International Journal of Chemical Studies

Madhusmita Patra
Department of Crop Physiology, Institute of Agricultural Sciences, Siksha 'O' Anusandhan Deemed to be University, Bhubaneswar, Odisha, India

Pragati Dash
Department of Plant Physiology, College of Agriculture, OUAT, Bhubaneswar, Odisha, India

Raj Kumari Bhol
Department of Plant Physiology, College of Agriculture, OUAT, Bhubaneswar, Odisha, India

Gyana Ranjan Rout
Department of Agricultural Biotechnology, College of Agriculture, OUAT, Bhubaneswar, Odisha, India

Satya Ranjan Das
Department of Plant Breeding and Genetics, College of Agriculture, OUAT, Bhubaneswar, Odisha, India

Assessment of Genetic Variability for Quantitative and Physiological traits in *Sub-1* introgressed lines and their parental strains in rice (*Oryza sativa*)

Madhusmita Patra, Pragati Dash, Raj Kumari Bhol, Gyana Ranjan Rout and Satya Ranjan Das

Abstract
The present investigation aimed at to evaluate twenty rice genotypes including Sub 1 introgressed lines along with their parents and four check varieties namely Lalat, Pratikshya, Mahanadi and PSBRc-68. The trial was laid out in randomized block design with three replications. Different yield attributing traits, physiological parameters and biochemical traits were examined to study the availability and extent of genetic variability and to assess the physiological and genetic bases of yield variations in Sub-1 introgressed lines and their parental strains. The analysis of variance showed significant variation among the test genotypes for all the traits except panicle number. Moderate to high degree of heritability estimates were observed for all the traits except for panicle number and leaf area index. The characters like chlorophyll content, carbohydrate content, Super oxide dismutase content, catalase content, glutathione peroxidase content, different growth parameters, grain yield per plant and plot yield exhibited high genotypic coefficient of variation coupled with high heritability and high genetic advance. The genotypes like Swarna, Ciherang, Pratikshya, BR 11-Sub 1, Swarna-Sub 1, Ciherang-Sub 1, PSBRc 68, BR 11 and PSRBc 18 were identified as promising cultures.

Keywords: rice, sub-1, genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance

Introduction
Rice is the staple food for more than 60 percent of the global population. It is the predominant dietary energy source for people in all of East and South-East Asia. Adding 30-50 percent of agricultural income to the millions of farm house holds, it is a staple food for 75% of Indian population. In terms of acreage, rice is grown in about 44.0 million hectares in India and it accounts for 40.5 percent of total food grain production and 43.42 percent of total cereal production, thus continues to hold the key to sustain food sufficiency in the country (Babu *et al.,* 2015) [5]. In India, 26% of the total cultivated area and 4.6% of the total rice-growing area are under flood-prone rice ecosystems. Out of 16.1 million ha of rainfed low land rice nearly 5.2 million ha is constantly affected by flash flood submergence and stagnant flooding, which profoundly influenced the overall productivity of the country. There has been remarkable success in breeding for tolerance to submergence during the last two decades and many *Sub-1* introgressed lines were developed by marker assisted back crossing (MABC). The *Sub1* varieties have been thoroughly field tested and has been widely adopted by the farmers (Mackill *et al*., 2012) [13]. It is interesting to note that as flooding stress is not a recurrent problem, therefore, the promising stress tolerant lines should have higher yield potential and greater stability of production under normal non-stress situations for greater acceptability of varieties by the farming community. Realizing the importance of high yield and greater stability of production of submergence tolerant lines, the present investigation was undertaken to assess the genetic variability for different traits and to examine the physiological and genetic bases of yield variations in *Sub-1* introgressed lines and their parental strains in rice.

Corresponding Author:
Madhusmita Patra
Department of Crop Physiology, Institute of Agricultural Sciences, Siksha 'O' Anusandhan Deemed to be University, Bhubaneswar, India

Materials and Methods

The experimental material consisted of twenty rice genotypes including Sub 1 introgressed lines along with their parents and four check varieties namely Lalat, Pratikshya, Mahanadi and PSBRc-68. The test genotypes were evaluated under normal cultural conditions at the Instructional Farm, Orissa University of Agriculture and Technology, Bhubaneswar during *kharif,* 2016 in randomized block design (RBD) with three replications as 7 row plots of 3.9m length with a row to row distance of 20 cm and plant to plant spacing of 15 cm in lowlands. The recommended crop management practices were followed including need based plant protection measures to raise a normal crop. Observations were recorded in respect of twelve metric traits like Days to 50% flowering (DF), Plant height (PH), Panicle length (PL), Panicle number (PN), Flag leaf angle (FLA), Flag leaf area (FLAr), Fertile grain number (FGN), Fertility percentage (F%), 100-grain weight (100-GW), Harvest index (HI), Grain yield/plant (GYP) and Plot yield (PY); thirteen physiological traits like Relative Growth Rate (RGR), Crop growth rate (CGR), Net assimilation rate (NAR), Relative leaf growth rate (RLGR), Relative leaf area growth rate (RLAGR), Leaf area ratio (LAR), Leaf weight ratio (LWR), Specific leaf weight (SLW), Specific leaf area (SLA), Leaf area index (LAI), Leaf area duration (LAD), Post-flowering photosynthetic contribution to grain yield (PPCG), including chlorophyll content and four biochemical traits like Carbohydrate content, Superoxide dismutase content (SOD), Catalase content and Glutathione peroxidase content during the course of investigation. Metric traits were

