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GENETIC VARIABILITY AND PHYSIOLOGICAL, BIOCHEMICAL, AGRO-MORPHOLOGICAL RESPONSE TO DROUGHT RESISTANCE IN UPLAND RICE (*Oryza sativa* L.)

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SUMMARY

Eighteen genotypes of upland rice were evaluated for grain yield and 17 biochemical traits for estimation of direct selection parameters. The entries were evaluated in Randomized Block Design with 3 replications under normal and drought condition during wet season in 2 years. Starch at maturity, soluble carbohydrate upper root, leaf starch, proline content and CHO lower root exhibited high phenotypic (PCV) and genotypic (GCV) coefficients of variation along with high heritability and high genetic advance under irrigated conditions. Under drought conditions, starch at maturity, starch lower root, starch at flowering, CHO at maturity, CHO lower root, leaf CHO, CHO at flowering, grain yield, starch upper root, chlorophyll b, CHO upper root and leaf starch showed high estimates of PCV, GCV, heritability and genetic advance in per cent of mean. The traits mentioned above emerged as ideal traits for improvement through selection in respective environments owing to their high variability and transmissibility. The results revealed that the estimates GCV, PCV, heritability and genetic advance were higher in drought conditions as compared to normal conditions for majority of biochemical traits under study. The adverse drought conditions appeared to unfurl greater degree of variability and transmissibility in the yield as well as biochemical traits. Therefore, greater possibility of improvement in biochemical traits through selection appears in drought condition than control condition.

Key words: Rice, drought, genetic evaluation, drought resistant parameters, yield physiological and biochemical characters

Key findings: Various physiological and biochemical characters confer drought resistance. Investigation of genetic variation of compatible characters and proficient screening techniques are exigent for selecting desirable genotypes.

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INTRODUCTION

Rice (*Oryza sativa* L.) is the single most important food crop for more than one third of world's population. To meet the needs of the growing population the present annual rice production of 560 million tons must be increased to 850 million tons by 2025 (Khush, 1997). Rice production is the biggest water consumer among the cereals and it is also very sensitive to water deficit. Interestingly, irrigated rice has got very low water use efficiency as it consumes 3000-5000 liter of water to produce 1 kg of rice. To ensure the food security and reduce the water shortage, development of drought tolerant (DT) and water-saving rice varieties has become increasingly important. Breeding rice for drought-prone conditions has had less success than breeding for favorable irrigated environments. There is a lower return on plant breeding for lower yielding upland environments, compounded by a more costly and slower uptake of new varieties. The plant breeding process for drought adaptation can be made more efficient when traits other than yield are added to the selection process. In rice, various researchers have identified putative traits for drought resistance. There has been a large effort to evaluate their effectiveness under a range of drought conditions. Limited work has been conducted on evaluating the contribution of putative drought resistance traits to grain yield in rice (Fukai and Cooper, 1995). This needs to be rectified, particularly considering their importance relative to upland conditions in Asian countries. Wade *et al*. (1999) suggested that intensive physiological-genetic research efforts onto clearly defined, major target environments should provide a basis for increasing the relevance of stress physiology and the efficiency of breeding programs for development of drought-resistant genotypes. Crops have many mechanisms of response and survival to drought and include some physiological, biochemical and agro-morphological response (Levitt, 1972 and Graff, 1980). Multidisciplinary approach involving genetics, biochemistry, biotechnology, physiology, plant breeding and crop science will be appropriate to assess the complicated and integrated response of plants to drought and to evolve superior drought resistant genotypes (Mitra, 2001). Furthermore, the functional significance of the physiological and biochemical characteristics and their relationship with yield, are still not clearly established in rice. Therefore, present study was undertaken to analyze the physiological, biochemical and agro-morphological responses of upland rice genotypes to drought at flowering stages in order to compare the responses of genotypes to water stress; to study the genetic variability and to identify drought tolerant genotypes through drought susceptibility index.

MATERIALS AND METHODS

Experimental sites, genotypes and years of screen

The present investigation was carried out in wet season, during 2007 and 2008 at the Instructional Farm of Department of Crop Physiology, N. D. University of Agriculture & Technology Kumarganj (Faizabad), U.P., India. The genotypes of upland rice (*indica* and *japonica* type) from different geographical regions (Table 1) were screened for drought tolerance. These genotypes responded well under severe drought conditions and displayed good drought score, recovery and early vegetative vigor, simultaneously, substantial yield also.

