genotypic variance and σ_g^2 = Penotypic variance

RESULTS AND DISCUSSION

Phenotypic performance of the populations : Tolerance to abiotic stresses is very complex at the whole plant and cellular levels (Foolad *et al.,* 2003). Several studies have been conducted in the past to show the effectiveness of selection based on yield under drought in a segregating population derived from a drought tolerant donor and a high yielding variety (Venuprasad *et al.,* 2007, 2008; Kumar *et al.,* 2008, 2009). The results related to yield attributes of rice genotypes under drought stress at reproductive stage and irrigated condition have been presented in **Table 1**. Rice genotypes grown under water stress condition produced significantly lower grain yields than flooded rice. Yield decline was observed almost in all the rice genotypes from 13.94 to 59.36 % grown under drought stress condition. Single plant yield under stress condition ranged from 11.05 g to 21.20 g. Among the BILs, CB-229, CB-193-3 outperformed IR64 under ROS condition and on par with IR64 under non stress condition. Several QTLs have been previously reported to have had a significant effect on GY under moisture stress but being highly specific to the background parent they were originally detected in (Maccaferri et al., 2008). Similarly QTL mapping studies were undertaken to identify QTLs for tolerance to drought (Bernier *et al.,* 2007; Venuprasad *et al.,* 2009; Vikram *et al.,* 2011; Ghimire *et al.,* 2012).

Table 1. Mean performance of various plant characters studied under controlled and moisture stress condition

Genotype	ENVN	Biometrical traits											
		DF		PH (cm)		PT		FP (%)		TP (mg g^{-1})		YPP (g)	
		Mean	R%	Mean	R%	Mean	R%	Mean	R%	Mean	R%	Mean	R%
IR64	C	87.75	12.54	81.75	5.20	18.00	44.44	93.43	21.39	25.60	73.44	27.18	59.36
	S	76.75		77.50		10.00		73.44		6.80		11.05	
APO	C	91.00	11.26	114.25	4.38	14.25	10.53	93.34	13.41	23.40	46.58	23.16	13.94
	S	80.75		109.25		12.75		80.83		12.50		19.93	
CB-229	C	85.75	14.29	77.25	10.03	17.75	29.58	93.89	13.98	24.80	33.47	27.13	21.86
	S	73.50		69.50		12.50		80.77		16.50		21.20	
CB -193-1	C	88.50	16.38	79.75	1.88	18.75	45.33	92.07	13.69	20.70	30.92	24.84	27.06
	S	74.00		78.25		10.25		79.46		14.30		18.12	
CB -193-2	C	91.25	12.05	82.50	1.52	17.75	33.80	91.91	13.06	21.60	31.02	25.46	22.66
	S	80.25		81.25		11.75		79.91		14.90		19.69	
CB -193-3	C	84.25	13.65	88.00	2.56	17.00	36.76	92.24	13.19	24.30	35.00	26.24	23.15
	S	72.75		85.75		10.75		80.08		15.79		20.16	
Mean ±SE	C	88.08±1.14		87.25±5.59		17.25±0.64		92.81±0.34		23.40±0.78		25.67±0.63	
	S	76.33±1.43		83.58±5.58		11.33±0.48		79.08±1.15		13.47±1.45		18.36±1.52	

DF - Days to flowering, PH - Plant height, PT - Productive tillers, FP - Fertility per cent,
TP - Total protein content, YPP - Yield per plant, R% - Per cent reduction over control

Phenotypic variation for GY and yield-related traits : The means, percentage reduction over control and heritability, GCV, PCV and Genetic advance as per cent of mean are presented in **Table 1 and 2**. Among the phenotypic traits studied, the GCV and PCV were higher in the case of plant height and number of productive tillers under controlled condition whereas under stress condition the GCV and PCV were higher for fertile grains per panicle followed by osmotic adjustment. The lowest GCV was observed for the trait fertility percentage in both control and stress condition. Broad sense heritability was estimated for different traits and computed across two environments. The trait *viz.,* hundred grain weight, osmotic adjustment and total protein recorded the highest h2 values of 0.99 under stress condition and hundred grain weight had higher heritability under controlled condition. The trait fertile grains per panicle recorded the highest genetic advancement under stress condition which was followed by the osmotic adjustment (Table 2).

