Research Note
Impact of drought and detection of potential donors for reproductive stage tolerance in rice

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Abstract
In present study, 48 drought tolerant lines along with two susceptible genotypes of upland and lowland rice ecologies were tested at Central Rice Research Institute during dry season of 2011 and 2012, to identify the reproductive stage drought tolerant lines and to exploit the genetic variations. In support of various estimates of morpho-physiological parameters, genotypes Nan Te Hao, Purbachi (Chinese 1), Saita, NSIC Rc 222, Binnatoha, CO18, Ai Jiao Nan Te, Brown Gora, Black Gora (NCS 12), Jhona 349, Kalakeri are adjudged as good donors for reproductive stage drought tolerance in rice.

Rice is a primary food source for more than two third of the world's population, that account for nearly 21% of global calorie intake (Maclean *et al*., 2002). Nearly 75% of the global rice production comes from irrigated ecosystem that covers around 55% of the total rice cropped area. Rainfed upland and lowland contributes only 21% of the total production from 34 % of the cropped area. Frequent occurrence of drought and submergence are considered as the key factor for low productivity of rice in rainfed environments. Drought stress during cropping season directly affects the grain yield; particularly the stress at reproductive stage is most devastating (Venuprasad *et al*., 2009; Lanceras *et al*., 2004). Drought stress during anthesis stage accompanied by high temperature reduces the duration and rate of grain filling, thereby reduce mean kernel weight. Grain yield is the result of many developmental and physiological events that occur during the life cycle of the plant, as determined by three main components; the number of panicles/plant, number of grain/panicle and weight of grains (Poehlman, 1987). Hence, identification of suitable gemplasm lines possessing reproductive stage drought tolerance traits and their utilization in breeding programme is a pre-requisite for success of drought tolerance breeding in rice.

Plant material and field layout:The experimental materials consisted of 48 drought tolerant lines including two susceptible genotypes of upland and lowland rice ecologies (Table 3) collected from gene bank of Central Rice Research Institute (CRRI), Cuttack, India and International Rice Research Institute (IRRI), Manila, Philippines. The field experiment was conducted during dry season 2011 and 2012 in alpha lattice design with two replications. Each genotype was raised in five rows with a row length of 4.5 m, to identify potential donors for reproductive stage tolerance. The germplasm lines were direct seeded with spacing of 20 x 15cm and subsequently normal package of practices were followed for raising a good crop. The selected drought tolerant genotypes are almost similar in flowering duration. Therefore, drought stress was applied simultaneously to all genotypes. Reproductive stage drought stress was applied by withholding irrigation water just before panicle initiation stage and stress was maintained for 20 days till soil moisture was up to 40-60 kilo Pascal. Five representative plants from each genotype in each replication were randomly selected to record observations on plant height (cm), ear bearing tillers per plant, panicle length, spikelet sterility %, total dry matter production (TDM), harvest index, *per se* yield, 1000 grain weight, kernel length and kernel breadth. Days to 50% flowering were computed on plot basis. The mean data after computing for each character was pooled from two years and subjected to standard methods of analysis. Analysis of variance was worked out by following the method suggested by Panse and Sukhatme (1985). The genotypic and phenotypic coefficients of variation (GCV and PCV) were worked out according to the method given by Singh and Chaudhary (1977). Heritability in broad sense and expected genetic advance on the basis of per cent of mean at five per cent selection intensity were worked out according to the method given by Allard (1960). Principle component analysis (PCA) analysis was used to estimate the Euclidean distance

between two genotypes and correlation between the variables (Anandan *et al*., 2011; Anandan *et al*., 2012). These analysis were performed using the Windowstat 7.5 software (Indostat Services, Hyderabad, India).

Analysis of variance for traits indicated significant differences among the genotypes studied for *per se* yield, ear bearing tiller, Total Dry Matter at harvest, spikelet sterility, days to 50% flowering and harvest index and found to be influenced under reproductive stage drought stress (Table 1). Therefore, these traits are useful for selection of genotypes for reproductive stage drought tolerance. Other traits like test weight, kernel length and kernel breadth were observed to be least variable under reproductive stage drought stress.