recorded on five competitive plants selected randomly from the middle rows of each plot, whereas, the characters like plot yield and days to 50% flowering were recorded on whole plot basis. The data recorded were subjected to statistical analysis based on the sample mean of the various characters under observation. The analysis of variance was carried out separately for each trait following the procedures of randomized block design analysis (Panse and Shukhatme, 1954). Based on the analysis of variance the different parameters of variability like mean, range, standard error of mean (SE_m), standard error of difference (SE_d), critical difference (CD), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2_{bs}) and genetic advance (GA) were estimated. The genotypic and phenotypic correlations coefficients between character pairs were computed according to Robinson *et al.* (1951) [17], Johnson *et al.* (1955) [11] and Al-Jibouri *et al.* (1958) [1].

Results and Discussion

The analysis of variance (Table 1) revealed significant variation among the test genotypes for all the traits except panicle number. The magnitude of genetic variance was moderate to high for majority of traits except for days to flowering, plant height, panicle length, panicle number, fertility percentage, leaf area index, specific leaf weight and specific leaf area, indicating the existence of sufficient variation in the material studied. A perusal of the relative magnitude of variation from.

**Table 1:** Analysis of variance for various characters (Mean sum of squares)

Sl. No.	Characters	Source of variation (df)		
		Replication (2)	Genotype (19)	Error (38)
1	Days to 50% flowering	2.09*	168.45**	0.42
2	Plant height (cm)	81.99**	208.75**	8.41
3	Panicle length (cm)	1.50	7.30**	0.64
4	Panicle number	0.72	2.84	1.79
5	Flag leaf angle (0^0)	4.05	106.23**	13.03
6	Flag leaf area (cm^2)	12.92	55.04**	9.25
7	No. of fertile grains/panicle	1378.89*	1697.96**	270.25
8	Fertility percentage	189.08*	294.98**	51.81
9	100-grain weight (g)	0.02	0.55**	0.02
10	Harvest index	47.87*	133.59**	14.13
11	Relative growth rate (g/g/week)	0.00	0.03**	0.001
12	Net assimilation rate (g/cm²/week)	0.00	0.001**	0.00
13	Leaf area index at 50% flowering	1.69	1.38	0.78
14	Leaf area ratio (cm²/g)	1.25	380.90**	13.41
15	Leaf weight ratio (g/g)	0.00	0.01**	0.00
16	Specific leaf weight (mg/cm²)	0.03	0.97**	0.11
17	Specific leaf area (cm²/g)	257.22	1059.50**	159.41
18	Crop growth rate (g/week)	0.01	1.19**	0.01
19	Relative leaf growth rate (g/g/week)	0.00	0.03**	0.001
20	Relative leaf area growth rate (cm²/ cm²/week)	0.00	0.02**	0.00
21	Leaf area duration (week)	6.19	14.28**	2.61
22	Post-flowering photosynthetic contribution to grain yield (%)	12.04	468.90**	15.14
23	Chlorophyll content at 50% flowering(mg/g)	0.07	0.40**	0.06
24	Carbohydrate content at 50% flowering (mg/g)	5.17**	16114.13**	0.89
25	Superoxide Dismutase content at 50% flowering (Units/mg of protein)	0.02	0.52**	0.02
26	Catalase content at 50% flowering (Units/mg of protein)	0.001	0.04**	0.001
27	Glutathione Peroxidase content at 50% flowering (Units/mg of protein)	0.01	71.89**	0.003
28	Grain yield / plant (g)	36.01**	25.34**	6.16
29	Plot yield (q/ha)	119.13**	157.58**	4.93

* and ** Significant at 5% and 1% level of probability respectively.
Figures in parentheses indicate degrees of freedom (df) for corresponding sources of variation

Table 2: Mean, Range, and Coefficient of variation, Genotypic and phenotypic coefficient of variation, Heritability and Genetic advance estimates of various characters

