

Original Research Article

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## Phenotypic Screening and Evaluation of *Sub1* Introgressed Lines in Popular Rice Varieties Ranjit and Bahadur of Assam, India

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### ABSTRACT

Phenotypic screening during *kharif* 2015 and evaluation of *Sub1* introgressed lines in Ranjit and Bahadur for submergence tolerance was done with the 35 genotypes. Out of 35 genotypes 32 were *Sub1* introgressed BC<sub>2</sub>F<sub>3</sub> lines (24 BC<sub>2</sub>F<sub>3</sub> lines of the cross -Ranjit x Swarna-*Sub1* and 8 BC<sub>2</sub>F<sub>3</sub> lines of the cross -Bahadur x Swarna-*Sub1*) with three parents i.e. Ranjit, Bahadur, and Swarna-*Sub1*. The phenotypic screening of genotypes showed that all *Sub1* introgressed lines had significantly higher survival rates as compared with the original recipient parents whereas less change in plant height was observed. The *Sub1* introgressed lines in BC<sub>2</sub>F<sub>3</sub> generation showed lesser elongation during submergence as compared to the parents and the susceptible check IR42. The analysis of variance revealed the existence of significant variation among the genotypes for grain yield and all other morpho-physiological quantitative traits. High estimates of genotypic and phenotypic variation in case of morphological characters like stem thickness, panicle number per plant indicated that selection would be effective for these characters. Amongst all the morpho-physiological quantitative traits, high heritability (>80) with high genetic advance (>20) as percent of mean estimates were recorded for leaf length of blade, stem thickness, leaf width of blade, grain weight of 1000 fully developed grains and grain width. The high estimates of heritability for these characters also indicated considerable genetic variation and lower influence of environment in the expression of these characters. High genetic advance coupled with high heritability estimates indicates that these traits are apparently controlled by additive genes. Thus these traits deserve top most priority in selection.

#### Keywords

Bahadur, Phenotyping, Ranjit, Rice, *Sub1*, Submergence tolerance

#### Article Info

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### Introduction

Rice (*Oryza sativa* L.) is the staple food of more than half of the world population. It is the dominant and only suitable crop in the rainfed and lowland areas of India. Submergence stress is a major constraint to rice production in areas of high rainfall and it

adversely affects farmers living on 10-15 million hectares of rainfed lowland rice in South and Southeast Asia (Neeraja *et al.*, 2007). To meet the demand of the ever increasing global population, greater production of rice is needed from this flood prone ecosystem. According to the estimate of World Bank (World Bank, 2008), flood

affected areas increased to 40 million hectares from 19 million hectares within one decade in India. Short-term submergence regularly affects over 20 million ha of rice in the tropic (Mackill *et al.*, 2012).

Assam is one of the major rice growing states in the country and *Sali* rice is grown as rainfed crop and it occupies around 1.8 million hectares. Around 0.5 million hectares *Sali* rice growing areas are chronically affected by flood. Flood is the major problem in the state, which affect all the three classes of rice. *Sali* rice is damaged in its vegetative stage due to inundation of low lying areas. Nearly 4 lakh hectares rice is chronically flood prone and the flood affected area is around 10 lakh hectares. Submergence due to inundation causes mortality of tillers and the extent of yield loss depends on the intensity and the duration of flood. Hence, sustainable and permanent solutions are needed to overcome this problem. One of the most promising solutions is to develop high yielding varieties that are submergence tolerant and that are more likely to be rapidly adopted by farmers in the target regions (Septiningsih *et al.*, 2009). Submergence tolerance is controlled by a single major quantitative trait locus (QTL) on chromosome 9, along with a number of minor QTLs (Xu and Mackill, 1996). All these studies have used the landrace FR13A (Nandi *et al.*, 1997; Xu and Mackill, 1996) which is one of the most submergence-tolerant donor varieties. Swarna-*Sub1* as well as other *Sub1* introgressed varieties such as Samba Mahsuri-*Sub1*, IR 64-*Sub1*, BR 11-*Sub1*, CR 1009-*Sub1* and TDK-*Sub1* is not adopted by the farmers of the state as they prefer the agronomic qualities of the variety Ranjit and Bahadur. Ranjit and Bahadur (semi-tall varieties) are the most popular varieties of Assam and they cover about 65 per cent of *Sali* rice growing areas in the state. However, these varieties are not tolerant to submergence. Thus, development of *Sub1*

QTL introgressed submergence tolerant version of these varieties i.e. Ranjit-*Sub1* and Bahadur-*Sub1* will definitely help the farmers of the flood prone areas of Assam. Hence, the present investigation has been undertaken with the objective phenotypic screening and evaluation of *Sub1* introgressed lines for submergence tolerance.

