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SCREENING OF TRANSPLANT *AMAN* RICE GENOTYPES FOR SUBMERGENCE TOLERANCE BASED ON MORPHO-GENETIC PARAMETERS

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ABSTRACT

Rice (*Oryza sativa* L.) is the staple food of more than three billion people in the world. The trend of increasing submergence has a negative effect on the rice yield but some of the rice genotypes show the excellent performance to give a satisfactory yield under submergence stress. Screening is very effective and reliable technique for submergence stress. The total of thirty rice genotypes including four modern varieties and twenty-six advanced lines were used for screening them against submergence tolerance by morphological analysis in the farm yard of Genetics and Plant Breeding division at Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh following modified hydroponic method. The experimental treatments comprised two factors, Factor A: Thirty T. *aman* rice genotypes; Factor B: Submerged condition and non-submerged control condition. The rice genotypes with diverse genetic background were used for screening of submergence tolerance at reproductive stages. The phenotypic co-efficient of variation (PCV) was higher than the genotypic co-efficient of variation (GCV) for all the characters studied indicating that they all interacted with the environment to some extent. The heritability for all characters was in the range of 62.44% to 99.42% and the highest heritability was found in number of filled grain panicle^{-1} (99.42%). The performance of the genotypes with respect to yield and yield components differed from each other under submergence and non-submergence conditions. Yield and yield components of the genotypes reduced in submergence condition. IR 28, IR 16, IR 18, IR 05, IR 06, IR 07, IR 24 were identified as tolerant to submergence stress. All tolerant genotypes showed higher plant height, number of total tillers plant^{-1} number of effective tillers plant^{-1}, panicle length, number of filled grains panicle^{-1}, 1000-grain weight and yield plant^{-1}, respectively. Therefore, identified genotypes are considered promising rice varieties tolerant to submergence stress.

Keywords: Rice genotype, Phenotypic co-efficient, Genotypic co-efficient, Submergence tolerance.

INTRODUCTION

As a cereal grain, rice is the most widely consumed staple food for a large part of the world's human population, especially in Asia. In Bangladesh, around 75.61% of cropped area is used for rice production; with annual production of 36.28 million tons from 11.62 million hectares of land (BBS, 2018). But rice is the most vulnerable cultivated crop to future changing climate (Mohanty *et al.,* 2013). Submergence stress is considered as a major challenge for rice production in South and Southeast Asia, causing annual losses of over one billion US dollars (Mackill *et al.,* 2006; Xu *et al.,* 2006; Khanh *et al.,* 2013). The most common climatic events in Bangladesh are floods, especially monsoon and flash floods that causes submergence of rice plants for 10- 15 days (Dewan, 2015; Rahman and Zhang, 2016; Dar, 2017). About one million hectares of land is flash flood prone in Bangladesh, which may occur more than one times. Flash floods and excessive rainfalls regularly affect rain-fed lowland rice (RLR) ecosystems in many parts of the country where flood water remains for around two weeks. Due to monsoon rains *aman* rice suffers from flash flood in different parts of the country. To cope with this environmental condition, it is obvious to find out new breeding strategies to improve yield by changing and adopting characteristics that has direct relation to increase rice yield under submergence condition.

Submergence tolerance, which is partially a function of the character of flood water (Ram *et al.,* 1999), is an important breeding objective intended to reduce, to the barest minimum, yield losses recorded in rain-fed lowland and deep-water rice areas (Mackill, 1986; Mohanty and Chaudhary, 1986; Kawano *et al.,* 2002; Kawano *et al.,* 2009). *Sub1* gene is an ethylene-response-factor that enhances submergence tolerance of rice. Plant adopts different mechanisms to tolerate the submergence stress. Quiescence and elongation are two opposite strategies by which rice adapts to flood depending upon the nature of flooding (Luo *et al.,* 2011). Rice plants that exhibit only limited elongation during submergence often show tolerance to flash flooding. This is probably due to energy conservation during flooding for maintenance and survival processes. A strong negative correlation between percent survival and elongation growth is commonly observed (Ella and Ismail, 2006). The most important mechanisms may be the formation of aerenchyma in the roots and leaves and their inter-connections that allows smooth gas movement especially O_2 from shoot to root to promote root growth and plant survival under O_2 deficient conditions (Vartapetian and Jackson, 1997), maintenance of high level of non-structural carbohydrate such as starch and soluble sugars. But the ideal response to flooding is submergence tolerance (survival under water) together with some elongating ability (Mackill *et al.,* 2010; Bailey-Serres and Voesenek, 2010).

The areas affected by flooding are expected to increase substantially as a consequence of sea-level rise and the predicted increases in frequencies and intensities of flooding caused by extreme weather events (Bates *et al.,* 2008). Although floods destroy millions of tons of rice every year, but there is little research on rice production under flooding condition. For up surging the rice production under the stress condition to feed the overgrowing population, it is very important to find out new promising submergence tolerant genotypes. And to identify novel sources of tolerance, we have to conduct a faster, easy and scorable germplasm screening. Greater efforts are now being devoted to identify more sources and bases of submergence tolerance. Cultivars are needed that have faster growth after submergence so that it could produce sufficient biomass in a shorter period (Sarkar and Bhattacharjee, 2011). Because, regeneration capacity of submerged rice seedlings is crucial for high productivity (Panda *et al.,* 2008). Therefore, the present study was undertaken to screen and find out the promising high yielding T. *aman* rice genotypes under submergence condition based on morpho-genetic parameters.

MATERIALS AND METHODS

Experimental site

This study was conducted in the farm yard of Plant Breeding division at Bangladesh Institute of Nuclear Agriculture, Mymensingh from June to December 2017. The soil type of the experimental site was silty clay loam under the AEZ 9 (Old Brahmaputra Flood Plain).

Experimental materials

A total of thirty rice genotypes including four checks with diverse genetic background were used for screening of submergence tolerance. Among them, twenty-six genotypes were advanced *T. aman* rice lines (Table 1) and the rest four checks were released varieties of submergence tolerant (Binadhan-11, Binadhan-12, BRRI dhan51, BRRI dhan52). These genotypes were selected for screening at the reproductive stage to exhibit various degrees of tolerance to submergence condition.