Sl. No.	Characters	Mean	Range	CV (%)	GCV (%)	PCV (%)	h² (%)	GA (10%)	GA as percentage of mean
1	Days to 50% flowering	101.08	87.33-110.00	0.64	7.40	7.41	99.75	13.16	13.01
2	Plant height (cm)	95.12	81.44-110.00	3.05	8.59	8.77	95.97	14.09	14.81
3	Panicle length (cm)	23.29	20.42-25.87	3.44	6.40	6.70	91.19	2.50	10.75
4	Panicle number	8.70	6.66-10.22	15.37	6.83	11.20	37.17	0.64	7.32
5	Flag leaf angle (0^0)	25.75	12.88-38.19	14.02	21.65	23.11	87.73	9.19	35.69
6	Flag leaf area (cm^2)	19.92	12.20-28.43	15.27	19.61	21.50	83.18	6.27	31.48
7	No. of fertile grains/panicle	111.58	71.33-151.67	14.73	19.55	21.32	84.08	35.21	31.55
8	Fertility percentage	71.85	57.09-91.22	10.02	12.53	13.80	82.44	14.39	20.02
9	100-grain weight (g)	2.32	1.41-3.00	5.65	18.24	18.53	96.90	0.73	31.61
10	Harvest index	40.49	25.78-54.68	9.29	15.59	16.48	89.42	10.50	25.94
11	Relative growth rate (g/g/week)	0.38	0.24-0.63	6.79	25.81	26.10	97.75	0.17	44.90
12	Net assimilation rate (g/cm²/week)	0.06	0.03-0.11	7.71	33.93	34.22	98.31	0.03	59.22
13	Leaf area index at 50% flowering	3.69	2.17-4.72	23.91	12.10	18.36	43.46	0.52	14.04
14	Leaf area ratio (cm²/g)	54.61	37.43-80.16	6.71	20.27	20.63	96.48	19.13	35.03
15	Leaf weight ratio (g/g)	0.27	0.17-0.34	7.34	17.32	17.83	94.35	0.08	29.61
16	Specific leaf weight (mg/cm²)	5.12	4.11-6.80	6.35	10.47	11.09	89.08	0.89	17.39
17	Specific leaf area (cm²/g)	198.29	170.38-243.66	6.37	8.74	9.48	84.95	28.10	14.17
Sl. No.	Characters	Mean	Range	CV (%)	GCV (%)	PCV (%)	h² (%)	GA (10%)	GA as percentage of mean