Management of water stress

The experiments were conducted with well defined protocol for water management under natural field conditions during wet season in both the years.

Irrigated control (E_1)

The experimental field was left uncovered to receive natural rainfall. In addition to this, experimental plots were irrigated using well laid channels for supplying tube well water, as and when required, to maintain appropriate moisture levels as recommended for irrigated rice.

Reproductive stage drought stress (E_2)

The experiment field was covered by constructing temporary rainout shelter at a height of 10-12 ft using polythene sheets to exclude any possibility of natural rainfall falling in the experimental plots with proper drainage channel. Care was taken to check the inflow or seepage of water from the adjoining areas by

Table 1. Description of rice genotypes.

Improved varieties/ cultivars	Description			
	Origin	Group	Plant Height	Particular characteristics
Moroberekan	West Africa	Tropical Japonica	70.0	Upland cultivar, course grain, high yielder, broad leaf, selection landraces.
TN-1	Taiwan	Japonica	85.0	Susceptible for multi disease and insect dwarf plant, low yield, short gold grain
Azucena	Philippine	Japonica	87.5	Highly green broad leaf, drought tolerant, course grain
Vandana	Orissa	Indica	98.5	Upland cultivar, tall plant and drought tolerant
NDR-359	NDUA&T, INDIA	Indica	85.8	Irrigated (ecology) long gold high yielder semi dwarf plant
NDR-97	NDUA&T, INDIA	Indica	76.8	Upland cultivar, dwarf plant, short duration, drought tolerant (escaping fine grain, eating quality good)
IR64	IRRI	Indica	88.2	Highly susceptible for drought, tiny fine grain semi dwarf
Saita	INDIA	Indica	76.0	Highly susceptible for drought and sheath blight, semi dwarf plant, land races
DGI-21	IRRI (IR64 x Azucena)	Indica x Japonica	79.5	Double haploid
DGI-75	IRRI (IR64 x Azucena)	Indica x Japonica	76.7	Double haploid
DGI-138	IRRI (IR64 x Azucena)	Indica x Japonica	100.5	Double haploid
DGI-152	IRRI (IR64 x Azucena)	Indica x Japonica	81.5	Double haploid
DGI-379	IRRI (IR64 x Azucena)	Indica x Japonica	99.5	Double haploid
DSU-18-6	IRRI (IR64 x Azucena)	Indica x Japonica	89.2	Double haploid
P-0088	IRRI (IR64 introgessed)	Indica x Japonica	97.2	Introgression line
P-0090	IRRI (IR64 introgessed)	Indica x Japonica	73.3	Introgression line
P-0326	IRRI (IR64 introgessed)	Indica x Japonica	92.5	Introgression line
P-0397	IRRI (IR64 introgessed)	Indica x Japonica	104.8	Introgression line

making adequate bunds around the experiment and covered with polythene in drought conditions. The heading stage drought was created by withholding the irrigation for 15 days up to 80 K Pa at 0-15 cm soil profile and 60 K Pa at 30 cm soil depth. Plants were exposed for 2 weeks (60-80 KPa.). Soil moisture content (SMC) during stress period was monitored through periodical soil sampling at 0-15, 15-30 cm soil depth. Drought was released by irrigation. Recovery was measured at 10th days after released of drought. Genotypes were scored for leaf rolling and leaf drying at the peak stress period using the IRRI Standard Evaluation System (IRRI, 1996).

Experimental Design

The genotypes were seeded and seedling establishment was done in dry beds and transplanting was done 21 days after seeding. Each genotype was transplanted in randomized block design with 3 replications in a 3 m length row. Row spacing was 20 x 15 cm and 1 seedling per hill was used. Recommended agronomic practices were followed. Pesticides and bird nets were used to protect the plants against pests. All other crop management practices were at the optimum level.