Experimental design

Design of the experiment was Completely Randomized Design (CRD) with two factors, Factor A: Thirty (30) T. *aman* rice genotypes; Factor B: Submerged condition and non-submerged control condition. Drum and pot screening method was used. Germinated seeds of thirty different rice entries were sown in each of the two replications in pot filled with fertilized soil containing 50 N, 25 P and 25 K mg/kg of soil. Two glass fibre trays were filled with ordinary tap water and pots were placed on these trays. Those served as a water bath and then the seedlings were grown for eight weeks under normal condition. Eight weeks old seedlings were then transferred into 100 cm long drum with 49 cm diameter and submerged with 95 cm depth of tank water. The water depth was maintained 95 cm throughout the experiment. Then the seedlings are fully submerged for 15-20 days. After 15-20 days of submergence the seedlings were taken from the drum and get of the water and kept it under normal condition until maturity. Weeding, thinning, irrigation, pesticide etc. were followed as and when necessary to ensure the normal plant growth and development. Upon maturity data on yield and yield components were taken. The considered traits for data collection were plant height (cm), number of total tillers plant^{-1}, number of effective tillers plant^{-1}, panicle length (cm), number of filled grains panicle^{-1}, number of unfilled grains panicle^{-1}, 1000-grain weight (g) and yield plant^{-1} (g). Percent reduction was calculated using the following formula:

% reduction= {(traits of normal- traits in submergence)/ Traits in normal} x100

Statistical analysis

MSTAT-C software was used to perform statistical analysis of data on yield and yield components from normal and submerged condition. Duncan's Multiple Range Test (DMRT) was used for lettering the mean performance of rice genotypes. Genetic parameters such as genotypic and phenotypic variance, heritability, genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV), genetic advance and correlation co-efficient were estimated as follows:

i.	Genotypic variance, σ^2_g (Johnson *et al.,* 1955)	$\sigma^2 g = \frac{GMS-EMS}{r}$	Where, GMS = Genotypic mean square EMS = Error mean square r = Number of replication
ii.	Phenotypic variance, σ^2_p (Johnson *et al.,* 1955)	$\sigma^2_p = \sigma^2_g + EMS$	Where, σ^2_g = genotypic variance EMS = Error mean square
iii.	Heritability, h^2_b (Johnson *et al.,* 1955 and Hanson *et al.,* 1956)	$h^2_b = \frac{\sigma^2_g}{\sigma^2_p} \times 100$	Where, σ^2_g = genotypic variance σ^2_p = phenotypic variance
iv.	Genotypic co-efficient of variations, GCV (Burton and Devane, 1953 and Singh and Choudhruy, 1985)	$GCV = \frac{\sigma^2_g}{\bar{x}} \times 100$	Where, σ^2_g = genotypic variance $\bar{x}$ = population mean
v.	Phenotypic co-efficient of variations, PCV (Burton and Devane, 1953 and Singh and Choudhruy, 1985).	$PCV = \frac{\sigma^2_g}{\bar{x}} \times 100$	Where, σ^2_g = phenotypic variance $\bar{x}$ = population mean
vi.	Genetic advance, GA (Johnson *et al.,* 1955)	$GA = h^2_b.K.\sigma_p$	Where, h^2b = heritability K = selection differential, the value of which is 2.06 at 5% selection intensity σ_p = phenotypic standard deviation
vii.	Genetic advance in percentage of mean, GA (%) (Comstock and Robinson, 1952)	$GA (\%) = \frac{GA}{\bar{x}} \times 100$	Where, GA = genetic advance $\bar{x}$= population mean
viii.	Genotypic correlation, $rg_{1.2}$ (Miller *et al.,* 1985)	$rg_{1.2} = \frac{CoV.g^{1.2}}{\sqrt{\sigma^2 g^1 \times \sigma^2 g^2}}$	Where, CoV. $g^{1.2}$ = genotypic covariance between the trait x_1 and x_2. $\sigma^2 g^1$ = genotypic variance of the trait x_1 $\sigma^2 g^2$ = genotypic variance of the trait x_2
ix.	Phenotypic correlation, $rp_{1.2}$ (Miller *et al.,* 1985).	$rp_{1.2} = \frac{CoV.p^{1.2}}{\sqrt{\sigma^2 p^1 \times \sigma^2 p^2}}$	Where, CoV.$p^{1.2}$= phenotypic covariance between the trait x_1 and x_2. $\sigma^2 g^1$ = phenotypic variance of the trait x_1 $\sigma^2 g^2$ = phenotypic variance of the trait x_2