18	Crop growth rate (g/week)	1.85	1.03-2.96	4.35	33.91	34.00	99.45	1.10	59.52
19	Relative leaf growth rate (g/g/week)	0.29	0.13-0.55	10.97	34.83	35.40	96.80	0.18	60.30
20	Relative leaf area growth rate (cm²/ cm²/week)	0.26	0.11-0.43	7.92	34.71	35.01	98.29	0.16	60.56
21	Leaf area duration (week)	9.71	5.56-15.28	16.62	20.30	22.45	81.74	3.14	32.31
22	Post-flowering photosynthetic contribution to grain yield (%)	60.27	32.03-76.33	6.46	20.41	20.74	96.77	21.29	35.33
23	Chlorophyll content at 50% flowering(mg/g)	1.87	1.27-2.55	13.05	17.98	19.50	85.07	0.55	29.19
24	Carbohydrate content at 50% flowering (mg/g)	247.51	114.59-400.06	0.38	29.61	29.61	99.99	128.98	52.11
25	Superoxide Dismutase content at 50% flowering (Units/mg of protein)	2.22	1.46-3.01	5.80	18.36	18.67	96.79	0.71	31.80
26	Catalase content at 50% flowering (Units/mg of protein)	0.00027	0.00004-0.00047	9.14	42.43	42.75	98.48	0.20	74.10
27	Glutathione Peroxidase content at 50% flowering (Units/mg of protein)	0.0 885	0.0172-0.1615	0.59	55.31	55.32	100.00	8.62	97.35
28	Grain yield / plant (g)	12.07	6.87-17.06	20.55	20.94	24.07	75.70	3.87	32.07
29	Plot yield (q/ha)	43.37	26.42-52.44	5.12	16.45	16.71	96.87	12.36	28.49
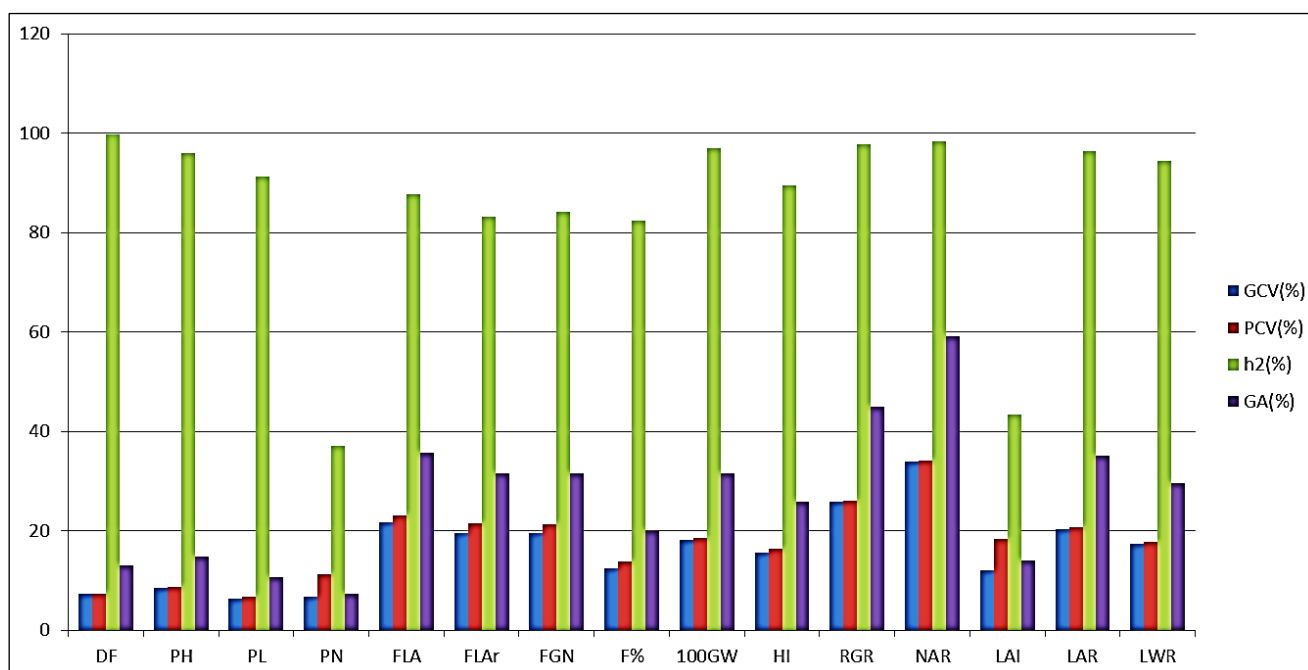
Fig 1: Cumulative representation of different genetic parameters GCV, PCV, Heritability and GA for 29 characters in rice
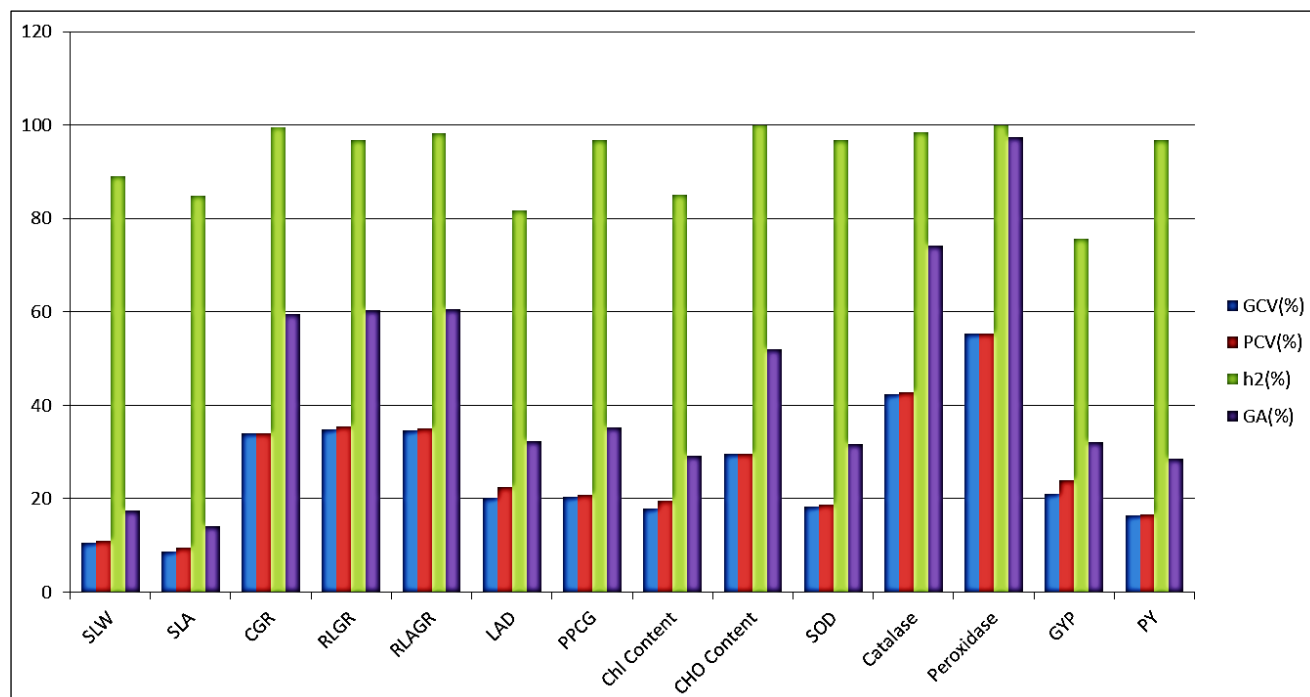
Fig 2: Cumulative representation of different genetic parameters GCV, PCV, Heritability and GA for 29 characters in rice