It is interesting that *$qDTY_{8.1}$* showed a positive effect on GY under stress. The effect of this QTL was also seen on yield related traits such as number of productive tillers per plant and panicle length under drought conditions. In general it has been observed that the effect of QTLs for yield under drought declines with decreasing severity of stress. Such pattern of effects has been seen for *$qDTY_{12.1}$* (Bernier *et al.,* 2009). Palanog *et al.* (2014) found that *$qDTY_{2.2}$* showed an effect on MTU1010 background but not on the IR64 background. Previously, in the study conducted by Swamy et al. (2013), *$qDTY_{2.2}$* showed effect in the advanced backcross mapping population developed by the cross of AdaySel and IR64 in contrast to the present study which had used a BC_1 derived mapping population. This indicated the effect of source of QTL allele and effect of genetic background on the expression of a QTL.

Table 2. Estimation of different genetical parameters under both control and stress condition

Characters	Control				Stress			
	GCV	PCV	HERT (h^2)	GA (%) of mean	GCV	PCV	HERT	GA (%) of mean
DF	3.14	3.26	0.92	6.21	4.54	4.72	0.93	8.99
PH (cm)	15.93	16.07	0.98	32.52	16.08	16.23	0.98	32.80
PT	8.82	9.96	0.79	16.11	7.70	15.74	0.24	7.754
PL (cm)	3.92	4.07	0.93	7.77	6.02	6.24	0.93	11.95
FG	5.44	5.66	0.92	10.76	36.02	36.77	0.96	72.71
FP	0.81	1.16	0.49	1.16	2.97	4.91	0.37	3.70
CH a	3.09	4.03	0.59	4.88	3.87	4.24	0.83	7.24
OA	-	-	-	-	33.55	33.65	0.99	68.93
TP (mg g^{-1})	8.08	8.35	0.94	16.11	26.23	26.30	0.99	53.87
HGW (g)	5.02	5.05	0.99	10.23	5.54	5.56	0.99	11.38
YPP (g)	5.90	6.21	0.90	11.55	20.20	20.41	0.98	41.15

PL - Panicle length, FG - Filled grains per panicle, CH a - Chlorophyll a, HGW - Hundred grain weight, OA - Osmotic adjustment

Table 3. Genotypic correlation coefficient for all traits under control and moisture stress condition

Characters	Environment	DF	PH	PT	PL	FG	FP	CH a	OA	TP	HGW	YPP
DF	C	1	0.453	-0.317	-0.199	-0.782**	-0.227	-0.88**	-	-0.538*	-0.737**	-0.689**
	S	1	0.594*	0.545*	-0.193	0.125	-0.002	-0.073	0.18	-0.324	-0.515*	-0.077
PH (cm)	C		1	-1	-0.242	-0.75**	0.248	-0.86	-	0.052	-0.429	-0.791**
	S		1	0.483	-0.422	0.328	0.363	0.328	0.526*	-0.09	-0.462	0.21
PT	C			1	0.301	0.595*	-0.334	0.686**	-	-0.202	0.198	0.669**
	S			1	0.242	0.988**	0.978**	0.963**	0.983**	0.619*	0.452	0.939**
PL (cm)	C				1	0.404	0.066	0.21	-	0.505*	0.003	0.523*
	S				1	0.265	-0.153	0.01	-0.083	0.099	0.848**	0.039
FG	C					1	0.126	0.981**	-	0.542*	0.848**	0.967**
	S					1	0.675**	0.624*	0.705**	0.346	0.465	0.577*
FP	C						1	0.136	-	0.862	0.526	0.321
	S						1	0.991**	0.989**	0.981**	0.351	0.971**
CH a	C							1	-	0.5*	0.95**	0.976**
	S							1	0.985**	0.924**	0.412	0.981**
OA	C								-	-	-	-
	S								1	0.753**	0.246	0.934**
TP (mg g^{-1})	C									1	0.671**	0.597*
	S									1	0.537*	0.942**
HGW (g)	C										1	0.78**
	S										1	0.445
YPP (g)	C											1
	S											1

*Significance at 0.05%, **Significance at 0.01%.