The genotypes showed considerable differences in grain yield and varied from 0.14 t ha^{-1} (UPLRI 7) to 1.959 t ha^{-1} (Nan Te Hao). The other genotypes exhibiting high *per se* yield were Pyari (1.942 t ha^{-1}), Vandana (1.640 t ha^{-1}), Tam Cau 9A (1.663 t ha^{-1}), N22 (1.65 t ha^{-1}), Black Gora (NCS 12) (1.31 t ha^{-1}), Muey Nong (1.308 t ha^{-1}) and Jhona 349 (1.314 t ha^{-1}) under reproductive stage drought stress. A wide range of genotypic coefficient of variation was observed for spikelet sterility, besides exhibited high inheritance (75%). Hence, spikelet sterility can be taken as selection criteria for identification of genotypes at reproductive stage. Besides, high GCV was also observed for TDM at harvest, harvest index and ear bearing tiller. These traits are also exhibiting high heritability during reproductive stage of the crop. Hence, these traits along with spikelet sterility are to be used for identification of donors at reproductive stage drought stress tolerance. It is reported that yield QTLs are also inherited under drought stress and play role for *per se* yield of the trait. Here, *per se* yield showed high GCV coupled with high heritability under drought stress. Thus, combination of traits like spikelet sterility, TDM at harvest, harvest index and ear bearing tillers with *per se* yield will be useful to differentiate the tolerant donors from susceptible genotypes.

Estimates of various morpho-physiological parameters of genotypes under reproductive stage drought stress of 50 rice genotypes are presented in Table 2. Genotypes studied in the present experiment, showed a wide variation in yield components such as ear bearing tiller hill^{-1} (EBT) and harvest index (HI). A high number of productive tillers have been considered a crucial diagnosis index along with a high spikelet m^{-2} resulting in a higher yield of crops. Results revealed that high EBT was recorded in Nan Te hao (13.45) followed by Pyari

(13.1), Muey Nong (12.85) and Vandana (12.1) under stress with low sterility (Table 3). Saita and Koshihikari were also good performer in case of total dry matter production 117.47 and 117.46 respectively. In contrast, the HI of all high yielding genotypes recorded more than 0.21 under stress condition. T 136 showed high panicle number (24.3) followed by T1 (23.4) and Taichung Native1 (23.3). Other germplasm lines like BR1, Kalakeri, IRRI 119 and T1 exhibited high grain yield along with low spikelet sterility, high panicle number and high harvest index may be good donors under reproductive stage drought stress.

Biplot diagram derived from first and second factor components for 50 genotypes is shown in Fig. 1. Genotypes with higher PC1 and PC2 scores had the high yields. The second quarter of biplot, which has the positive values of PC1 and PC2, are the suitable regions to identify the high-performance genotypes. Golabadi et al. (2006) obtained the similar results in drought tolerance of segregating populations of durum wheat. The development of reproductive organs, which is under the control of photoassimilate production and partitioning by the source tissues, is the most critical (Taiz and Zeiger, 2002; Wahid and Rasul, 2004). Therefore, increased drought at reproductive stage has pronounced effect on grain development and yield.

Cultivar-by-trait biplot analysis (Fig. 1) of 50 genotypes with spikelet sterility, TDM at harvest, harvest index, ear bearing tiller and *per se* yield, indicated that the pair wise trait of drought donor genotypes exhibited an acute angle for most of these traits. The figure indicated that these traits are correlated and may be considered as selection criteria for reproductive stage drought stress tolerance donors. From the figure, the genotypes can be divided into four groups. Based on spikelet sterility, TDM at harvest, harvest index, ear bearing tiller and *per se* yield, genotypes from group II (second quarter) may be considered as reproductive stage drought tolerant. This group contains promising genotypes like Nan Te Hao, Purbachi (Chinese 1), Saita, NSIC Rc 222, Binnatoha, CO18, Ai Jiao Nan Te, Brown Gora, Black Gora (NCS 12), Jhona 349, Kalakeri. The group III contains PSBRC 80, BR 2, Dhagad deshi, BR 1, IR74371-46-1-1, T 1, Asse Y Pung, Pyari, Muey Nong (Wang Din). These genotypes are moderately drought tolerant. But group I and group IV contains drought susceptible genotypes like Basmati 370, IR64, JC 148, IR 36, UPLRI 7, Ratna, Jaya, Samba Mahsuri, MTU1010, Magawk Dong 269-7-7 (9), CO 25, Dholiboro, GS 529 and Dular. The genotypes present in group I and

IV may be rejected as they form separate group when compared with pair wise trait. Based on the estimates of various morpho-physiological parameters and biplot analysis, genotypes like Nan Te Hao, Purbachi (Chinese 1), Saita, NSIC Rc 222, Binnatoha, CO18, Ai Jiao Nan Te, Brown Gora, Black Gora (NCS 12), Jhona 349, Kalakeri are considered as potential donors for reproductive stage drought tolerance in rice.