RESULTS AND DISCUSSION

Analysis of Variance

Analysis of variance of thirty rice genotypes for yield and yield attributing traits revealed that significant differences were present among the genotypes for all the studied traits under submergence treatment except number of effective tiller plant^{-1} for genotype-treatment interaction (supplementary Table 1 and 2). BRRI dhan51 (16.07%), IR 06 (15.43%) and Binadhan-11 (8.45%) showed highest plant height reduction under the submergence stress (Table 3). On the other hand, lowest plant height reduction was observed by IR 12 (6.52%) followed by IR 16 (6.81%). These results indicated that plant height reduced under the submergence stress. This result agrees with that of Sugai *et al.,* 1999 and Kotera *et al.,* 2005. Submergence stress might inhibit cell division or cell enlargement so that plant height was reduced. Increase of plant height is a submergence adaptive trait occurred in most of the cases where water stagnation is common (Sugai *et al.,* 1999). Under submergence stress IR 01 (26.48%) showed highest reduction in number of total tiller plant^{-1} followed by BRRI dhan52 (21.18%). IR 24 (33.38%), IR 01 (31.93%), IR 04 (22.22%) and IR 02 (20.00%) showed greater number of effective tiller plant^{-1} reduction under the submergence stress whereas IR 05 (1%), IR 28 (3.30%), IR 08 and IR 19 (5.58%) exhibited the lowest number of effective tiller plant^{-1} reduction under the submergence stress (Table 3). Number of effective tiller plant^{-1} was highest at non-submergence condition (IR 18) and lowest at submergence condition (IR24) (Table 2). A decreasing trend in effective tillers plant^{-1} was shown by all the varieties as the duration of submergence increased (Table 2). The number of the effective tillers plant^{-1} is one of the major yield determinants. The genotype in which the reduction of effective tiller plant^{-1} due to submergence is lower is considered as submergence tolerant because the high tilling ability is desirable for achieving maximum yield. Due to submergence the formation of tiller bud might hamper which decreased the tiller number. Hanada *et al.,* (1990) suggested that the lack of oxygen for respiration or accumulation of ethylene might inhibit tiller bud formation and growth. However, the loss in tillers per unit area could not be compensated for in the sensitive genotypes because of the drastic decrease (up to 98 %) in survival (Singh *et al.,* 2014). Panicle growth was also retarded by the submergence stress. At this study, in reproductive stage several genotypes showed highest panicle length reduction. IR 14 showed highest panicle length reduction (15.77%) followed by IR 21 (11.13%), IR 17 (9.32%) and Binadhan-11 (9.12%). On the other hand, IR 13 showed lowest (2.16%) panicle length reduction (Table 3). Panicle length was highest at non-submergence condition (IR 05) and lowest at submergence condition (Binadhan-12) (Table 2). The results are conformity with Hushine (2004) who stated that panicle length was affected by the number of seedlings hill^{-1}. Though submergence decreased the panicle length, the reduction rate was very low. Considering filled grain, genotypes IR 10 (0.00%), IR 06 (3.12%), IR 19 (3.99%) and IR 20 (4.11%) showed lowest reduction. On the other hand, IR 23 (7.41%), Binadhan-12 (7.12%), IR 16 (6.71%) and BRRI dhan51 (6.66%) showed highest reduction (Table 3). Submergence tolerant genotypes showed lower reduction of number of filled grain panicle^{-1} than the non-submergence tolerant. This is because of loss of biomass production was lower in tolerant genotypes which increased the assimilation and ultimately produced the high number of grains (Table 3). Mahapatra (2017) found a significant difference among the cultivars as regard to number of grains panicle^{-1}.1000-grain weight was also highest at non-submergence stage and lowest at submergence stress. 1000-grain weight decreased with increase in the duration of submergence in every variety (Table 2). IR 25 (14.71%), Binadhan-12 (10.34%), IR 24 (5.92%), IR 27 (5.32%) and IR 23 (5.22%) showed greater 1000-grain weight reduction under the submergence stress. On the other hand, lowest 1000-grain weight reduction was observed by IR 29 (1.18%) followed by IR 05 (2.33%), Binadhan-11 (2.45%) and IR 08 (2.73%) (Table 3). Decreased grain size in submerged treatment might be due to improper grain filling; though the difference was not significant. Nugraha *et al.,* (2012) stated that the lowest 1000-grain weight under submergence conditions was due to improper grain filling and uneven filling stage, therefore, at harvest the grains had different maturity stages thus lowered grain weight. Zhang *et al.,* (2015) did not found any significant difference between control and submergence treated plant. Yield plant^{-1} was also greater at non-submergence stage and lower at submergence stress (Table 2). On the basis of yield, IR 24 (6.25%), Binadhan-12 (7.69%), Binadhan- 11 (8.31%) and IR 13 (8.33%) showed lowest reduction. On the other hand, IR 11 (15.35%), IR 05 (15.00%), IR 08 (14.83%) and IR 15 (14.56%) showed highest reduction (Table 3). Wang *et al.,* (2014) investigated the influence of slight submergence (2 days and 4 days) on midseason rice at the final phase of the tilling stage and found that the yields of the experimental groups were close to those of the control group. Different yield components like number of total tiller plant^{-1}, number of panicle plant$^{-1,}$ panicle length was greatly affected by submergence stress in rice (Voesenek and Bailey-Serres, 2015).

Estimation of genetic parameters of rice genotypes

Genetic parameters for all studied yield attributing traits are presented in Table 4. In this study all the traits showed significant genotypic and phenotypic variance (Table 4). This study indicated that for all the traits phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) (Table 4). Similar result was found by Bhadru *et al.,* (2012). The difference between the PCV and GCV indicated the environmental influence. In this study the lowest value of GCV and PCV was found for the trait plant height while the highest value of GCV and PCV was found for the trait yield plant^{-1} (Table 4). The estimates of GCV reflect the total amount of genotypic variability. However, the study of PCV and GCV is not only useful for comparing the relative amount of phenotypic and genotypic variations among different traits but also very useful to estimate the scope for improvement by selection. Heritability estimates are of great important in plant breeding. In this study, most of the studied traits showed high heritability (Table 4). Heritability of all the traits ranging from 62.44% to 99.42%; while the highest heritability was found in number of filled grain panicle^{-1} (99.42%) (Table 4). High heritability values indicate that the characters under study are less influenced by environment in their phenotypic expression and have the greater possibility of genetic improvement through selection methods. Character showing high heritability may not necessarily give high genetic advance. Johnson *et al.,* (1955) showed high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion. The highest value of genetic advance was found in trait 1000-grain weight (60.34). The lowest genetic advance was in number of unfilled grain panicle^{-1} (1.8) (Table 4). High heritability and low genetic advance was observed for number of filled grain panicle^{-1} and number of unfilled grain panicle^{-1} (Table 4). These may be attributed to non-additive gene action governing the traits, and these characters could be improved through the use of hybridization and hybrid vigor. The highest value in genetic advance as percent of mean was found for the trait number of effective tiller plant^{-1} (178.23 %); while the lowest value (4.32 %) for the trait number of unfilled grain panicle^{-1} (Table 4).

Phenotypic correlations among the traits

Supplementary Table 1: Analysis of variance (mean square) of the data for yield and yield contributing characters of rice.

Sources	df	Plant height (cm)	No. of total tiller plant^{-1}	No. of effective tiller plant^{-1}	Panicle length (cm)	No. of filled grain panicle^{-1}	No. of unfilled grain panicle^{-1}	1000-grain weight	Yield plant^{-1}
Variety	29	283.77**	8.62**	12.14**	38.37**	1565.40**	209.51**	85.05**	113.95**
Treatment	1	1450.67**	57.80**	89.61**	125.83**	3108.36**	16.81**	48.15**	206.93**
Variety × Treatment	29	50.14*	10.12*	0.69	1.26**	6.98**	304.15**	9.12*	43.32*
Error	120	18.08	0.78	0.97	0.51	3.02	34.99	0.43	0.79

**- Significant at 1% level of probability, *- Significant at 5% le vel of probability, df- Degrees of freedom.

Supplementary Table 2: Performance of rice genotypes under submergence treatments.