Observation and evaluation

Observations were recorded on 5 competitive plants of the middle row of each plot for yield and 18 biochemical traits. The biochemical traits estimated by chlorophyll according to Arnon (1949), protein content by Lowery *et al*. (1951), soluble sugar by Yamn and Willis (1954), starch estimation according to Mc Cready *et al*. (1950), proline content by Bates *et al*. (1973), Superoxide dismutase activity (SOD) according to Asada *et al*. (1974), Nitrate reductage (NR) estimated by Jowarski (1971) method, α-amylase activity estimated by Chance and Maechly (1955). While, identifying the promising genotypes for limited irrigation, drought susceptibility index (DSI) suggested by Fischer and Maurer (1978) was also taken into consideration. The data of biochemical and grain yield were analyzed by appropriate statistical analysis (Gomez and Gomez, 1984) using CropStat 7.2 (IRRI, 2009) program. Phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability (broad sense) and genetic advance as percentage of mean were computed following Singh and Chaudhury (1985).

RESULTS

Analysis of variance

The ANOVA of 18 genotypes including 2 checks with respect to 19 biochemical traits and grain yield revealed that the mean sum of squares due to genotypes were highly significant for all the characters studied indicating genetic variability among the experimental materials except protein, NR, SOD 3 days, SOD 0 days under E_1 and SOD 0 day under drought conditions.

Genetic parameters

The estimation of mean of all 19 characters for 2 environments over the seasons showed lower value under drought compared to irrigated condition except Proline, α amylase and SOD. However, differences in mean values of all the characters are higher except protein, soluble sugar and chlorophyll which showed marginal differences between the 2 environments. A wide range of variation was observed in the rice genotype for all the biochemical characters, yield and yield attributes. However, widest range of variation was recorded for proline, NR, α amylase, soluble sugar and starch at flowering and maturity under the environments and Chlorophyll b, SOD 3 and 0 days in E_2.

The genotypic coefficient of variation (GCP) and phenotypic coefficient of variation (PCV) were computed separately for the pooled irrigated and pooled stress environment. The results revealed that highest GCV and PCV were recorded for soluble sugar in lower root (GCV = 33.12 & PCV = 33.26) under E_1 and starch at maturity (GCV = 46.43 & PCV = 46.52) under E_2 followed by starch at maturity (GCV = 27.87 & PCV = 27.97) under E_1 and starch lower root (GCV = 33.64 & PCV = 33.81) under E_2 whereas, the lowest values of GCV and PCV were observed in case of SOD at 3 day as well as SOD at 0 days under both the conditions (Table 2). The high GCV and PCV values (> 20.00%) were observed for proline, leaf starch, soluble sugar in upper root under E_1 while the characters viz., chlorophyll b, soluble sugar at flowering and maturity, leaf soluble sugar, starch at maturity, soluble sugar upper root and lower root, leaf starch and starch in upper root. The low estimates (> 10.0%) of these 2 parameters were noted for protein and amylase under both the conditions while, chlorophyll a and NR under E_1 and proline under E_2. Simultaneously, rest of the characters recorded moderate estimate for GCV and PCV under both the conditions.

In this study, high heritability coupled with high genetic advance (Ga) were estimated for Chlorophyll b, proline, soluble sugar and starch at flowering, soluble sugar and starch at maturity, leaf soluble sugar and starch, soluble sugar upper and lower root and grain yield under both the conditions.

Table 2. Estimates of range, grand mean, phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability in broad sense (h^2) and genetic advance in per cent of mean (Ga) for 19 characters in rice germplasm under irrigated (E_1) and drought (E_2) conditions.