## Materials and Methods

The present study was undertaken with the aim of evaluation of *Sub1* introgressed lines for submergence tolerance in Ranjit and Bahadur. Ranjit and Bahadur are popular rice varieties of Assam covering more than 60 percent area during *kharif*. Field experiments were conducted during *Sali/Kharif 2015* at Regional Agriculture Research Station (RARS), Assam Agricultural University, Titabar, Assam, India. The experimental material comprised of 32 *Sub1* introgressed BC<sub>2</sub>F<sub>3</sub> lines (24 *Sub1* introgressed lines in Ranjit background and 8 *Sub1* introgressed lines in Bahadur background). Rice genotypes having tolerance to submergence namely Swarna-*Sub1* and FR13A were used as resistant check variety and Swarna, Ranjit, Bahadur and IR42 were used as susceptible check variety in phenotypic screening.

## Screening for submergence tolerance

Phenotyping of the 32 *Sub1* fixed lines for submergence tolerance were carried out during *Sali/Kharif 2015* (Table 1). Phenotypic screening was carried out in phenotypic tank of dimension (10.0m X 10.0m X 2.0 m). The seeds of the *Sub1* introgressed lines along with the checks were sown into the tank. The 10 days old seedlings were then submerged for 12 days and water level was maintained at 1.1 m. Desubmergence was carried out after 12 days and the genotypes were assessed on the basis of survival percentage and plant height (elongation ability).

### **Evaluation of *Sub1* introgressed lines**

The lines were evaluated on the basis of yield and other morpho-physiological quantitative characters by using experimental design RBD (Table 2). The mean values of the observations recorded for 38 genotypes using CRD experimental design were subjected to the statistical and biometrical analyses. The partitioning of the total variance assignable to different sources was done according to Fisher's method. Genetic parameters were estimated for each character from ANOVA. The mean data for each of the eleven morpho-physiological characters were subjected to analysis of variance by following randomized block design. Genetic parameters were estimated for each character from ANOVA. Genotypic variances ( $\sigma^2_g$ ), phenotypic variance ( $\sigma^2_p$ ) and environmental variance ( $\sigma^2_e$ ) were computed according to Burton and Devane (Burton and Devane, 1953). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated from these variances in terms of standard deviation as percentage of the grand mean. Heritability ( $h^2$ ) in broad sense was calculated following Allard (Allard, 1960). Expected genetic advance for each character was calculated by using the formula suggested by Hanson (Hanson *et al.*, 1956).

### **Results and Discussion**

#### **Phenotyping**

The phenotypic screening of the 32 genotypes along with resistant check varieties i.e. Swarna-*Sub1* and FR13A and susceptible check varieties i.e. Swarna, Ranjit, Bahadur and IR42 have shown that all *Sub1* introgressed lines had significantly higher survival rates as compared with the original recipient parents and less change in plant height was observed. Further it was observed that the *Sub1* introgressed lines in BC<sub>2</sub>F<sub>3</sub> generation showed

lesser elongation during submergence compared to the parents and the susceptible check IR42. The *Sub1* introgressed lines have shown survival rate in between the range 78-92 percent whereas the susceptible cultivars showed 0-24 percent and resistant check cultivars showed survival percentage in the range of 83-91 (Table 3). The plant height before survival in *Sub1* introgressed lines ranges from 19-28 percent whereas plant height after survival in *Sub1* introgressed lines ranges from 22-34 percent. In case of resistant check variety the plant height before survival ranges from 20-34 and plant height after survival ranges from 26-40 (Fig. 2). In susceptible check cultivars the plant height before survival was recorded in the range of 20-23 and plant height after survival was found 0-38. The *Sub1* introgressed lines have shown elongation rate (plant height) in between the ranges 7.40 - 32.00 percent whereas the susceptible cultivars showed 0-65.21 percent and in resistant check cultivars it was found in range of 17.64-30 percent. Based on the observed data the CD value for survival percentage was found to be 4.12 and for percentage change in plant height was 2.33 at 5 percent probability level.