The analysis of variance and range of variations in respect of all the characters under study (Table 1 and 2), it is revealed that there is presence of ample genetic variability in the material, thus providing enormous scope for selection of genotype, which could be used in the future breeding program for realization of high and stable yields in rice. It is not surprising to note that there exists enormous amount of variability in all most all the characters, as the materials under study were mid-early to late in maturity duration varieties, combining many quantitative and physiological traits from diverse parental sources of different origin, maintaining wider range of genetic diversity with respect to plant type, maturity duration, grain features, yielding ability, were proved efficient in inducing variability for various traits.

The overall mean, range, CV, Genotypic and phenotypic coefficient of variation for yield and its component traits along with physiological and biochemical characters of twenty elite rice genotypes are presented (Table 2). The genotypic and phenotypic coefficient of variation in different traits maintained correspondence for most of the characters except for leaf area index, panicle number and grain yield per plant. Majority of the traits showed smaller difference between PCV and GCV indicating little influence of the environment, therefore selection on the basis of phenotypic value for most of the traits is expected to be effective. In general, phenotypic coefficient of variation was higher than the genotypic co-efficient of variation suggesting the influence of environment factor. Particularly in leaf area index, panicle number and grain yield per plant the difference between the two estimates was fairly wide enough indicating the greater influence of environment on expression of these traits. Both GCV and PCV were observed to be high (more than 15%) for traits like flag leaf angle, flag leaf area, number of fertile grains per panicle, 100-grain weight, harvest index, relative growth rate, net assimilation rate, leaf area ratio, leaf weight ratio, crop growth rate, relative leaf growth rate, relative leaf area growth rate, leaf area duration, post-flowering photosynthetic contribution to grain yield, chlorophyll content, carbohydrate content, superoxide dismutase content, catalase content, glutathione peroxidase

content, grain yield per plant and plot yield, suggesting that these traits are under the influence of genetic control. Hence these traits can be relied upon and simple selection can be practiced for further improvement. A review of literature from published reports on genetic variability indicates very inconsistent and contrasting results by Tuwar *et al*. (2013) [25], Singh *et al*. (2013) [25] Ganapati *et al*. (2014), Anis *et al*. (2016) [3], Mishu *et al*. (2016) [15], Rukmini *et al*. (2017) [18] and Goswami (2018) [8]. However in majority of cases these estimates were found to be low for panicle length, panicle number, plant height, days to 50% flowering moderate to high for fertile grains/panicle, 100-grain weight and harvest index.

Moderate to high degree of heritability estimates were observed for all the traits except for panicle number and leaf area index. Traits like flag leaf angle, flag leaf area, number of fertile grains per panicle, fertility percentage, 100-grain weight, harvest index, relative growth rate, net assimilation rate, leaf area ratio, leaf weight ratio, crop growth rate, relative leaf growth rate, relative leaf area growth rate, leaf area duration, post-flowering photosynthetic contribution to grain yield, chlorophyll content, carbohydrate content, superoxide dismutase content, catalase content, glutathione peroxidase content, grain yield per plant and plot yield exhibited higher values of genetic advance. Moderate levels of genetic advance were recorded for days to 50% flowering, plant height, leaf area index, specific leaf weight and specific leaf area. Lower values of genetic advance were recorded for panicle length and panicle number.

Considering the importance GCV value simultaneously with heritability and genetic advance in increasing the reliability and response of selection, efforts were made to indicate both heritability and genetic advance values along with GCV for various traits during the present investigation (Figure 1). The characters like flag leaf angle, flag leaf area, number of fertile grains per panicle, 100-grain weight, harvest index, relative growth rate, net assimilation rate, leaf area ratio, leaf weight ratio, crop growth rate, relative leaf growth rate, relative leaf area growth rate, leaf area duration, post-flowering photosynthetic contribution to grain yield, chlorophyll content, carbohydrate content, superoxide dismutase content,

catalase content, glutathione peroxidase content, grain yield per plant and plot yield exhibited high GCV coupled with high heritability and high genetic advance indicates the preponderance of additive gene and hence selection based on phenotypic performance for these traits would be effective (Augustina *et al.* 2013; Sandhya *et al.* 2014; Savitha and Usha Kumari,2015; Mishu *et al.* 2016 [15]; Islam *et al.* 2016, Srujana *et al.* 2017; and Ali *et al.* 2018) [4, 2, 15, 10, 24, 2].

The traits like flag leaf angle, flag leaf area, number of fertile grains per panicle, fertility percentage, 100-grain weight, harvest index, relative growth rate, net assimilation rate, leaf area ratio, leaf weight ratio, crop growth rate, relative leaf growth rate, relative leaf area growth rate, leaf area duration, post-flowering photosynthetic contribution to grain yield, chlorophyll content, carbohydrate content, superoxide dismutase content, catalase content, glutathione peroxidase content, grain yield per plant and plot yield exhibited high heritability coupled with high genetic advance indicates the preponderance of additive gene effect and hence selection based on phenotypic performance for these traits would be effective (Augustina *et al.*, 2013, Sandhya *et al.* 2014; Mishu *et al.* 2016; Islam *et al.* 2016) [4, 20, 15, 10].

Days to 50% flowering, plant height, panicle length, specific leaf weight and specific leaf area exhibited high heritability value and moderate to low genetic gain suggested that the inheritance of such traits might be under the control of both additive and non-additive gene effects. Therefore, selection of genotypes on the basis of phenotypic performance of the above traits may not be effective (Dhanwani *et al.* 2013; Haque *et al.* 2014; Sarwar *et al.* 2015; Kumar *et al.* 2015; Sala and Shanti, 2016; and Sumanth *et al.* 2017) [6, 9, 21, 12, 19, 24].

It was interesting to note that panicle number and leaf area index exhibited low heritability with low genetic gain suggested that inheritance of such traits might be under the control of non-additive gene effects. Therefore, selection of genotypes on the basis of phenotypic performance of the above traits may not be effective (Mulugeta *et al.*, 2012) [14]

Mean Performance of Different Genotypes for Various Traits

The mean performance of different genotypes with respect to various characters including plot yield has been presented in Table 3. It was interesting to note that none of the introgressed lines out yield their parents in the present study except for BR11, PSBRc 18 and Thadokkham 1 (Fig 2).The increase or decrease in plot yield was not associated with the corresponding increase or decrease of related traits under study. This discrepancy might have resulted due to undetected sampling errors during recording of observations. Although maximum care has been taken for recording data from a large number of samples for estimating the mean, yet the experimental bias in favour of single plants cannot be ruled out. As during the present investigation, the *per se* performance of the varieties is more meaningful, therefore, major emphasis was given to plot yield than other yield components estimated on per plant basis to identify the most promising cultures for their future use.