Characters	Environments	Mean	Range	Coefficient of Variation		Heritability h^2 (b)	GA in per cent of mean
				GCV	PCV		
Chlorophyll a	Irrigated	0.783 ±0.025	0.73-0.87	5.30	5.45	94.60	10.21
	Drought	0.521 ±0.024	0.25-0.66	19.47	19.51	99.60	40.30
Chlorophyll b	Irrigated	0.259 ±0.023	0.21-0.45	18.91	18.97	99.30	42.47
	Drought	0.209 ±0.010	0.13-0.35	23.91	24.02	99.10	47.84
Protein	Irrigated	3.982 ±0.015	3.54-4.36	9.35	9.43	58.30	19.24
	Drought	3.12 ±0.004	2.45-3.84	0.79	1.61	24.40	7.53
Proline	Irrigated	23.03 ±2.11	17-34	23.25	23.26	99.90	47.85
	Drought	33.68 ±1.62	27-38	9.25	9.30	98.90	18.44
Nitrate reductage	Irrigated	168.00 ±5.78	148-181	14.48	14.87	94.80	30.03
	Drought	102.52 ±4.22	76-128	3.03	4.56	44.20	4.14
Amylase	Irrigated	512.231 ±17.10	410-581	9.11	9.14	99.40	18.70
	Drought	655.82 ±22.22	568-735	5.82	5.85	98.90	11.99
SOD 3 Day	Irrigated	449.24 ±12.11	442-454	0.01	0.64	46.70	7.60
	Drought	1018.49 ±13.10	854-1079	3.68	3.69	29.40	7.55
SOD 0 Day	Irrigated	449.24 ±12.81	442-454	0.01	0.64	0.21	16.62
	Drought	910.62 ±19.53	747-958	0.00	1.61	0.17	4.7
Soluble sugar at flowering	Irrigated	210.11 ±6.48	166-245	10.87	10.95	98.60	21.28
	Drought	145.31 ±3.77	78-218	27.54	27.70	98.80	56.37
Starch at flowering	Irrigated	151.60 ±3.12	113-192	14.93	15.20	96.40	30.18
	Drought	112.10 ±2.09	60-158	29.22	29.31	99.40	60.00
Soluble sugar at maturity	Irrigated	140.62 ±2.66	119-214	18.54	18.65	98.80	37.96
	Drought	94.31 ±1.53	38-140	28.91	29.03	99.10	59.29
Starch at maturity	Irrigated	131.24 ±3.26	83-195	27.87	27.97	99.30	57.23
	Drought	88.88 ±2.09	33-180	46.43	46.52	99.60	75.47
Leaf Soluble sugar	Irrigated	68.63 ±2.66	43-85	14.94	15.55	92.30	29.56
	Drought	48.00 ±1.53	35-71	24.97	25.53	95.70	50.30
Leaf starch	Irrigated	46.95 ±3.54	32-74	24.67	25.19	96.00	49.79
	Drought	34.14 ±2.25	23-53	26.91	27.72	94.20	53.78
Soluble sugar in upper root	Irrigated	0.175 ±0.018	0.12-0.24	25.06	25.15	99.30	51.42
	Drought	0.123 ±0.016	0.09-0.19	20.45	20.55	99.00	40.75
Starch upper root	Irrigated	0.214 ±0.007	0.14-0.32	23.37	23.72	97.10	49.18
	Drought	0.122 ±0.004	0.05-0.21	17.57	21.26	68.30	28.03
Soluble sugar in lower root	Irrigated	0.129 ±0.008	0.06-0.21	33.12	33.26	99.00	69.76
	Drought	0.079 ±0.006	0.03-0.11	27.61	27.84	98.40	50.63
Starch lower root	Irrigated	0.104 ±0.009	0.08-0.16	19.32	27.91	47.90	28.84
	Drought	0.068 ±0.005	0.04-0.11	33.64	33.81	99.00	73.83
Grain yield	Irrigated	520.69 ±7.12	390-664	16.69	16.70	99.90	34.36
	Drought	371.57 ±6.68	228-550	25.35	25.37	7.90	32.19

Table 3. Drought resistance parameters; drought susceptibility index (DSI) and drought tolerance efficiency (DTE) for morpho-physiological and biochemical characters for tested rice genotypes.