#### **Evaluation of *Sub1* introgressed lines**

The evaluation of *Sub1* introgressed lines was done with eleven quantitative characters by using experimental design RBD. The rice genotypes were distinguished from each other in respect of length of leaf blade (LLB) which ranged from 29.5 cm in Swarna-*Sub1* to 61.53 cm in E-6 genotype with a mean value 42.11cm. The genotypes exhibited less variability (CV= 0.97). Leaf width (LWdB) ranged from 1.08 cm in Ranjit to 1.98 cm in genotype 1189-1 with a mean value 1.64 cm. The genotypes exhibited more variability (CV= 2.44). Stem thickness (ST), which ranged from 0.45 cm in W-167 to 1.56 cm in N-3 genotype with a mean value 0.62 cm. The

genotypes exhibited more variability (CV= 9.88). Stem length (SL), which ranged from 79.16 cm in D-160 and 130.166 cm in 1189-1 genotype with a mean value 102.26 cm. The genotypes exhibited more variability (CV=1.14). The rice genotypes were distinguished from each other in respect of panicle number per plant (PNP), which ranged from 3 in N-3 and 13 in U-86 genotype with a mean value of 8.73. The genotypes exhibited more variability (CV= 14.77). Grain weight of 1000 fully developed grains (GW) which ranged from 11.56 g in L-3 to 22.83 g in Bahadur genotype with a mean value of 17.35 g. The genotypes exhibited more variability (CV= 1.54). Grain length (GL) which ranges from 7.19 mm in 1398-1 to 8.40 mm in 1324-1 genotypes with a mean value of 7.76 mm. The genotypes exhibited variability (CV= 2.15). Grain width (GWd) which ranged from 1.42 mm in J-164 to 2.32 mm in the genotype Swarna-Sub1 with a mean value of 1.64 mm. The genotypes exhibited variability (CV= 2.02). Decorticated grain length (DGL) which ranged from 4.77 mm in D-160 to 5.89 mm in N-3 genotype with a mean value 5.49 mm. The genotypes exhibited more variability (CV= 3.69). Decorticated grain width (DGWd) which ranged from 1.27 mm in C-210 and D-136 to 1.92 mm in Bahadur genotype with a mean value 1.45 mm. The genotypes exhibited variability (CV= 2.35). Yield per plot which ranged from 3.13 kg in D-136 to 6.25 Kg in Bahadur. Remaining cultivars fell between these ranges. The genotypes exhibited more variability (CV= 9.80). The significant difference was found for all the eleven quantitative characters under study.

### **Analysis of variance for eleven morpho-physiological characters**

Analysis of variance (ANOVA) for eleven morpho-physiological quantitative characters are presented in (Table 4). The results showed

that the mean sum of squares were highly significant for all the characters. It means that there is sufficient variability among the different genotypes and hence desirable improvement can be brought through selection for different characters. There were significant differences among the genotypes for all the characters under study.

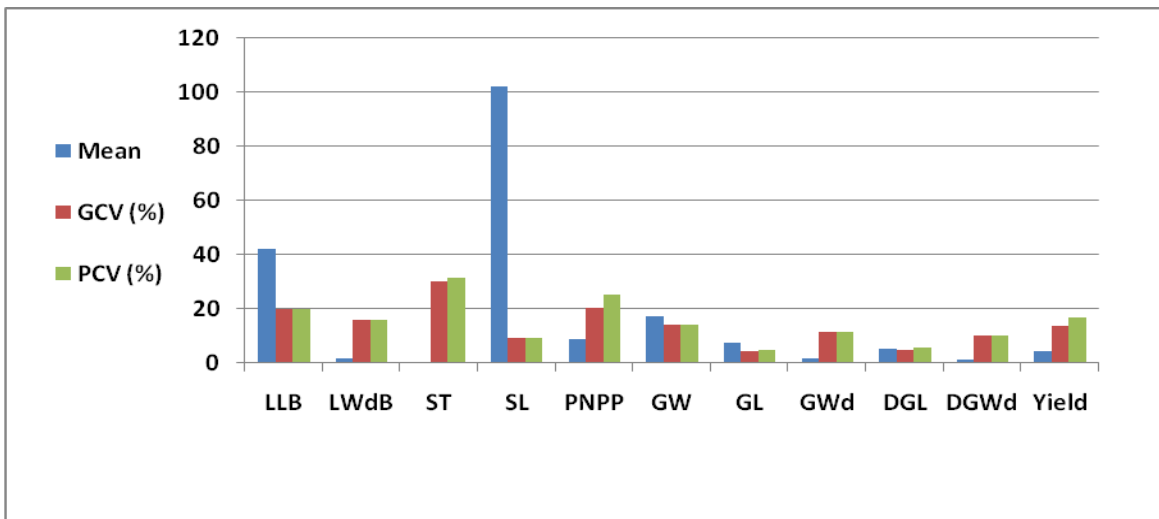
### **Extent of genetic variation for eleven morpho-physiological characters**