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Table 1. Analysis of variance for various morpho-physiological traits of 50 rice genotypes under reproductive stage drought stress

Characters	Sources of variation		
	Rep	**Genotype**	**Error**
Days to 50% flowering	30.00	263.99*	30.54
Plant height	34.75	297.36*	37.27
Ear bearing tiller	20.00	14.06*	3.44
Panicle length	9.85	6.51*	1.66
Total dry matter production	390.19	840.83*	134.53
Harvest index	0.00067	0.0077	0.0021
Sterility %	376.87	270.55*	43.67
Yield	30.48	53.44*	24.66
1000 grain weight	0.0013	0.47	0.017
Kernel length	0.021	0.46	0.043
Kernel breadth	0.0012	0.66	0.0109

Table 2. Estimation of genetic parameters for various morpho-physiological traits during reproductive stage drought tolerance of 50 rice genotypes

Characters	Mean	GCV(%)	PCV(%)	h^2(BS)	GA% as mean
Days to 50% flowering	73.98	14.6	15.53	0.88	20.92
Plant height(cm)	80.61	14.15	15.13	0.87	21.96
Ear bearing tiller	8.64	26.65	30.66	0.75	4.12
Panicle length(cm)	20.74	7.5	8.7	0.74	2.76
Total dry matter production(g)	97.32	19.31	21.07	0.84	35.48
Harvest index(%)	0.21	24.33	28.33	0.72	0.09
Sterility %	37.28	28.56	31.19	0.83	20.09
Yield (g)	25.98	14.6	19.9	0.53	5.73
1000 grain weight(g)	2.12	22.44	22.86	0.96	0.96
Kernel length(mm)	0.81	56.7	59.55	0.9	0.9
Kernel breadth(mm)	6.2	9.23	9.3	0.98	1.16

Table 3. Mean performance of 50 rice genotypes of various traits under reproductive stage drought stress.