Genotypes	Plant height (cm)	No. of total tiller plant^{-1}	No. of effective tiller plant^{-1}	panicle length (cm)	No of filled grain panicle^{-1}	No. of unfilled grain panicle^{-1}	1000-grain weight (g)	Yield plant^{-1} (g)
IR 01	78.83 b-f	9.83	7.00 fg	27.03 ab	127.17 pq	23.00 c	24.97 efgh	19.00 cdef
IR 02	75.83 c-f	11.17	9.00 b-g	23.43 e-h	164.17 c-h	31.17 bc	16.62 n	16.00 e-i
IR 04	81.00 b-e	10.83	8.00 d-g	26.77 abc	151.67 i-l	35.83 abc	23.78 hij	28.50 a
IR 05	75.00 def	11.83	9.50 a-f	28.33 a	179.83 ab	39.00 abc	25.50 c-h	18.50 c-g
IR 06	68.00 fg	12.50	9.33 a-g	26.20 a-d	185.00 a	47.00 ab	27.17 abc	16.83 efgh
IR 07	83.00 a-d	11.17	9.17 a-g	24.15 c-f	160.50 e-i	36.00 abc	29.05 a	16.00 e-i
IR 08	77.00 c-f	12.83	11.67 ab	25.32 b-f	166.83 c-g	40.00 abc	27.82 ab	16.67 efgh
IR 09	83.00 a-d	11.67	7.50 efg	26.25 a-d	136.83 nop	37.00 abc	26.62 b-g	20.83 bcd
IR 10	75.33 c-f	11.50	9.83 a-e	24.05 d-g	168.00 c-f	43.17 abc	19.60 m	22.50 b
IR 11	83.00 a-d	10.67	10.17 a-e	25.50 b-e	138.67 mno	39.50 abc	28.18 ab	16.00 e-i
IR 12	84.17 a-d	13.00	10.00 a-e	26.37 a-d	172.00 bcd	49.17 ab	26.87 bcde	17.83 d-h
IR 13	76.00 c-f	11.33	9.33 a-g	27.50 ab	169.83 b-e	40.17 abc	26.77	23.00 b
IR 14	83.00 a-d	12.83	10.50 a-d	20.27 ij	158.33 f-j	43.50 abc	24.77 ghi	13.17 ij
IR 15	85.00 abc	10.83	7.50 efg	26.38 a-d	141.17 lmn	45.33 ab	25.60 c-h	14.83 hij
IR 16	89.83 ab	13.67	11.50 ab	25.05 b-f	158.50 f-j	53.00 a	25.55 c-h	15.83 fghi
IR 17	84.00 a-d	12.33	10.50 a-d	23.83 d-h	153.67 h-k	37.00 abc	27.93 ab	16.83 efgh
IR 18	78.00 cdef	13.17	11.83 a	25.17 b-f	167.00 cdef	41.33 abc	25.53 c-h	15.00 hij

continued…

IR 19	70.00 efg	13.50	11.67 ab	25.20 b-f	163.67 d-h	39.50 abc	25.10 d-h	12.33 j
IR 21	83.00 abcd	12.33	8.50 c-g	22.67 fghi	137.00 nop	34.50 abc	22.93 ijk	17.83 d-h
IR 22	75.17 def	9.83	8.00 defg	26.1a-e	145.00 klmn	36.17 abc	24.90 fgh	19.17 cde
IR 23	81.67 bcd	11.33	8.33 c-g	21.43 ghi	130.00 opq	38.00 abc	22.40 jkl	18.83 cdef
IR 24	78.67 b-f	9.00	6.67 g	26.15 abcd	123.00 q	34.67 abc	20.83 lm	31.00 a
IR 25	86.83abc	12.83	9.33 a-g	25.50 bcde	160.50 e-i	37.17 abc	22.23 jkl	22.83 b
IR 27	76.83 cdef	10.83	8.67 c-g	23.42 efgh	149.00 jklm	43.00 abc	21.42 klm	18.83 cdef
IR 28	93.67 a	11.33	9.83 a-e	25.47 bcde	156.00 ghij	48.00 ab	27.63 ab	21.00 bcd
IR 29	84.83 abcd	12.83	11.00 abc	26.02 a-e	174.67 abc	40.67 abc	25.15 d-h	21.50 bc
Binadhan-11	68.00 fg	10.83	8.67 c-g	18.18 j	136.33 nop	34.17 abc	26.93 bcd	15.33 ghij
Binadhan-12	63.33 g	11.83	10.67 abcd	18.17 j	139.83 mno	33.50 abc	11.00 o	12.50 j
BRRI dhan51	68.67 fg	12.83	10.83 abc	21.22 hi	145.00 klmn	35.17 abc	24.10 hij	13.33 ij
BRRI dhan52	74.83 defg	9.83	8.67 c-g	25.03 b-f	141.83 lmn	39.50 abc	21.73 kl	22.67 b
Level of sig.	**	NS	**	**	**	**	**	**
$LSD_{0.05}$	1.27	0.24	0.27	0.42	2.52	1.57	0.58	0.69
Max	93.67	13.67	11.83	28.33	185.00	53.00	29.05	31.00
Min	63.33	9.00	6.67	18.17	123.00	23.00	11.00	12.33
Average	78.85	11.68	9.44	24.54	153.37	39.17	24.29	18.48
CV	8.72	10.26	3.21	10.31	10.53	9.13	5.30	8.23

**- Significant at 1% level of probability, Similar letter indicates there is no significant difference at 5% level of probability as per DMRT whereas different letter indicates significant difference at 5% level of probability as per DMRT, NS= Non significant.

Table 1: List of rice genotypes used in this study.

Genotypes	Sources
IR 01, IR 02, IR 04, IR 05, IR 06, IR 07, IR 08, IR 09, IR 10, IR 11, IR 12, IR 13, IR 14, IR 15, IR 16, IR 17, IR 18, IR 19, IR 21, IR 22, IR 23, IR 24, IR 25, IR 27, IR 28, IR 29	International Rice Research Institute (IRRI)
Binadhan-11, Binadhan-12	Bangladesh Institute of Nuclear Agriculture (BINA)
BRRI dhan51, BRRI dhan52	Bangladesh Rice Research Institute (BRRI)

Table 2: Effect of genotype and submergence treatment interactions on yield and yield contributing traits.