The estimates of genotypic and phenotypic variances, heritability, genotypic and phenotypic coefficients of variations, genetic advance as a percentage of mean and expected genetic advance at 5 percent selection intensity are presented in (Table 5). In case of morpho-physiological characters a comparison of the genotypic and phenotypic variances of the characters clearly revealed that there was a close correspondence between the two estimates for all the characters. A better comparison of the extent of genetic variation in the traits could be made from the estimates of genotypic and phenotypic coefficients of variations. The GCV estimate for yield was found to be 13.57 percent which were moderate. The maximum GCV was reflected for stem thickness (30.07) followed by panicle number per plant (20.44) (Fig. 1). The lowest GCV was reflected for grain length (4.30) followed by decorticated grain length (4.73) and stem length (9.32). Rest of the characters exhibited moderate GCV. For these characters GCV estimates had a close correspondence with PCV estimates along with their high heritability estimates. Highest heritability with genetic advance was observed for leaf length of blade (99.76, 41.13), stem thickness (89.74, 58.69), leaf width of blade (97.16, 32.44), grain weight of 1000 fully developed grains (98.83, 28.97) and grain width (97.22, 23.12) (Fig. 2). High heritability with moderate genetic advance was observed for the traits like stem length (98.51, 19.06) and

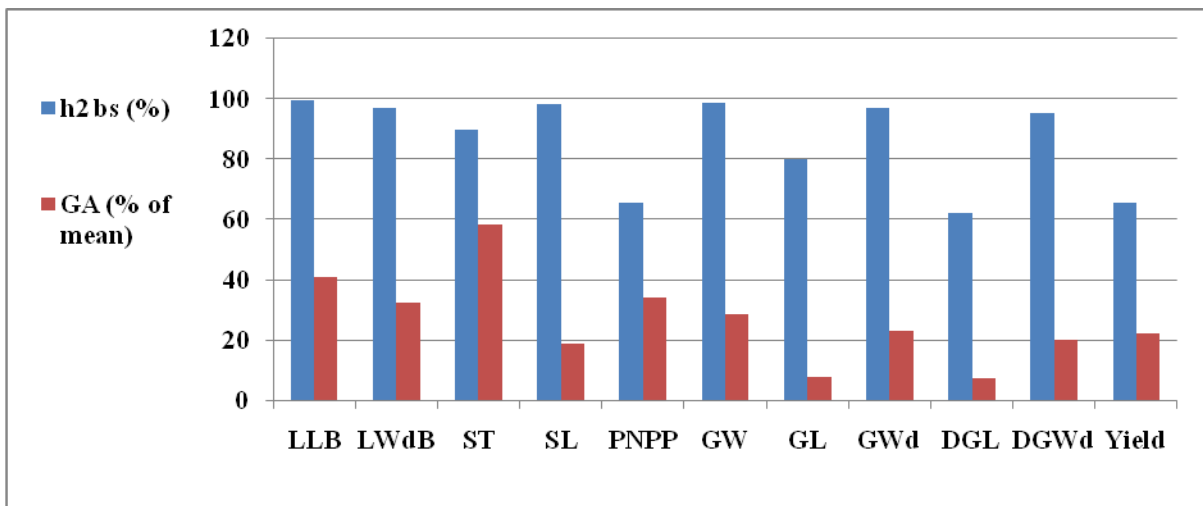
decorticated grain width (95.58, 20.44). Moderate heritability with low genetic advance was observed for the traits like grain length (79.95, 7.93), and decorticated grain length (62.26, 7.69). Moderate heritability

with high genetic advance was observed for the traits like yield (65.79, 22.67) and panicle number per plant (65.79, 34.14). The genetic advance as percentage of mean was observed at 5% selection intensity.

**Fig.1** Genetic variability parameters (Mean, GCV, PCV) of eleven quantitative morpho-physiological characters viz. Leaf Length of blade (LLB), Leaf width of blade (LWdB), Stem thickness (ST), Stem length (SL), Panicle number per plant (PNPP), Grain weight of 1000 fully developed grains (GW), Grain length (GL), Grain width (GWd), Decorticated grain length (DGL), Decorticated grain width (DGWd), Yield



**Fig.2** Genetic variability parameters ( $h^2_{bs}$ , GA (% of mean)) of eleven quantitative morpho-physiological characters viz. Leaf Length of blade (LLB), Leaf width of blade (LWdB), Stem thickness (ST), Stem length (SL), Panicle number per plant (PNPP), Grain weight of 1000 fully developed grains (GW), Grain length (GL), Grain width (GWd), Decorticated grain length (DGL), Decorticated grain width (DGWd), Yield



**Table.1** List of genotypes used in the present study

Plant material	Genotypes
Resistant check variety	Swarna- <i>Sub1</i> , FR13A
Susceptible check variety	IR 42, Swarna, Ranjit, Bahadur
Test entries	Y-374, C-210, 1160-2, Y-219, N-6, S-4, 1160-1, N-9, 1316-2, W-167, J-329, C-376, Y-350, L-2, C-196, U-86, N-3, J-164, L-3, D-160, C-367, Z-1, E-6, D-65, Z-8, D-136, A-193, 1241-1, 1189-1, 1324-1, 1398-1, 1384-1.