| Sl No.	Genotype	Ear Bearing Tiller	Total Dry Matter	Harvest Index(%)	Sterility %	Yield (t/ha)
1	ZHENSHAN 2	12.15	86.98	0.21	40.05	0.76
2	GS 529;DULAR	8.90	86.74	0.26	30.25	0.48
3	BINNATOHA	7.00	111.32	0.21	30.00	1.07
4	PURBACHI (CHINESE 1)	13.00	126.60	0.15	24.25	0.95
5	SAITA	7.15	117.47	0.18	23.95	0.97
6	NSIC Rc 222	11.60	110.26	0.16	27.15	1.00
7	SAMBA MAHSURI	5.40	79.60	0.18	78.50	0.16
8	KASALATH	9.30	98.98	0.21	43.05	1.09
9	BR 21	10.65	102.55	0.31	25.65	0.75
10	T 1	7.40	128.90	0.31	31.60	1.23
11	CO18	7.35	121.25	0.23	41.50	0.67
12	IR 64	12.45	128.90	0.13	74.60	0.13
13	BASMATI 370	6.50	61.50	0.28	75.90	0.16
14	MAGAWK DONG 269-7-7 (9)	6.25	106.72	0.11	39.20	0.44
15	JHONA 349	14.25	120.84	0.22	29.00	1.31
16	TAICHUNG NATIVE 1	6.75	65.80	0.21	38.05	0.12
17	PSBRC 80	12.70	83.16	0.25	37.30	0.63
18	MTU1010	5.50	79.95	0.16	69.42	0.20
19	BR 2	13.00	99.72	0.25	32.75	0.55
20	KOSHIHIKARI	10.45	117.47	0.33	26.55	1.03
21	UPLRI 7	8.00	82.19	0.24	78.95	0.14
22	ASSE Y PUNG	11.05	109.99	0.31	30.25	0.67
23	DUBRAJ	5.00	59.05	0.17	72.15	0.19
24	NAN TE HAO	13.45	116.28	0.21	19.40	1.96
25	IRRI 119	7.65	99.35	0.30	25.70	1.01
26	KALAKERI	14.20	107.20	0.13	26.95	1.25
27	AI JIAO NAN TE	9.70	90.59	0.21	28.50	1.09
28	NIAW	8.70	91.86	0.23	43.20	0.89
29	Dhagad deshi	12.75	79.71	0.28	36.60	0.76
30	JC 148	6.75	97.51	0.35	45.00	0.38
31	MUEY NONG (WANG DIN)	12.85	135.76	0.29	28.25	1.31
32	DHOLI BORO	6.10	106.32	0.24	39.15	0.73
33	BR 1	7.90	109.98	0.28	29.75	1.09
34	RATNA	6.85	46.95	0.23	77.40	0.19
35	BROWN GORA	9.60	96.43	0.22	43.25	1.25
36	CHAU	9.10	117.91	0.17	38.90	0.34
37	NSIC Rc 192	9.50	111.00	0.32	39.70	0.30
38	CO 25	7.20	104.83	0.21	45.70	0.63
39	JAYA	6.05	52.50	0.19	62.95	0.37
40	IRRI 123	9.30	96.28	0.31	42.20	0.67
41	Vandana	12.10	136.94	0.31	26.10	1.64
42	TAM CAU 9 A	9.20	94.40	0.31	25.90	1.66
43	N 22	8.05	112.39	0.23	26.30	1.65
44	BLACK GORA (NCS 12)	8.25	103.19	0.22	26.10	1.31
45	IR 36	6.05	11.50	0.25	68.90	0.11
46	RD 25	7.55	101.78	0.17	43.05	0.97
47	IR74371-70-1-1	6.60	103.83	0.17	51.10	0.82
48	IR74371-46-1-1	10.65	73.27	0.27	24.05	1.32
49	Pyari	13.10	96.00	0.29	23.40	1.94
50	T 136	5.10	60.25	0.16	46.65	0.90
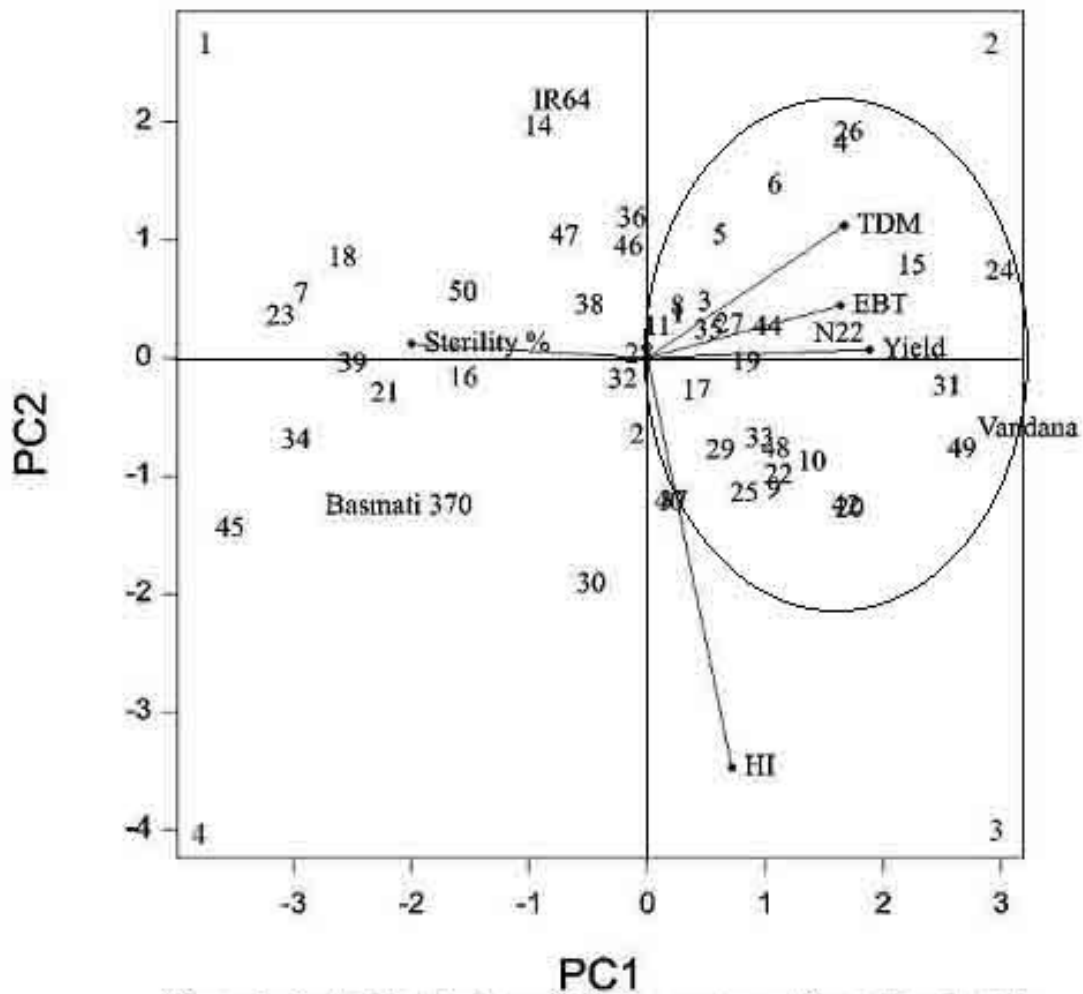
Figure 1. Spatial distribution of 50 rice genotypes for yield and yield related traits for reproductive stage drought tolerance in rice.