Out of twenty cultures evaluated during the present investigation, as many as ten cultures showing yield level of more than 45 q/ha could be sorted out to be promising. The yield performance of these promising entries along with other metric traits is presented for ease of better comprehension (Table.4). The most promising cultures identified during the present investigation

Table 3: Mean performance of different genotypes with respect to various characters

Sl. No.	Variety	DF	PH (cm)	PL (cm)	PN	FLA (0^0)	FLAr (cm^2)	FGN	F (%)	100-GW (g)	HI	RGR	NAR	LAI	LAR	LWR
1	BR11	103.00	101.74	23.86	8.44	23.32	19.29	138.00	68.02	2.27	44.49	0.31	0.05	3.99	49.87	0.27
2	BR11-Sub1	102.67	106.44	25.87	7.55	24.97	23.90	151.67	69.46	2.43	43.21	0.32	0.04	4.63	59.25	0.29
3	Ciherang	92.00	96.00	23.67	9.55	25.79	18.24	118.67	91.22	2.63	48.10	0.50	0.11	4.71	42.38	0.22
4	Ciherang-Sub1	93.00	93.36	24.70	8.77	27.54	20.24	124.00	89.24	2.66	47.50	0.43	0.07	3.73	51.92	0.26
5	Savitri	110.00	94.29	22.66	8.55	27.29	18.22	100.00	58.89	2.15	29.26	0.35	0.05	4.27	61.04	0.34
6	Savitri-Sub1	110.00	92.88	22.70	9.66	30.59	22.12	105.00	60.79	2.09	25.78	0.32	0.04	3.64	62.13	0.32
7	IR64	87.33	85.38	24.23	8.44	28.22	17.73	81.33	84.58	2.41	40.90	0.28	0.03	3.89	42.18	0.21
8	IR64-Sub1	89.33	85.70	24.58	8.33	29.24	15.28	71.33	81.00	2.48	34.52	0.31	0.05	3.78	44.76	0.21
9	PSBRc 18	88.33	108.66	23.77	6.66	38.19	28.43	122.33	78.61	2.34	54.68	0.24	0.04	3.20	37.43	0.17
10	PSBRc 18-Sub1	103.00	91.89	24.54	8.22	28.69	20.05	95.67	71.64	2.32	38.60	0.31	0.04	2.67	66.45	0.31
11	Samba Mahsuri	104.33	81.44	20.42	9.00	23.42	15.77	150.33	81.94	1.41	40.91	0.47	0.04	3.47	78.62	0.32
12	Samba Mahsuri-Sub1	104.33	83.99	21.72	9.22	24.96	18.73	143.00	71.51	1.42	39.02	0.63	0.07	3.10	80.16	0.34
13	Swarna	106.33	86.83	20.45	9.44	20.95	17.03	113.67	69.99	1.95	44.09	0.46	0.07	3.87	58.96	0.29
14	Swarna-Sub1	105.00	88.89	20.57	10.00	18.52	12.20	117.67	74.30	1.96	43.85	0.28	0.04	3.17	52.79	0.28
15	Thadokkham	105.00	98.00	22.74	7.55	22.56	17.35	92.33	72.06	2.99	36.60	0.49	0.08	3.06	56.52	0.33
16	Thadokkham- Sub1	106.33	98.61	23.65	8.55	23.03	18.23	90.00	63.38	3.00	41.72	0.46	0.08	2.17	46.87	0.27
17	PSBRc 68	103.00	110.00	24.89	7.00	30.74	28.22	87.33	57.09	2.83	35.60	0.41	0.07	4.72	47.02	0.23
18	Lalat	93.67	94.83	24.91	10.22	36.05	26.96	83.33	68.22	2.53	40.60	0.34	0.06	4.29	49.05	0.23
19	Pratikshya	105.00	99.11	23.18	9.77	12.88	18.18	131.67	61.70	2.13	45.83	0.29	0.03	4.03	49.81	0.25
20	Mahanadi	110.00	104.44	22.77	9.00	17.99	22.20	114.33	63.40	2.31	34.43	0.37	0.06	3.42	55.04	0.28
	Grand mean	101.08	95.12	23.29	8.70	25.75	19.92	111.98	71.85	2.32	40.49	0.38	0.06	3.69	54.61	0.27
	CD	1.07	4.79	1.33	2.21	5.97	5.03	27.17	11.90	0.22	6.21	0.04	0.01	1.46	6.05	0.03

Table 3: Mean performance of different genotypes with respect to various characters