**Table.2** List of quantitative morpho-physiological characters used in evaluation of *Sub1* introgressed lines

Sl. No	Morpho-physiological quantitative characters	Sl. No	Morpho-physiological quantitative characters
1.	Leaf length of blade (cm)	8.	Grain width (mm).
2.	Leaf width of blade (cm).	9.	Decorticated grain length (mm).
3.	Stem thickness (cm).	10.	Decorticated grain width (mm).
4.	Stem length (cm).	11.	Yield
5.	Panicle no per plant.	6.	Grain weight of 1000 fully developed grains (gm).
7.	Grain length (mm).		

**Table.3** Survival percentage and percentage changes in plant height due to submergence of the rice cultivars after 12 days of submergence

Test Entries	Survival Percentage	Plant Height		
		Before Survival (cm)	After Survival (cm)	Percentage Change
IR 42	0	21	-	-
FR 13A	91	34	40	17.64
Swarna <i>Sub1</i>	83	20	26	30.00
Swarna	14	20	33	65.00
Ranjit	20	23	36	56.52
Bahadur	24	23	38	65.21
Y-374	83	19	23	21.05
C-196	87	25	33	32.00
E-6	88	25	31	24.00
C-210	83	24	30	25.00
U-86	85	23	28	21.73
1189-1	90	27	31	14.81

1160-2	89	24	28	17.05
N-3	78	24	31	29.16
1324-1	87	22	28	27.27
Y-219	83	21	27	28.57
J-164	90	28	34	21.42
1398-1	92	23	29	25.00
N-6	89	24	29	20.83
L-3	91	19	22	15.78
D-65	88	28	33	17.85
S-4	87	23	27	17.39
D-160	84	26	30	15.38
Z-8	81	22	26	18.18
1160-1	85	26	30	14.06
C-367	89	20	24	20.00
D-136	90	27	29	7.40
N-9	88	23	29	26.08
Z-1	85	21	24	14.28
1384-1	84	24	28	16.66
1316-2	86	26	31	19.23
L-2	81	22	25	13.63
A-193	79	23	28	21.73
W-167	88	21	23	9.52
Y-350	81	22	24	9.09
1241-1	82	25	33	32.00
J-329	86	24	28	16.66
C-376	83	22	25	13.63
CD(0.05)	4.12			2.33

**Table.4** Analysis of variance (Mean squares) for eleven quantitative morpho-physiological characters

Mean squares												
Source of variance	D.F	LLB	LWdB	ST	SL	PNPP	GW	GL	GWd	DGL	DGWd	Yield
Replication	2	0.41	0.01**	0.01	19.84**	15.72**	0.64**	0.36**	0.02**	0.30**	0.01**	0.16
Genotypes	34	212.85**	0.20**	0.10**	274.05**	11.23**	18.15**	0.36**	0.10**	0.24**	0.06**	1.35**
Error	68	0.16	0.002	0.004	1.36	1.66	0.071	0.02	0.001	0.04	0.001	0.20

\*Significant at p=0.005

\*\*Significant at p=0.001

Leaf Length of blade (LLB), Leaf width of blade (LWdB), Stem thickness (ST), Stem length (SL), Panicle number per plant (PNPP), Grain weight of 1000 fully developed grains (GW), Grain length (GL), Grain width (GWd), Decorticated grain length (DGL), Decorticated grain width (DGWd), Yield.

**Table.5** Genetic variability parameters of eleven quantitative morpho-physiological characters

Characters	Range		Mean	$(\sigma^2_g)$	$(\sigma^2_p)$	GCV (%)	PCV (%)	$h^2_{bs}$ (%)	GA (% of mean)
	Min.	Max.							
LLB	29.5	61.53	42.11	70.89	71.06	19.99	20.01	99.76	41.13
LWdB	1.08	1.98	1.64	0.06	0.07	15.97	16.20	97.16	32.44
ST	0.45	1.56	0.62	0.03	0.039	30.07	31.74	89.74	58.69
SL	79.16	130.16	102.2	90.89	92.26	9.32	9.39	98.51	19.06
PNPP	3	13	8.73	3.18	4.85	20.44	25.22	65.69	34.14
GW	11.56	22.83	17.35	6.02	6.09	14.14	14.23	98.83	28.97
GL	7.19	8.40	7.76	0.11	0.13	4.30	4.81	79.95	7.93
GWd	1.42	2.32	1.64	0.035	0.036	11.38	11.54	97.22	23.12
DGL	4.77	5.89	5.49	0.06	0.10	4.73	5.99	62.26	7.69
DGWd	1.27	1.92	1.45	0.021	0.022	10.15	10.38	95.58	20.44
Yield	3.13	6.25	4.57	0.38	0.58	13.57	16.73	65.79	22.67