Genotypes	NR		Shoot Starch		Leaf Starch		Shoot SS		Leaf SS		Total Chlorophyll		Protein Content	
	DSI	DTE	DSI	DTE	DSI	DTE	DSI	DTE	DSI	DTE	DSI	DTE	DSI	DTE
Azucena	0.82	67.24	0.31	90.22	1.13	68.22	0.84	62.08	0.62	81.41	0.81	76.53	1.05	79.47
DGI 138	1.18	52.91	0.80	74.40	0.41	88.39	0.56	74.74	0.70	78.84	1.04	69.70	1.24	75.85
DGI 152	1.17	53.43	1.49	52.59	1.28	63.95	1.21	45.65	1.60	51.70	1.18	65.66	0.75	85.30
DGI 21	0.54	78.68	1.34	57.40	1.29	63.75	0.55	75.38	0.95	71.46	0.67	80.65	1.39	72.86
DGI 379	0.77	69.52	1.88	39.96	1.03	70.97	0.96	56.89	1.52	54.33	1.20	64.95	0.08	98.51
DGI 75	0.84	66.48	0.94	70.12	1.39	61.05	1.43	35.44	1.50	54.72	1.06	69.07	1.21	76.46
DSU 18-6	1.11	55.81	0.69	77.95	0.91	74.31	0.27	87.75	0.85	74.29	1.06	69.15	0.90	82.51
IR64 (C)	0.98	61.12	2.13	32.16	1.52	57.36	1.16	47.67	1.26	62.10	1.25	63.64	0.30	94.08
Moroberekan	0.65	73.97	0.45	85.77	0.51	85.76	1.08	51.18	0.41	87.78	0.74	78.57	0.79	84.56
NDR 359	0.63	75.03	0.40	87.34	0.90	74.72	0.29	86.75	0.51	84.71	0.78	77.32	0.95	81.47
NDR 97	0.60	76.09	0.23	92.55	0.84	76.31	0.20	91.01	0.59	82.28	0.99	71.13	0.63	87.69
P 0088	1.38	44.94	0.85	72.82	0.77	78.47	1.70	23.40	1.19	64.30	1.20	64.95	1.79	65.07
P 0090	1.74	30.90	1.40	55.43	0.43	87.85	0.44	79.98	1.37	58.77	1.17	65.98	0.64	87.57
P 0326	1.00	60.02	1.81	42.23	0.89	75.01	1.22	45.29	0.49	85.38	0.80	76.84	1.14	77.69
P 0397	1.12	55.48	0.79	74.88	1.73	51.46	1.98	11.00	1.45	56.44	0.59	82.72	1.33	74.10
Saita	1.34	46.75	1.80	42.43	0.87	75.56	1.75	21.20	1.83	44.94	1.56	54.74	1.67	67.50
TN 1	1.26	49.95	1.36	56.60	1.18	66.75	0.32	85.71	0.59	82.30	1.16	66.33	1.85	63.88
Vandana	0.67	73.16	0.40	87.35	0.55	84.45	0.19	91.50	0.34	89.80	0.65	81.05	0.33	93.66

Genotypes	RWC		Biomass		HI		TW		Grain Yield		Per cent increase		
	DSI	DTE	DSI	DTE	DSI	DTE	DSI	DTE	DSI	DTE	Amylase	Proline	LWP (-bar)
Azucena	0.68	87.43	0.84	75.77	0.83	82.42	0.58	91.42	0.55	85.08	20.26	11.46	66.10
DGI 138	0.63	88.40	0.53	84.93	1.12	76.35	1.01	84.90	1.17	68.61	41.08	30.78	27.94
DGI 152	0.87	84.05	1.43	58.95	1.00	78.80	1.19	82.28	1.50	59.58	25.49	59.94	23.36
DGI 21	0.92	83.08	1.11	68.18	0.88	81.49	0.62	90.69	1.34	63.99	41.54	68.49	15.73
DGI 379	0.72	86.78	1.10	68.36	0.74	84.30	1.26	81.17	1.45	60.90	5.60	23.73	47.83
DGI 75	1.28	76.56	0.87	74.99	0.97	79.60	0.41	93.96	1.46	60.61	34.98	64.56	79.31
DSU 18-6	0.53	90.17	0.92	73.48	0.88	81.47	0.92	86.26	1.09	70.72	46.68	56.17	31.34
IR64 (C)	1.47	73.02	1.44	58.58	1.41	70.18	1.09	83.78	1.27	65.74	34.96	82.00	73.91
Morobereken	0.41	92.41	0.41	88.10	0.46	90.34	0.81	87.86	0.60	83.88	9.66	55.00	12.16
NDR 359	0.49	91.01	0.47	86.49	0.70	85.22	1.23	81.61	0.47	88.45	23.16	66.67	25.42
NDR 97	3.11	42.93	1.38	60.27	1.19	74.89	0.71	89.38	1.28	60.38	21.75	12.31	19.57
P 0088	1.65	69.64	1.48	57.48	1.30	72.51	1.21	81.96	1.47	60.38	35.52	6.72	87.67
P 0090	1.17	78.50	0.89	74.44	0.89	81.25	0.95	85.85	1.41	62.11	26.81	21.38	28.79
P 0326	0.47	91.30	1.14	67.17	0.70	85.14	0.50	92.50	0.74	80.10	10.99	20.69	23.77
P 0397	0.84	84.59	1.14	67.31	1.23	74.08	1.20	82.09	1.36	63.40	26.53	87.32	80.30
Saita	1.42	73.83	1.63	53.16	1.53	67.65	2.72	59.52	1.99	46.49	44.10	82.99	92.65
TN 1	0.68	87.58	0.30	91.43	1.25	73.60	1.17	82.61	0.81	78.26	1.91	81.30	16.88
Vandana	0.59	89.17	0.59	82.97	0.93	80.46	0.24	96.47	0.42	88.66	17.52	43.74	17.86