Genotypes	Treat-ments	Plant height (cm)	No. of total tiller plant^{-1}	No. of effective tiller plant^{-1}	Panicle length (cm)	No. of filled grain panicle^{-1}	No. of unfilled grain panicle^{-1}	1000-grain weight (g)	Yield plant^{-1} (g)
IR 01	T_1	81.67 b-h	11.33 a-f	8.33 c-g	28.00 ab	131.00 z	20.00 h	25.53 e-n	20.00 gh
	T_2	76.00 c-l	8.33 fg	5.67 fg	26.07 a	123.33 h	26.00 fgh	24.40 j-p	18.00 jkl
IR 02	T_1	79.00 b-k	12.00 abcd	10.00 a-e	24.43 abc	169.00 fgh	30.00 efgh	17.03 yz	17.00 klmn
	T_2	72.67 e-m	10.33 b-g	8.00 c-g	22.43 ab	159.33 lmn	32.33 d-h	16.20 yz	15.00 pqrs
IR 04	T_1	84.00 a-h	12.00 abcd	9.00 b-f	28.00 a-e	156.00 nop	30.00 efgh	24.23 k-s	30.00 b
	T_2	78.00 c-k	9.67 defg	7.00 efg	25.53 abcd	147.33 rst	41.67 b-g	23.33 n-v	27.00 c
IR 05	T_1	78.00 c-k	12.00 abcd	10.00 a-e	29.00 a-e	185.00 ab	31.00 efgh	25.80 e-m	20.00 gh
	T_2	72.00 g-m	11.67 a-e	9.00 b-f	27.67 a-e	174.67 def	47.00 a-e	25.20 f-p	17.00 klmn
IR 06	T_1	73.67 lm	13.00 abc	10.00 a-e	27.10 a-e	188.00 a	33.00 c-h	27.60 bcde	18.00 jkl
	T_2	62.30 d-m	12.00 abcd	8.67 b-g	25.30 a-e	182.00 bc	61.00 ab	26.73 b-i	15.67 nopq
IR 07	T_1	86.00 a-g	12.00 abcd	10.00 a-e	25.30 a-f	166.00 ghij	33.00 c-h	30.00 a	17.00 klmn
	T_2	80.00 b-j	10.33 b-g	8.33 c-g	23.00 a-f	155.00 nopq	39.00 c-h	28.10 abcd	15.00 pqrs
IR 08	T_1	80.00 b-j	13.00 abc	12.00 ab	26.10 b-g	171.00 fg	41.00 b-g	28.20 abcd	18.00 jkl
	T_2	74.00 d-m	12.67 abcd	11.33 abc	24.53 a-f	162.67 i-m	39.00 c-h	27.43 b-f	15.33 opqr
IR 09	T_1	86.00 a-g	12.00 abcd	8.00 c-g	27.10 b-g	140.00 vwx	42.00 b-g	27.10 b-h	22.00 ef
	T_2	80.00 b-j	11.33 a-f	7.00 efg	25.40 b-g	133.67 yz	32.00 efgh	26.13 c-l	19.67 hi
IR 10	T_1	78.00 c-k	12.00 abcd	11.00 abcd	25.00 b-g	168.00 ghi	42.00 b-g	20.00 yz	23.67 d
	T_2	72.67 e-m	11.00 a-g	8.67 b-g	23.10 b-g	168.00 ghi	44.33 b-g	19.20 yz	21.33 fg
IR 11	T_1	86.00 a-g	11.00 a-g	11.00 abcd	26.00 b-g	143.00 tuvw	49.00 a-e	28.63 ab	17.33 klm
	T_2	80.00 b-j	10.33 b-g	9.33 bcde	25.00 b-g	134.33 xyz	30.00 efgh	27.73 bcde	14.67 pqrs
IR 12	T_1	87.00 a-e	13.00 abc	11.00 abcd	27.10 b-g	177.00 cde	46.00 a-f	27.43 b-f	19.00 hij
	T_2	81.33 b-i	13.00 abc	9.00 b-f	25.63 b-g	167.00 ghi	52.33 abcd	26.30 c-k	16.67 lmno
IR 13	T_1	79.00 b-k	12.00 abcd	10.00 a-e	27.80 b-g	174.00 def	46.00 a-f	27.20 b-h	24.00 d
	T_2	73.00 e-m	10.67 b-g	8.67 b-g	27.20 b-g	165.67 g-k	34.33 c-h	26.33 c-k	22.00 ef
IR 14	T_1	86.00 a-g	13.00 abc	11.00 abcd	22.00 c-i	163.67 h-l	53.00 abc	25.23 f-p	14.00 rstu
	T_2	80.00 b-j	12.67 abcd	10.00 a-e	18.53 c-h	153.00 opqr	34.00 c-h	24.30 k-r	12.33 vw

continued…..

IR 15	T_1	88.00 abcd	11.00 a-g	8.00 c-g	27.00 d-i	145.00 stuv	65.00 a	26.07 c-l	16.00 mnop
	T_2	82.00 b-h	10.67 b-g	7.00 efg	25.77 d-i	137.33 wxy	25.67 gh	25.13 g-p	13.67 stuv
IR 16	T_1	93.00 ab	14.00 a	12.00 ab	26.00 e-i	164.00 h-l	65.00 a	26.03 c-l	17.00 klmn
	T_2	86.67 a-f	13.33 ab	11.00 abcd	24.10 d-i	153.00 opqr	41.00 b-g	25.07 g-p	14.67 pqrs
IR 17	T_1	87.00 a-e	13.00 abc	11.00 abcd	25.00 e-j	157.00 mno	37.00 c-h	28.27 abc	18.00 jkl
	T_2	81.00 b-i	11.67 a-e	10.00 a-e	22.67 e-j	150.33 pqrs	37.00 c-h	27.60 bcde	15.67 nopq
IR 18	T_1	81.00 b-i	14.00 a	13.00 a	26.00 e-j	171.00 fg	40.00 c-h	26.00 d-l	15.67 nopq
	T_2	75.00 d-m	12.33 abcd	10.67 abcd	24.33 e-j	163.00 ijkl	42.67 b-g	25.07 g-p	14.33 qrst
IR 19	T_1	73.00 e-m	14.00 a	12.00 ab	26.10 f-k	167.00 ghi	40.00 c-h	25.60 e-m	13.00 tuvw
	T_2	67.00 i-m	13.00 abc	11.33 abc	24.30 e-j	160.33 j-n	39.00 c-h	24.60 i-q	11.67 w
IR 21	T_1	86.00 a-g	13.00 abc	9.00 b-f	24.00 g-k	141.00 uvw	30.00 efgh	23.27 o-v	19.00 hij
	T_2	80.00 b-j	11.67 a-e	8.00 c-g	21.33 g-k	133.00 yz	39.00 c-h	22.60 q-x	16.67 lmno
IR 22	T_1	78.00 c-k	10.00 c-g	9.00 b-f	27.00 g-l	149.00 rs	37.00 c-h	25.50 e-o	20.00 gh
	T_2	72.33 f-m	9.67 defg	7.00 efg	25.20 g-l	141.00 uvw	35.33 c-h	24.30 k-r	18.33 ijk
IR 23	T_1	85.00 a-h	12.00 abcd	9.00 b-f	22.43 g-l	135.00 xyz	37.00 c-h	23.00 p-w	20.00 gh
	T_2	78.33 c-k	10.67 b-g	7.67 defg	20.43 g-l	125.00 z	39.00 c-h	21.80 t-y	17.67 jkl
IR 24	T_1	82.00 b-h	10.00 c-g	8.00 c-g	27.00 g-l	127.00 z	30.00 efgh	21.47 u-y	32.00 a
	T_2	75.33 d-l	8.00 g	5.33 g	25.30 g-l	119.00 z	39.33 c-h	20.20 yz	30.00 b
IR 25	T_1	90.00 abc	13.00 abc	10.00 a-e	26.43 i-m	166.00 ghij	33.00 c-h	24.00 l-t	24.00 d
	T_2	83.67 a-h	12.67 abcd	8.67 b-g	24.57 h-m	155.00 nopq	41.33 b-g	20.47 xyz	21.67 ef
IR 27	T_1	80.00 b-j	12.00 abcd	9.00 b-f	24.53 klmn	153.00 opqr	33.00 c-h	22.00 s-y	20.00 gh
	T_2	73.67 dem	9.67 defg	8.33 c-g	22.30 j-n	145.00 stuv	53.00 abc	20.83 wxyz	17.67 jkl
IR 28	T_1	97.00 a	12.00 abcd	10.00 a-e	26.00 klmn	160.00 klmn	47.00 a-e	28.10 abcd	22.00 ef
	T_2	90.33 abc	10.67 b-g	9.67 a-e	24.93 klmn	152.00 opqr	49.00 a-e	27.17 b-h	20.00 gh
IR 29	T_1	88.00 abcd	13.00 abc	12.00 ab	27.03 lmn	178.00 cd	43.00 b-g	25.30 f-o	23.00 de
	T_2	81.67 b-h	12.67 abcd	10.00 a-e	25.00 lmn	171.33 efg	38.33 c-h	25.00 h-p	20.00 gh