Sl. No.	Variety	SLW	SLA	CGR	RL GR	RLA GR	LAD	PPCG	Chl. Con.	Car. Con.	SOD	Catalase	Peroxidase	GYP	Plot yield (q/ha)
1	BR11	5.57	181.17	1.17	0.34	0.23	9.69	74.68	1.57	277.98	1.79	0.00026	0.0172	13.59	45.88 (9)
2	BR11-Sub1	5.07	170.38	2.07	0.31	0.33	11.09	65.60	1.62	209.14	1.81	0.00029	0.0487	14.39	50.83 (4)
3	Ciherang	5.22	191.62	1.90	0.29	0.24	10.55	62.25	2.41	265.22	2.43	0.00029	0.0362	16.96	51.86 (2)
4	Ciherang-Sub1	5.23	191.88	2.34	0.27	0.15	8.33	76.33	2.33	262.39	1.54	0.00040	0.0432	15.47	47.67 (6)
5	Savitri	6.80	180.78	1.13	0.31	0.30	15.28	66.54	2.55	323.53	2.41	0.00020	0.1615	10.23	37.00
6	Savitri-Sub1	5.25	191.14	1.03	0.26	0.11	13.40	64.99	2.24	183.03	2.73	0.00018	0.1575	10.66	26.42
7	IR64	4.99	200.39	1.75	0.18	0.25	10.07	72.31	1.58	158.12	2.57	0.00015	0.0207	8.01	34.56
8	IR64-Sub1	4.74	211.08	1.41	0.15	0.23	10.31	58.26	2.13	114.59	2.08	0.00004	0.0403	6.87	29.98
9	PSBRc18	4.61	217.21	1.15	0.25	0.26	7.75	63.54	2.05	201.65	1.46	0.00012	0.0414	11.59	45.84 (10)
10	PSBRc18-Sub1	4.81	209.95	1.87	0.22	0.25	8.12	36.53	1.93	204.49	2.17	0.00029	0.0574	9.05	46.00 (8)
11	Samba Mahsuri	4.11	243.66	2.82	0.37	0.43	10.47	75.97	1.27	230.20	2.94	0.00042	0.1498	9.78	45.20 (11)
12	Samba Mahsuri-Sub1	4.29	233.27	2.96	0.55	0.42	9.07	47.94	1.83	259.96	2.29	0.00037	0.1197	10.16	44.48
13	Swarna	4.96	201.61	2.67	0.34	0.29	8.71	56.38	2.15	145.98	2.34	0.00043	0.1585	14.86	52.44 (1)
14	Swarna-Sub1	5.28	189.51	1.03	0.18	0.11	7.70	59.99	1.31	228.78	1.98	0.00016	0.0988	13.20	48.07 (5)
15	Thadokkham	5.57	178.73	2.47	0.45	0.41	7.07	41.15	1.61	237.69	2.43	0.00028	0.1117	10.68	37.46
16	Thadokkham-Sub1	5.77	173.56	1.88	0.39	0.29	5.56	32.03	1.78	347.22	2.29	0.00047	0.0822	13.18	40.67
17	PSBRc 68	5.05	198.11	2.54	0.26	0.21	11.43	59.28	1.93	332.04	2.06	0.00021	0.1260	9.75	46.52 (7)
18	Lalat	4.75	210.51	2.13	0.13	0.19	9.44	59.70	1.38	335.68	1.92	0.00017	0.0809	11.26	39.64
19	Pratikshya	5.07	197.15	1.37	0.22	0.20	9.51	61.25	1.81	232.42	3.01	0.00031	0.1341	17.06	51.71(3)
20	Mahanadi	5.16	194.02	1.38	0.34	0.28	10.75	70.66	1.98	400.06	2.23	0.00029	0.0841	14.73	45.19(12)
	Grand mean	5.12	198.29	1.85	0.29	0.26	9.71	60.27	1.87	247.51	2.22	0.00027	0.0885	12.07	43.37
	CD	0.54	20.87	0.13	0.05	0.03	2.67	6.43	0.40	1.56	0.21	0.00004	0.0009	4.10	3.67
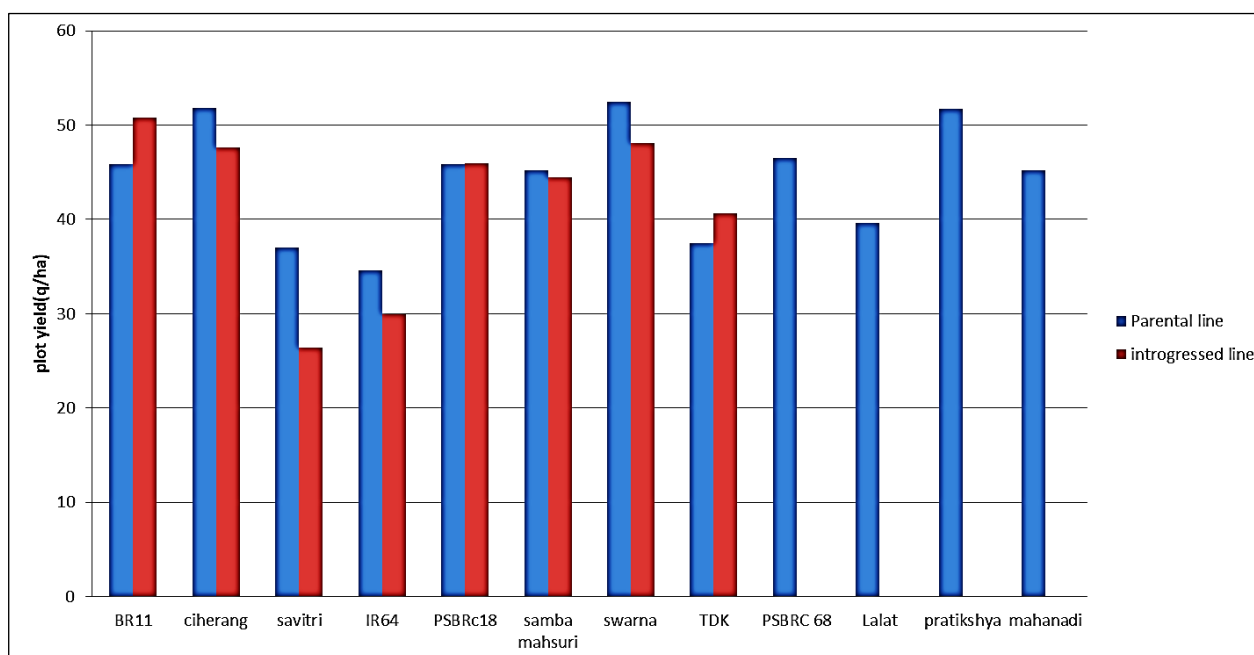
Fig 3: Plot yield of Sub1 introgressed lines along with their parent