Correlation studies : Under control conditions number of filled grains per panicle (0.967) and chlorophyll 'a' (0.976) content had recorded high and significant positive correlation with yield and chlorophyll 'a' (0.981) (**Table 3**). Days to flowering (-0.689) and plant height (-0.791) had negative correlation with yield. Under stress, fertility percentage (0.971), chlorophyll 'a' (0.981), osmotic adjustment and total protein content had high and positive correlation with grain yield. Similarly osmotic adjustment (0.934), total protein (0.942) and chlorophyll 'a' (0.981) recorded high and positive correlation with yield and days to flowering is negatively correlated with hundred grain weight (-0.515) and yield per plant (-0.077). Studies have also shown moderate correlation between yield performance of lines selected under managed dry season screening at IRRI and wet season screening in target environments like Eastern India (Verulkar *et al.,* 2010).

Physiological characterization : A significant difference in relative water content (RWC), photosynthetic rate, conductance, transpiration and Ci/Ca was observed among genotypes between drought stress and irrigated condition. In water stress condition, higher value of RWC was recorded in tolerant rice genotypes as compared to susceptible genotypes at reproductive stage (**Fig. 1**). There was a slow decline in transpiration rate in the resistant genotypes when compared to that of the susceptible parent IR 64. Chen *et al.* (1995) observed that elevating photosynthetic rate is beneficial to dry matter production and yield. Cao *et al.* (2001) reported that photosynthetic rate among rice varieties were significant and the net photosynthetic rate as a selection parameter for drought resistant genotypes.

Mohan *et al.* (2000) stated that the chlorophyll content is an indication of stress tolerance capacity of plants and its high value means that the stress did not have much effect on chlorophyll content of tolerant plants. Gowri (2005) observed decrease in chlorophyll content under water scarcity situation than irrigated environment. Thus the results indicated that grain yield under stress was limited due to decreased production and translocation of assimilates as the sink size, is not affected (Chaturvedi and Ingram, 1989; Ahmed, 1992). The results clearly indicated that water deficit during booting to anthesis initiation is more detrimental than anthesis stage stress.

Total protein content was found to be higher in drought tolerant genotypes. This was in agreement with the results of Jha and Singh (1997) and Beena *et al.* (2012) that water scarcity stress tolerant rice genotypes had comparatively higher protein content than susceptible lines under water stress condition. Reduction of soluble protein under water stress condition suggested that lipid peroxidation products hydrolyze protein coding mRNAs (Jiang *et al.,* 1992).

Graphical genotyping of rice BILs using SSR makers' data : Graphical genotypes are very useful for plant breeders to develop ideal genotypes ('ideotypes') which contain desirable marker alleles at multiple target loci throughout the genome. Two rice genotypes (CB-229, CB-193-3) which showed consistent yield enhancement under