continued…..

Binadhan-11	T_1	71.00 h-m	12.00 abcd	9.00 b-f	19.07 nop	140.00 vwx	43.00 b-g	27.27 b-g	16.00 mnop
	T_2	65.00 klm	9.67 defg	8.33 c-g	17.33 mno	132.67 yz	25.33 gh	26.60 b-j	14.67 pqrs
Binadhan-12	T_1	66.00 jklm	12.00 abcd	11.00 abcd	19.00 opq	145.00 stuv	30.00 efgh	11.60 z	13.00 tuvw
	T_2	60.67 m	11.67 a-e	10.33 a-e	17.30 nop	134.67 xyz	37.00 c-h	10.40z	12.00w
BRRI dhan51	T_1	74.67 d-m	13.00 abc	12.00 ab	22.00 pq	150.00 qrs	30.00 efgh	24.60 i-q	14.00rstu
	T_2	62.67 lm	12.67 abcd	9.67 a-e	20.43 opq	140.00 vwx	40.33 c-g	23.60 m-u	12.67uvw
BRRI dhan52	T_1	78.00 c-k	11.00 a-g	9.00 b-f	26.00 q	146.00 stu	30.00 efgh	22.13 r-y	24.00d
	T_2	71.67 g-m	8.67 efg	8.33 c-g	24.07 q	137.67 wxy	49.00 a-e	21.33 v-z	21.33fg
5 % lsd		1.24	0.23	0.27	0.41	2.47	1.54	0.57	0.67
Level of sig.		*	*	*	**	**	**	*	*
CV		8.72	10.26	3.21	10.31	10.53	9.13	5.30	8.23

T_1- Non submergence, T_2- Submergence, Similar letter indicates there is no significant difference at 5% level of probability as per DMRT whereas different letter indicates significant difference at 5% level of probability as per DMRT, **- Significant at 1% level of probability, *- Significant at 5% level of probability.

Table 3: Percent reduction of the genotypes in response on submergence and non-submergence conditions to plant height, no. of total tiller plant^{-1}, no. of effective tiller plant^{-1}, panicle length, no. of filled grain panicle^{-1}, 1000-grain weight and yield plant^{-1}.

Genotypes	Plant height (cm)	No. of total tiller plant^{-1}	No. of effective tiller plant^{-1}	Panicle length (cm)	No. of filled grain panicle^{-1}	1000-grain weight (g)	Yield plant^{-1} (g)
	% Reduction	% Reduction	% Reduction	% Reduction	% Reduction	% Reduction	% Reduction
IR 01	6.94	26.48	31.93	6.89	5.85	4.43	10
IR 02	8.01	13.92	20.00	8.19	5.72	4.87	11.76
IR 04	7.14	19.49	22.22	8.82	5.56	3.71	10
IR 05	7.69	2.75	1.00	4.59	5.58	2.33	15
IR 06	15.43	7.69	13.30	6.64	3.19	3.15	12.94
IR 07	6.98	13.92	16.70	9.09	6.63	6.33	11.76
IR 08	7.50	2.54	5.58	6.02	4.87	2.73	14.83

IR 09	6.98	5.58	12.50	6.27	4.52	3.58	10.59
IR 10	6.83	8.33	21.18	7.60	0.00	4.00	9.89
IR 11	6.98	6.09	15.18	3.85	6.06	3.14	15.35
IR 12	6.52	0.00	18.18	5.42	5.65	4.12	12.26
IR 13	7.59	11.08	13.30	2.16	4.79	3.19	8.33
IR 14	6.98	2.54	9.09	15.77	6.52	3.69	11.93
IR 15	6.82	3.00	12.50	4.56	5.29	3.61	14.56
IR 16	6.81	4.79	8.33	7.31	6.71	3.69	13.71
IR 17	6.90	10.23	9.09	9.32	4.25	2.37	12.94
IR 18	7.41	11.93	17.92	6.42	4.68	3.58	8.55
IR 19	8.22	7.14	5.58	6.89	3.99	3.91	10.23
IR 21	6.98	10.23	11.11	11.13	5.67	2.88	12.26
IR 22	7.27	3.30	22.22	6.67	5.37	4.71	8.35
IR 23	7.85	11.08	14.77	8.92	7.41	5.22	11.65
IR 24	8.13	20.00	33.38	6.29	6.29	5.92	6.25
IR 25	7.03	2.54	13.30	7.04	6.63	14.71	9.71
IR 27	7.91	19.42	7.44	9.09	5.23	5.32	11.65
IR 28	6.87	11.08	3.30	4.11	5.00	3.30	9.09
IR 29	7.19	2.54	16.66	7.51	3.74	1.18	13.04
Binadhan-11	8.45	19.41	7.44	9.12	5.23	2.45	8.31
Binadhan-12	8.07	2.75	6.09	8.94	7.12	10.34	7.69
BRRI dhan51	16.07	2.54	19.41	7.13	6.66	4.06	9.50
BRRI dhan52	8.11	21.18	7.44	7.42	5.7	3.61	11.13

Table 4: Genetic parameters of yield and yield contributing traits of rice genotypes.