Leaf Length of blade (LLB), Leaf width of blade (LWdB), Stem thickness (ST), Stem length (SL), Panicle number per plant (PNPP), Grain weight of 1000 fully developed grains (GW), Grain length (GL), Grain width (GWd), Decorticated grain length (DGL), Decorticated grain width (DGWd), Yield.

### Phenotyping and evaluation of *Sub1* introgressed lines

#### Phenotyping

The present study clearly demonstrated that all the *Sub1* introgressed lines exhibited significantly higher survival rates compared to the parents. Further it was observed that the *Sub1* introgressed lines in BC<sub>2</sub>F<sub>3</sub> generation showed lesser elongation during submergence compared to the parents and the susceptible check IR42. The *Sub1* introgressed lines have shown survival rate in between the range 78-92 percent whereas the susceptible cultivars showed 0-24 percent and resistant check cultivars showed survival percentage in the range of 83-91 these results are in accordance with Iftekharuddaula *et al.*, (2016), Singh *et al.*, (2016), Jena *et al.*, (2015) and John *et al.*, (2017). The plant height before survival in *Sub1* introgressed lines ranges from 19-28 percent whereas plant height after survival in *Sub1* introgressed lines ranges from 22-34 percent. In case of resistant check variety the plant height before survival ranges from 20-34 and plant height after survival ranges from

26-40. In susceptible check cultivars the plant height before survival was recorded in the range of 20-23 and plant height after survival was found 0-38. The *Sub1* introgressed lines have shown elongation rate in between the range 7.40-32.00 percent whereas the susceptible cultivars showed 0-65.21 percent and in resistant check cultivars it was found in range of 17.64-30 percent. The result corroborated with Sarkar *et al.*, (1996), Das *et al.*, (2005), Septiningsih *et al.*, (2009), Jena *et al.*, (2015) and Goswami *et al.*, (2017). Jena *et al.*, (2015) reported that in the submergence screening more than 75% survival rate was observed in the BC<sub>2</sub>F<sub>2</sub> generation *Sub1* introgressed lines in two popular semi lowland rice cultivars Pooja and Pratikshya of Orissa. A similar study was made by Septiningsih *et al.*, (2009) where it was observed that all mega varieties with *Sub1* introgression had a significantly higher survival rate than the original parents. In the study made by Das *et al.*, (2005) tolerant genotypes were identified and key traits such as high levels of non-structural carbohydrates (NSC, starch and soluble sugars) and limited underwater elongation were found to be



associated with tolerance. According to Sarkar *et al.*, (2009) the submergence tolerance mechanism in respect to seedling height, carbohydrate, chlorophyll and specific leaf weight (SLW) was studied in rice. Twenty five-day-old seedlings of five rice cultivars were submerged for 12 days. Submergence tolerant cultivars consumed more carbohydrates in the beginning of submergence to elongate the seedling height and later produce new carbohydrates after exposure of the leaves in the sunlight above water. Moreover, they maintained more chlorophyll and specific leaf weight as compared with susceptible cultivars during submergence.

### **Evaluation of *Sub1* introgressed lines**

#### **Extent of genetic variation**

The analysis of variance revealed the existence of significant variation among the genotypes for grain yield and all other morpho-physiological quantitative characters. In case of morphological quantitative characters, high estimates of genotypic and phenotypic variation in the present study as revealed from the estimates of GCV and PCV's for stem thickness, panicle number per plant indicated that selection would be effective for these characters. The high estimates (>80%) of heritability for these characters also indicated considerable genetic variation and lower influence of environment in the expression of these characters. These results were in accordance with De and Rao (1987), Deosarkar *et al.*, (1989), Bai *et al.*, (1992) and Ravindra Babu (1996). The difference between GCV and PCV values were relatively low in the present study, which indicated less influence of the environment for the characters. The GCV provides information for comparison of the genetic variability and indicates the validity of the traits for selection. However, it does

not provide a clear picture of the extent of genetic gain to be achieved from selection unless heritable fraction of variation is known (Burton, 1952), indicating the importance of heritability estimation. Heritability in broad sense being the ratio of genotypic variance to phenotypic variance indicates the extent of genetic control of a given trait and thus reflects the efficiency of selection of the trait. High heritability with high genetic advance was reported for the characters like grain per plant, 100-grain weight and grain number by Deo sarkar *et al.*, (1989). High heritability with high genetic advance for days to flowering was reported by Singh *et al.*, (1986) and Roy *et al.*, (1992).