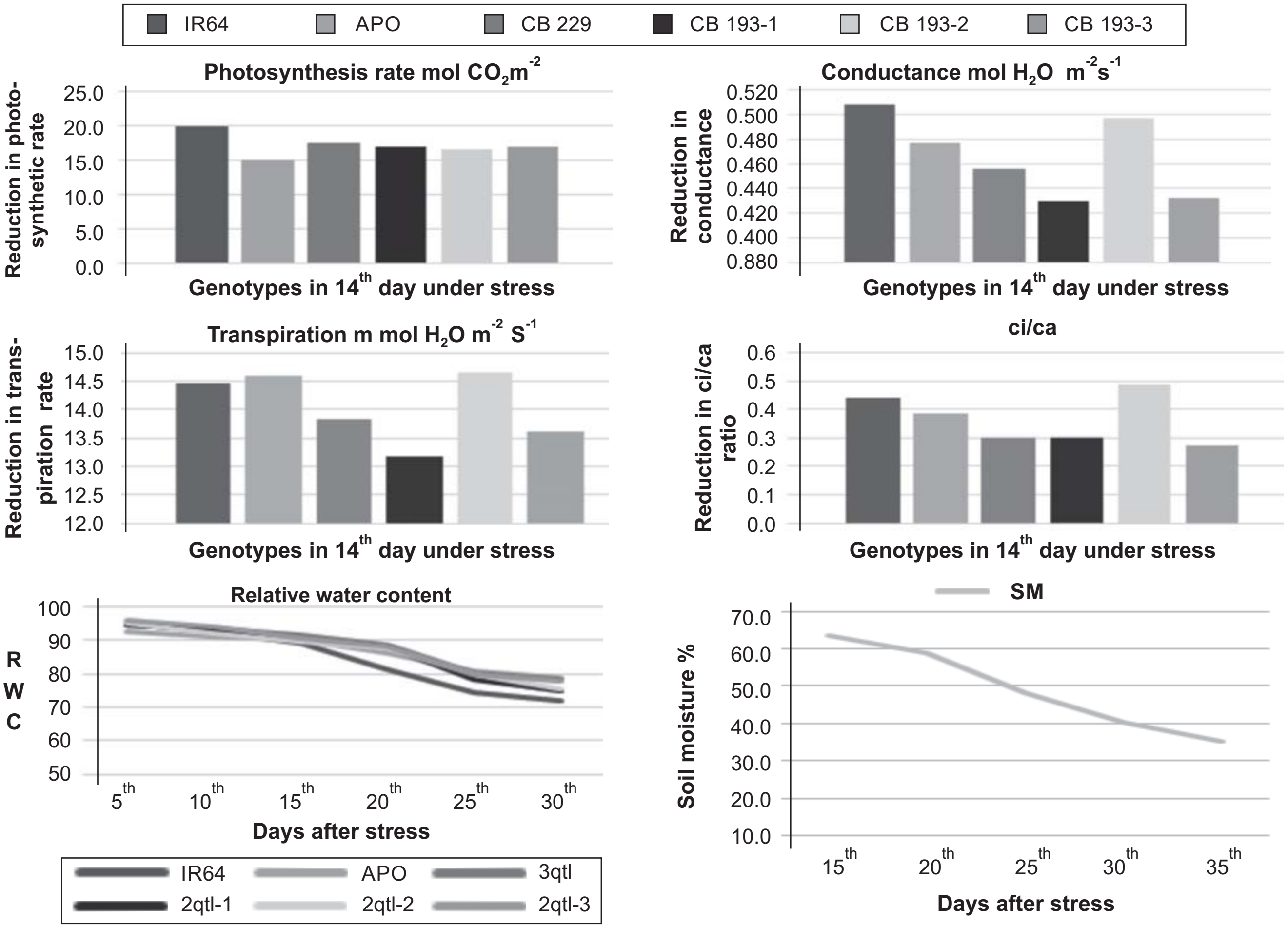

Fig. 1. Effect of drought stress condition on various physiological parameters of rice genotypes.

Table 4. Genome recovery per cent

Sr. No.	Genotypes	IR64 genome (%)	Apo genome (%)	Heterozygote (%)
1	CB-229	57.8	25.2	17.1
2	CB-193-3	58.8	23	18.2

stress was graphically genotyped. Among the 348 SSR markers distributed throughout 12 chromosomes of rice, 123 (35.34%) could detect polymorphism between IR64 and Apo. Finally, 123 polymorphic SSR markers equably distributed throughout 12 linkage groups were used to screen the genotypes of BILs. The genome recovery per cent of the BILs are given in the **Table 4**. The carrier chromosome namely 2,3 and 8 had six and seven segments from the donor parent in CB- 229 and CB 193-3 respectively. The non carrier chromosomes had more number of segments from Apo and some regions with heterozygosity. Further selfing and selection through MAS will enable in picking up lines with more recovery of recipient parent.