	Genotypic variance	Phenotypic variance	Heritability	Genotypic coefficient of variation	Phenotypic coefficient of variation	GA	% GA
Plant height (cm)	88.56	106.64	83.05	11.94	13.10	21.45	20.89
No. of total tiller plant^{-1}	2.61	3.39	77.07	13.85	15.77	4.98	6.34
No. of effective tiller plant^{-1}	3.72	4.70	79.30	20.44	22.96	16.23	178.23
Panicle length (cm)	12.62	13.13	96.13	14.48	14.77	22.34	89.34
No. of filled grain panicle^{-1}	520.79	523.81	99.42	14.88	14.92	1.92	6.99
No. of unfilled grain panicle^{-1}	58.17	93.16	62.44	19.47	24.64	1.80	4.32
1000-grain weight (g)	28.21	28.64	98.51	21.87	22.03	60.34	40.21
Yield plant $^{-1}$(g)	37.72	38.52	97.94	33.23	33.58	3.71	61.74

GA= Genetic Advance, GA (%) = Genetic Advance as percent of mean.

Table 5: Correlation between the yield contributing traits of rice genotypes.

	Plant height (cm)	No. of total tiller plant^{-1}	No. of effective tiller plant^{-1}	Panicle length (cm)	No. of filled grain panicle^{-1}	No. of unfilled grain panicle^{-1}	1000-grain weight (g)	Yield plant^{-1} (g)
Plant height (cm)	1							
No. of total tiller plant^{-1}	0.24**	1						
No. of effective tiller plant^{-1}	0.15*	0.75**	1					
Panicle length (cm)	0.40**	0.07	0.03	1				
No. of filled grain panicle^{-1}	0.09	0.54**	0.55**	0.37**	1			
No. of unfilled grain panicle^{-1}	0.20*	0.14*	0.20**	0.09	0.27*	1		
1000-grain weight (g)	0.38**	0.21**	0.17*	0.44**	0.26**	0.16*	1	
Yield plant^{-1} (g)	0.31**	-0.24**	0.27**	0.51**	0.57**	-0.06	0.61**	1

*= 5% level of significance, **= 1% level of significance.

Phenotypic correlation based on the effect of genotype on different traits was measured (Table 5). Majority of the traits gave significant and positive correlations with each other (Table 5). Highly significant positive association were observed between number of total tiller plant^{-1} and number of effective tiller plant^{-1} (r= 0.75), yield plant^{-1} and 1000-grain weight panicle^{-1} (r= 0.61), number of effective tiller plant^{-1} and number of filled grain panicle^{-1} (r= 0.55) (Table 5). Correlation coefficients give apparent relationship between two or more parameters. Submergence changed the growth pattern compared to the control. Yet several parameters showed distinct relationship among themselves (Table 5). It showed that the changes of different plant characteristics were simultaneous under submergence. Correlation analyses further revealed that maintenance of plant height, panicle length, number of effective tiller plant^{-1}, number of filled grain panicle^{-1} and 1000-grain weight was important for plant performance under submergence stress (Sarkar and Das, 2003; Kato *et al.,* 2014). Identification of the plant traits that were responsible for variations in yield stability could help rice breeders in developing high yielding genotypes adapted to submergence.

CONCLUSION

Submergence stress has frequently encountered in rice crop, is a widespread curb of rice production in Southeast Asia mainly having irrigated and high rainfall environment. Climate change accelerates the condition towards more damaging situation. The presently cultivated rice varieties may not be able to withstand this increased submergence. Hence, it is imperative to develop submergence tolerance rice variety with high yield potential and grain quality using modern tools of biotechnology. However, most of the works on selection of submergence tolerant rice considered only the vegetative stage. So, it is essential to develop submergence tolerant rice lines at reproductive stages. In this study thirty rice genotypes were evaluated at reproductive stage under submergence condition. The performance of the genotypes with respect to yield and yield components differed from each other under submergence and non-submergence conditions. Yield and yield components of the genotypes reduced in submergence condition. IR 28, IR 16, IR 18, IR 05, IR 06, IR 07, IR 24 were identified as tolerant to submergence stress. All tolerant genotypes showed higher plant height, number of total tillers plant^{-1}, number of effective tillers plant^{-1}, panicle length, number of filled grain panicle^{-1}, 1000-grain weight and yield plant^{-1} respectively. Adequate genetic diversity was present among the studied rice genotypes. High values of heritability and genetic advance for most of the yield attributes offer the more opportunity for further improvement of those following breeding program. Correlation study revealed the associated traits thus having influence on rice yield under submergence condition. Moreover, studied rice genotypes showed wide variations in submergence tolerance.

REFERENCES

Bailey-Serres, J. and L.A.C.J. Voesenek(2010) Life in the balance: a signaling network controlling survival of flooding. *Curr. Opin. Plant Biol*13:489–494.

Bates, B.C., Z.W. Kundzewicz, S. Wuand J.P. Palutikof (2008) Climate change and water, IPCC Secretariat, Geneva, 210.

B.B.S. (Bangladesh Bureau of Statistics) (2018) Statistical Year Book of Bangladesh, Bureau of Statistics, Statistics Division, Ministry of Planning, Government of People's Republic of Bangladesh, Dhaka,140.

Bhadru, D., V.T. Rao, Y.C. Mohan and D. Bharathi (2012) Genetic variability and diversity studies in yield and its component traits in rice (*Oryza sativa* L.). *SABRAO J. Breed. Genet* 44: 129-137.

Burton, G.W. and D.E. Devane (1953) Estimating heritability in tall fescue (*Festucaarundinacea*) from replicated clonal material. *Agron. J*45: 478-481.

Comstock, R.E. and H.F. Robinson (1952) Genetic parameters, their estimate and significance. Proceeding of 6th*International Grassland Congress* 1:284-291.

Dar, M.H. (2017) Transforming rice cultivation in flood prone coastal Odisha to ensure food and economic security. *Food Sec*9:711-722.

Dewan, T.H. (2015) Societal impacts and vulnerability to floods in Bangladesh and Nepal. *WeatherClim. Extremes* 7:36-42.

Ella, E.S. and A.M. Ismail (2006) Seedling nutrient status before submergence affects survival after submergence in rice. *Crop sci*46:1673-1681.

Hanada, K., K. Kagawa, Y. Yokoyama and S. Nomura (1990) Effects of air supply on the growth of tiller buds in floating rice. *Jpn. J. Trop. Agr*34:276–283.

Hanson, G., H.F. Robinson and R.E. Comstock (1956) Biometrical studies on yield in segregating population of Korean Lespedeza. *Agron. J*48: 268-274.