For effective selection high heritability estimates coupled with high genetic advance is a better criterion as suggested by Panse *et al.*, (1957). Genetic advance is dependent upon the heritability of trait, genetic variability and intensity of selection (1999). In the present investigation high magnitude of genetic advance as percent of mean (>20) were observed for stem thickness (58.69), leaf length of blade (41.13), panicle no per plant (34.14), leaf width of blade (32.44), grain weight of 1000 fully developed grains (28.97), grain width (23.12) and yield (22.67). In the present study high heritability (>80) with high genetic advance (>20) as percent of mean estimates were recorded for leaf length of blade, stem thickness, leaf width of blade, grain weight of 1000 fully developed grains and grain width. High genetic advance coupled with high heritability estimates indicates that these traits are governed by additive gene and therefore, selection based on phenotypic performance is likely to give beneficial results in improving these characters. These results indicated the involvement of increased additive gene action and therefore, phenotypic selection without progeny testing to increase the frequency of additive gene will be effective to a certain

extent. High heritability (>80) with moderate genetic advance (10-20) was observed for traits like stem length, decorticated grain width. Moderate heritability (60-80) with low genetic advance (<10) was observed for the traits like grain length and decorticated grain length whereas, moderate heritability (60-80) with high genetic advance (>20) was observed for traits like yield and panicle number per plant. The results corroborated with research conducted by Afrin *et al.*, (2018). Low heritability with low genetic advance was not observed. This indicated that these characters might be under the small effect of control of non-additive (dominance and epistasis) gene action. Hence, these traits do not offer much scope for improvement through simple selection. The use of population improvement concept and intermittent biparental mating and relaxation of selection in segregating generations could help in generation of useful recombinants for improvement of such traits. Many workers emphasized the application of recurrent selection in addition to conventional selection methods in autogamous crops like rice (Singh and Singh, 1991). Amongst all the morpho-physiological quantitative traits stem thickness and leaf length of blade was found to possess maximum genetic variation apparently controlled by additive genes. Thus this trait deserves top most priority in selection.

Submergence is a recurring problem where short term flash flooding damages rice in the rice-producing rainfed lowland areas. Developing rice cultivars with tolerance to submergence with yield and quality traits acceptable to farmers is a feasible approach to address this problem. Due to the heterogeneity in flood prone ecosystem many different types of traditional rice cultivars are being grown by the farmers. This necessitates development of high yielding varieties in popular rice variety background that are

submergence tolerant and are more likely to be rapidly adopted by farmers in the target regions. The present investigation was carried out with the objective of phenotypic screening and evaluation of *Sub1* introgressed lines for submergence tolerance in popular rice varieties (Ranjit and Bahadur) background. The *Sub1* introgressed lines in Ranjit and Bahadur background have exhibited expression of *Sub1* in submerged condition. The *Sub1* introgressed lines can survive for more than 12 days of continuous submergence. There were significant variations in the *Sub1* introgressed lines and therefore selection will be effective for further improvement.

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### **References**

- Afrin W, Nafis MH, Hossain MA, Islam MM and Hossain MA (2018) Responses of rice (*Oryza sativa* L.) genotypes to different levels of submergence. *C R Biologies* 341:85-96.
- Allard RW (1960) Principles of plant breeding. John Wiley and Sons, New York.
- Burton GW (1952) Quantitative inheritance in grasses. *Proc. 15th Int Grassland Cong* 1:227-283.
- Burton GW and Devane EM (1953) Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Agron J* 45:478-485.
- Das KK, Sarkar RK, Ismail AM (2005) Elongation ability and non-structural carbohydrate levels in relation to submergence tolerance in rice. *Plant Science* 168:131-136.