Table 4: Promising cultures in rice

Sl. No.	Variety	DF	PH (cm)	PN	FGN	F (%)	100-GW (g)	PY (q/ha)
1	Swarna	106.00	86.83	9.44	114.00	69.99	1.95	52.44
2	Ciherang	92.00	96.00	9.55	119.00	91.22	2.63	51.86
3	Pratikshya	105.00	99.11	9.77	132.00	61.70	2.13	51.71
4	BR 11-Sub 1	103.00	106.44	7.55	152.00	69.46	2.43	50.83
5	Swarna-Sub 1	105.00	88.89	10.00	118.00	74.30	1.96	48.07
6	Ciherang-Sub 1	93.00	93.36	8.77	124.00	89.24	2.66	47.67
7	PSBRc 68	103.00	110.00	7.00	87.00	57.09	2.83	46.52
8	PSBRc 18-Sub 1	103.00	91.89	8.22	96.00	71.64	2.32	46.00
9	BR 11	103.00	101.74	8.44	138.00	68.02	2.27	45.88
10	PSBRc 18	88.00	108.66	6.66	122.00	78.61	2.34	45.84

Were Swarna, Ciherang, Pratikshya, BR 11-Sub 1, Swarna-Sub 1, Ciherang-Sub 1, PSBRc 68, BR 11 and PSRBc 18.

The superior performance of Swarna, was due to higher tiller number, harvest index, RGR, NAR, LAI, LAR, LWR, SLA,

CGR, RLGR, RLAGR, chlorophyll content, SOD content, catalase content, glutathione peroxidase content and grain yield per plant. Similarly the high yield in Ciherang was due to superior expression of panicle number, fertility percentage, 100-grain weight, harvest index, RGR, NAR, LAI, LAD, chlorophyll content, carbohydrate content, SOD content, catalase content and grain yield per plant. The high yield in Pratikshya may be ascribed to higher panicle number, fertile grain number, harvest index, LAI, PPCG, SOD content, catalase content, glutathione peroxidase content and grain yield per plant. The high yield in BR-11 Sub1 was due to longer panicle length, higher flag leaf area, fertile grain number, 100-grain weight, harvest index, LAI, LAR, LWR, CGR, RLGR, RLAGR, LAD, PPCG, catalase content and grain yield per plant.. The superior yield performance of Swarna-Sub 1 was due to higher panicle number, fertility percentage, harvest index, LWR, SLW and grain yield per plant. The superior yield performance of Ciherang-Sub 1 was related to longer panicle length, higher fertile grain number, fertility percentage, 100-grain weight, harvest index, RGR, NAR, LAI, CGR, PPCG, chlorophyll content, carbohydrate content, catalase content and grain yield per plant. Similarly the high yield performance of PSBRc 68, may be explained due to longer panicle length, higher flag leaf angle, flag leaf area, 100-grain weight, RGR, NAR, LAI, CGR, LAD, chlorophyll content, carbohydrate content and glutathione peroxidase content.

Conclusion
It was interesting to note that the high yield performance of promising cultures was responsible for the superior expression of various traits under study and no definite trend of relationship has been established. However, it is imperative to identify various quantitative and physiological traits associated with the promising genotypes, which could be utilized for realization of higher yield and greater stability in rice. In general it is revealed that higher yield, in the promising genotypes may be due to longer panicle length, higher panicle number, higher grain number with improved spikelet fertility, higher 100-grain weight, higher harvest index, RGR, NAR, LAI, CGR, LAD, post flowering contribution to grain yield, higher chlorophyll content, carbohydrate content, SOD content, catalase content, glutathione peroxidase content at 50% flowering and grain yield per plant. These characters may serve as selection criteria for prediction and realization of higher yield, greater stability and better adaptation in rice.

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