Hushine, M.A. (2004) Effect of methods of transplanting and seedlings per hill on the growth and yield of transplant *aman*rice. M.S. Thesis, Department of Agronomy, BAU, Mymensingh, Bangladesh.

Johnson, H.W., H.F. Robinson and R.E. Comstock (1955) Estimates of genetic and environmental variability in soybean. *Agron. J*47:314-318.

Kawano, N., E. Ella, O. Ito, Y. Yamauchi and K. Tanaka (2002) Metabolic changes in rice seedlings with different submergence tolerance after de-submergence. *Environ. Exper. Bot*47:195– 203.

Kawano, N., O. Ito and J.I. Sakagami (2009) Morphological and physiological responses of rice seedlings to complete submergence (flash flooding). *Ann. Bot*103: 161–169.

Kato, Y., B.C.Y. Collard, E.M. Septiningsih and A.M. Ismail (2014) Physiological analyses of traits associated with tolerance of long-term partial submergence in rice. *AoBPlants* 6: plu058.

Khanh, T.D., L.H. Linh, T.H. Linh, L.H. Ham and T.D. Xuan (2013) Rapid and high-precision marker assisted backcrossing to introgress the SUB1 QTL into the Vietnanese elite rice varieties. *J. Plant Breed. Crop Sci*5:26-33.

Kotera, A., E. Nawata, L.V.Thao, N.V.Vuong and T. Sakuratani (2005) Effect of submergence on rice yield in the Red River Delta, Vietnam. *Jpn. J. Trop. Agr*49: 97–206.

Luo, F.L., K.A. Nagel, H. Scharr, B. Zeng, U. Schurr and S. Matsubara (2011) Recovery dynamics of growth, photosynthesis and carbohydrate accumulation after de-submergence: a comparison between two wetland plants showing escape and quiescence strategies. *Ann. Bot*107:49–63.

Mackill, D.J., B.C.Y. Collard, C.N. Neeraja, R.M. Rodriguez, S. Heuer and A.M. Ismail (2006) QTLS in ricebreeding: examples for abiotic stresses. In:Rice Genetics 5: Proceedings of International Rice Genetics Symposium, Brar, D.S., D.J. Mackill and B. Hardy (eds), International Rice Research Institute, Manila, 155-167.

Mackill, D.J. (1986) *Progress in Rainfed Lowland Rice*. Los Baños: International Rice Research Institute; Rainfed Lowland Rice Improvement in South and South East Asia; Results of a Survey,115–144.

Mackill, D.J., M.A. Ismail, M.A. Pamplona, L.D. Sanchez, J.J. Carandang and M.E. Septiningsih(2010) Stress tolerant rice varieties for adaptation to a changing climate. International Rice Research Institute, Metro Manila, Philippines. *Crop Environ. Bioinf*7: 250-259.

Miller, C.K., F.A. Kralios and R.L. Lux (1985) Correlation between refractory periods and activation-recovery intervals from electrograms: effects of rate and adrenergic interventions. *Circulation* 72:1372-1379.

Mohanty, S., R. Wassmann, A. Nelson, P. Moya and S.V.K. Jagadish (2013) Rice and climate change, significance for food security and vulnerability. International Rice Research Institute, Philippines, 14.

Mohanty, H.K. and R.C. Chaudhary (1986) Breeding for submergence tolerance in rice in India.In: Progress in Rainfed Lowland Rice, International Rice Research Institute, Los Baños, Philippines, 177-190.

Mahapatra, N. (2017) Yield and its attributing characters of different rice genotypes to submergence stress. *J. Pharm. Innov*6:315-319.

Nugraha, Y., G.V. Vergara, D.J. Mackill and A.I. Ismail (2012) Response of SUB1 introgression lines of rice to various flooding conditions. *Indones. J. Agric. Sci*14:15-26.

Panda, D., S.G. Sharma and R.K. Sarkar (2008) Chlorophyll fluorescence parameters, CO_2 photosynthetic rate and regeneration capacity as a result of complete submergence and subsequent re-emergence in rice (*Oryza sativa* L.). *Aquat. Bot*88: 127–133.

Ram, P.C., K. Singh, B.B. Singh, V.K. Singh, H.P. Singh, T.L. Setter, V.P. Singh and R.K. Singh (1999) Environmental characterization of floodwater in eastern India: relevance to submergence tolerance of lowland rice. *Exp. Agric*35:141–152.

Rahman, R.B. and J. Zhang (2016) Flood and drought tolerance in rice: opposite but may coexist. *Food Energy Secur*5:76-88.

Sarkar, K.R. and B. Bhattacharjee (2011) Rice genotypes with SUB1 QTL differ in submergence tolerance, elongation ability during submergence and re-generation growth at re-emergence. *Rice* 5:7.

Sarkar, R.K. and S. Das (2003) Yield of rainfed lowland rice with medium water depth under anaerobic direct seeding and transplanting. *Trop. Sci*43:192-198.

Singh, R.K. and B.D. Choudhury (1985) Biometrical method in quantitative genetic analysis. Kalyani Publishers, Ludhiana, New Delhi, 54-57.

Singh, S., D.J. Mackill and A.M. Ismail (2014) Physiological basis of tolerance to complete submergence in rice involves genetic factors in addition to the SUB1 gene. *AoBPlants*6: plu060.

Sugai, K., Y. Goto, M. Saito and I. Nishiyama (1999) Effects of stepwise raising of the water level on tiller number in rice plants (*Oryza sativa* L.). *Jpn. JCrop Sci*68:390–395.

Vartapetian, B.B. and M.B. Jackson (1997) Plant adaptations to anaerobic stress. *Ann. Bot*79: 3–20.

Voesenek, L.A.C.J. and J. Bailey-Serres (2015) Flood adaptive traits and processes: an overview.*New Phytol*206: 57-73.

Wang, B., Y.J. Zhou, Y.Z. Xu, G. Chen, Q.F. Hu and W.G. Wu (2014) Effects of waterlogging stress on growth and yield of middle season rice at the tillering stage. *China Rice* 20:68-75.

Xu, K., X. Xia, T.Fukao, P. Canlas, Maghirang-Rodriguez, S. Heuer, A.M. Ismail, J. Bailey-Serres, P.C. Ronald and D.J. Mackill(2006) Sub1A is an ethylene response factor-like gene that confers submergence tolerance to rice. *Nature* 442:705–708.

Zhang, Y., Z.L.L. Wang, Q. Zhou, Y. Xiao and X. Wei (2015) Short-term complete submergence of rice at the tillering stage increases yield. *PloSOne*10: e0127982.