Pyramiding multiple QTLs with differing efficiencies under diverse genetic backgrounds would result in gain in grain yield under moisture stress condition when compared to the other combinations of QTLs. These observations support the hypothesis that selection for yield under reproductive-stage drought stress is effective in rice, and that choice of donor is very important in breeding drought-tolerant rice. From the results it is clear that the genotype CB 229 had an increase in yield when compare to IR64 under both the environment indicating that three QTL combination in IR64 background is more tolerant to drought condition.

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REFERENCES

Ahmed A. 1992. Operational performance of the rural rationing programme in Bangaladesh. *Food Policy in Bangladesh*. Working paper No. 5, Washington DC. *International Food Policy Research Institute.*

Barrs H D and Weatherley P E. 1962. A reexamination of the relative turgidity technique for estimating water deficits in leaves. *Aust J Biol Sci.* **15 :** 415–428.

Beena R, Thandapani and Chandrababu R. 2012. Physio-morphological and biochemical characterization of selected recombinant inbred lines of rice for drought resistance. *Indian J. Plant Physiol*. **17** (2) **:** 189-193.

Berloo V R. 2008. GGT 2.0: versatile software for visualization and analysis of genetic data. *Journal of Heredity*. **99 :** 232–236.

Bernier J, Kumar A, Ramaiah V, Spaner D and Atlin G. 2007. A large-effect QTL for grain yield under reproductive-stage drought stress in upland rice. *Crop Sci*. **47:** 507–518.

Bernier J, Kumar A, Venuprasad R, Spaner D, Verulkar S, Mandal N P, Sinha P K, Peeraju P, Dongre P R, Mahto R N, Atlin G, 2009. Characterization of the effect of a QTL for drought resistance in rice, qtl12.1, over a range of environments in the Philippines and eastern India. *Euphytica*. **166 :** 207-217.

Cao S Q, Zhai H Q, Yang T N, Zhang R X and Kuang T Y. 2001. Studies on photosynthetic rate and function duration of rice germplasm resources. *Chin J Rice Sci.* **15** (1) **:** 29–34. (in Chinese with English abstract).

Chaturvedi G S and Ingram K T. 1989. Growth and yield of lowland rice in response to shad and drainage. *Philipp J Crop Sci*. **14** (2) **:** 61–67.

Chen W F, Xu Z J and Zhang B L. 1995. *Physiological Bases of Super High Yield Breeding in Rice.* Liao Ning Science and Technology Publishing Company, Shenyang, China.

Ghimire H K, Quiatchon L A, Vikram P, Swamy B P M, Dixit S, Ahmed H, Hernandez J E, Borromeo T H and Kumar A. 2012. Identification and mapping of aQTL (qDTY1.1) with consistent effect on grain yield under drought. *Field Crops Res.* **131 :** 88–96.

Gowri S. 2005. Physiological studies on aerobic rice (*Oryza sativa* L.). M.Sc., thesis submitted to TNAU, Coimbatore, India.

Jha B N and Singh R A. 1997. Physiological responses of rice varieties to different levels of moisture stress. *Indian J. Plant Physiol*. 2: 81-84.

Jiang M Y, Jing J M and Wang S T. 1992. Effect of osmotic stress on membrane lipid peroxidation and endogenous protective systems in rice seedlings. *Acta Phtophysiol. Sinica.* **17 :** 80-84.

Kumar A, Bernier J, Verulkar S, Lafitte H R, Atlin G N. 2008. Breeding for drought tolerance : direct selection for yield, response to selection, and use of drought tolerant donors in upland and lowland-adapted populations. *Field Crops Res*. **107 :** 221–231.

Lowry O H, Rosebrough N J, Farr A L and Randall R J. 1951 Protein measurement with the Folin phenol reagent. *J. Biol. Chem.* **193 :** 265-275.

Lush J L. 1940. Relative importance of dam's productivity, pig's own market score and pig's own growth rate, in selecting young boars and gilts for breeding. Research Item No. 18 of the Regional Swine Breeding Laboratory. Mimeographed. Ames, Iowa.