- De RN, Suriya Rao AV (1987) Genetic variability and correlation studies in rice under semi-deep water logged situation. *Oryza* 25:360-364.
- Deosarkar DB, Misal MB, Nerker YS (1989) Variability and correlation studies for yield and yield attributing characters in breeding lines of upland rice. *J Maharastra Agric Univ* 14:28-29.
- Goswami S, Kar RK, Paul A, Dey N (2017) Genetic potentiality of indigenous rice genotypes from eastern India with reference to submergence tolerance and deep water traits. *Curr Plant Biol* 11-12:23-32.
- Hanson CH, Robinson HF, Comstock RE (1956) Biometrical studies of yield in segregating population of Korean *Lespedeza*. *Agron J* 48:267-282.
- Iftekharruddaula KM, Ahmed HU, Ghosal S, Amin A, Moni ZR, Bisnu PR, Barman HN, Siddique MA, Collard BCY, Septiningsih EM (2016) Development of early maturing submergence tolerant rice varieties for Bangladesh. *Field Crop Res* 190:44-53.
- Jena PP, Bharathkumar S, Reddy JN, Mohapatra T (2015) Introgression of *Sub1* locus into highly preferred rice cultivars (Pooja and Pratikshya) in eastern region of India for submergence tolerance through marker assisted backcrossing. *Adv Biores* 6(1):45-53
- John D, Shylaraj KS (2017) Introgression of *Sub1* QTL into an elite rice (*Oryza sativa* L.) variety Jyothi through marker assisted backcross breeding. *Journal of Tropical Agriculture* 55:1-11.
- Mackill DJ, Ismail AM, Singh US, Labios RV, Paris TR (2012) Development and Rapid Adoption of Submergence Tolerant (*Sub1*) Rice Varieties. *Advances in Agronomy* 115.
- Nandi S, Subudhi PK, Senadhira D, Manigbas NL, Sen Mandi S, Huang N (1997) Mapping QTLs for submergence tolerance in rice by AFLP analysis and selective genotyping. *Mol Gen Genet* 225:1-8.
- Neeraja C, Rodriguez RM, Pamplona A, Heuer S, Collard B, Septiningsih E (2007) A marker-assisted backcross approach for developing submergence-tolerant rice cultivars. *Theor Appl Genetic* 115:767-776.
- Panase VG (1957) Genetics of quantitative characters in relation to plant breeding. *Indian J of Genetics* 17:318-327
- Rama B, Regina A, Devika R, Joseph CA (1992) Genetic variability and association of characters in medium duration rice genotypes. *Oryza* 29:19-22
- Ravindra Babu V (1996) Study of genetic parameters, correlations and path coefficient analysis of rice under saline conditions. *Ann Agric Res* 17:370-374.
- Roy A, Kar MK (1992) Heritability and correlation studies in upland rice. *Oryza* 29:195-199.
- Sarkar KR, De NR, Reddy NJ, Ramakrishnayya G (1996) Studies on the Submergence Tolerance Mechanism in Relation to Carbohydrate, Chlorophyll and Specific Leaf Weight in Rice (*Oryza sativa* L.). *J Plant Physiol* 149:623-625.
- Sarkar RK, Reddy JN, Sharma SG, Ismail AM (2006) Physiological basis of submergence tolerance in rice and implications for crop improvement. *Curr Sci* 91:899-906.
- Septiningsih EM, Pamplona MA, Sanchez DL, Neeraja CN, Chirravuri GV, Heuer S, Ismail AM, Mackill DJ (2009) Development of submergence-tolerant rice cultivars: the *Sub1* locus and beyond. *Ann Bot* 103(2):151-160.
- Singh R, and Singh A (1991). Combining ability for harvest index and other related characters in rice. *Oryza* 28:19-22.

- Singh R, Singh Y, Xalaxo S, Verulkar S, Yadav N, Singh S, Singh N, Prasad KSN, Kondayya K, Rao PVR, Rani MG, Anuradha T, Suraynarayana Y, Sharma PC, Krishnamurthy SL, Sharma SK, Dwivedi, JL, Singh AK, Singh PK, Nilanjay, Singh NK, Kumar R, Chetia SK, Ahmad T, Rai M, Perraju P, Pande A, Singh DN, Mandal NP, Reddy JN, Singh ON, Katara JL, Marandi B, Swain P, Sarkar RK, Singh DP, Mohapatra T, Padmawathi G, Ram T, Kathiresan RM, Paramsivam K, Nadarajan S, Thirumeni S, NagarajanM, Singh AK, Vikram P, Kumar A, Septiningsih E, Singh US, Ismail AM, Mackill D, Singh NK (2016) From QTL to variety harnessing the benefits of QTLs for drought, flood and salt tolerance in mega rice varieties of India through a multi-institutional network. *Plant Sci* 242:278-287
- Singh RK, Chaudhary BD (1999) *Quantitative Genetics Analysis*. Timberland Publishers, New Delhi, India Pp 180
- Singh RS, Chauhan SP, Maurya DM (1986) Genetic variability in 98 upland rice cultivars of India. *IRRN* 11(4): 9-10
- World Bank (2008) *Climate Change Impacts in Drought and Flood Affected Areas: Case Studies in India*. Report No. 43946:1-162
- Xu K, and Mackill DJ (1996) A major locus for submergence tolerance mapped on rice chromosome 9. *Mol Breed* 2:219-224.

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