Maccaferri M, Sanguineti M C, Corneti S, Araus J L, Ben Salem M, Bort J, DeAmbrogio E, Garcia delMoral L, Demontis A, El-Ahmed A, Elouafi I, Maalouf F, Machlab H, Martos V, Nachit M N, Nserallah N, Ouabbou H, Royo C, Slama A, Villegas D and Tuberosa R. 2008. Quantitative trait loci for grain yield and adaptation of durum wheat (*Triticum durum* Desf.) across a wide range of water availability. *Genetics.* **178 :** 489–511.

Mohan M M, Lakshmi S N and Ibrahim S M. 2000. Chlorophyll stability index (CSI): its impacton salt tolerance in rice. *IRRI Newsletter.* pp. 38-39. Monje and Bughree, 1992.

Monje O A. and Bughree. 1992. Inherent limitation of non-destructive chlorophyll meters. A comparison of two types of meters. *Hort. Sci.* **27 :** 71-89.

Murray M G and Thompson W F. 1980. Rapid isolation of high molecular weight plant DNA. *Nucleic Acid Res*. **8 :** 4321-4326.

Palanog A D, B.P. MallikarjunaSwamy, NoraziyahAbd Aziz Shamsudin, Shalabh Dixit, Jose E. Hernandez, Teresita H. Boromeo, Pompe C. Sta. Cruz, Arvind Kumar. 2014. Grain yield QTLs with consistent-effect under reproductive-stage drought stress in rice. *Field Crops Research.* **161 :** 46–54.

Panaud O, Chen X and McCouch S. 1996. Development of microsatellite markers and characterization of simple sequence length polymorphism (SSLP) in rice (*Oryza sativa* L.). *Mol Gen Genet.* **252 :** 597–607

Sakamoto T and Matsuoka M. 2008. Identifying and exploiting grain yield genes in rice. *Curr Opin Plant Biol.* **11 :** 209–223

Swamy Mallikarjuna B P, Ahmed H U, Henry A, Mauleon R, Dixit S, Vikram P, Tilatto R, Verulkar S B, Perraju P, Mandal N P , Variar M, Robin S, Chandrababu R, Singh O N, Dwivedi J L, Das S P, Mishra K K, Yadav R B, Aditya T L, Karmakar B, Satoh K, Moumeni A, Kikuchi S, Leung H and Kumar A. 2013. Genetic, physiological, and gene expression analyses reveal that multiple QTL enhance yield of rice mega-variety IR64 under drought. *Plos One*. **8** (5) **:** e62795.

Venuprasad R, Dalid C O, Del Valle M, Zhao D, Espiritu M, Sta Cruz M T, Amante M, Kumar A and Atlin G N. 2009. Identification and characterization of large-effect quantitative trait loci for grain yield under lowland drought stress in rice using bulk-segregant analysis. *Theor Appl Genet* . **120 :** 177–190

Venuprasad R, Sta Cruz M T, Amante M, Magbanua R, Kumar A and Atlin G N. 2008. Response to two cycles of divergent selection for grain yield under drought stressin four rice breeding populations. *Field Crops Res*. **107 :** 232–244.

Verulkar S B, Mandal N P, Dwivedi J L, Singh B N, Sinha P K, Mahato R N, Dongre P, Singh O N, Bose L K, Swain P, Robin, S, Chandrababu R, Senthil S, Jain A, Shashidhar H E, Hittalmani S, Vera Cruz C, Paris T, Raman A, Haefele S, Serraj R, Atlin G and Kumar A. 2010. Breeding resilient and productive rice genotypes adapted to drought-prone rainfed ecosystems of India. *Field Crops Res*. **117 :** 197–208.

Vikram P, MallikarjunaSwamy B P, Dixit S, Ahmed H U, Sta Cruz M T, Singh A K 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.* doi:10.1186/1471-2156-12-89

Xing Y and Zhang Q. 2010. Genetic and molecular bases of rice yield *Annu. Rev. Plant Biol.* 2010. **61 :** 11.1–11.22.

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