Simultaneously, starch upper root and NR under E_1 and starch lower root and chlorophyll a under E_2 estimated high heritability (> 75.0) and genetic advance (> 30.0). Moderate estimate for heritability (50.0-75.0) and genetic advance (10.0-30.0) were recorded by starch lower root under E_1 and starch upper root under E_2. While, rest of the characters showed low estimate for both the parameters, indicating that simple selection will not be good enough to do needful under respective environments.

Drought susceptibility index (DSI)

The drought susceptibility index is independent of yield potential and drought intensity, and potentially useful for comparisons of drought susceptibility of genotypes between drought levels experiments, since larger values of DSI indicate greater drought susceptibility.

Among the drought resistance parameters, DSI varied from 0.43 (NDR 359) to 1.99 (Saita) for grain yield; 0.24 (Vandana) to 2.72 (Saita) for test weight; 0.46 (Azucena) to 1.53 (Saita) for harvest index; 0.54 (DGI 21) to 1.74 (P 090) for NR; 0.23 (NDR 97) to 2.13 (IR 64) for shoot starch; 0.41 (DGI 138) to 1.73 (PO 397) for leaf starch; 0.19 (Vandana) to 1.98 (PO 397) for shoot soluble sugar; 0.34 (Vandana) to 1.83 (Saita) for leaf soluble sugar; 0.59 (PO 397) TO 1.56 (Saita) for chlorophyll; 0.08 (DGI 379) to 1.85 (TN 1) for protein and 0.30 (TN 1) to 1.63 (Saita) for biomass (Table 3). Of 18 genotypes, 6 indicated below average (ARI < 1), 11 were having above average (ARI > 1) and only 1 was having average (ARI ≈ 1) to drought condition for yield (Table 3). The genotypes viz., Vandana, NDR 97, Morobreken, P 0326 and TN 1 were emerged as most drought resistant genotypes (DSI < 1) for approximately all the characters under study. Interestingly, Saita was the most drought susceptible genotypes with low yield and high DSI for all the characters.

Drought Tolerance Efficiency (DTE)

Another parameter of drought resistance is drought tolerance efficiency, and the values of these parameters were ranged from 46.49% (Saita) to 88.66% (Vandana). Thus, Vandana (88.66%), NDR 359 (88.45%), Azucena (85.08), Moroberekan (83.88%) and PO 326 (80.10%) showed the highest DTE. Interestingly, above said genotypes was imparted by DTE (> 75%) for other characters under study on more than 8 characters out of 12 (Table 3). For instance high DTE genotypes Vandana showed high DTE estimated for all the characters except NR. Relatively greater value of DTE was recorded by most of the genotypes for all the characters under study. Six genotypes (33% of total) were identified as susceptible (i.e. DTE > 60%).

DISCUSSION

Genetic variability parameters

The phenotypic coefficients of variation (PCV) values were greater than genotypic coefficient of variation (GCV) values indicating the effect of environment on the manifestation of these traits and prominent role of genotype in creating variability. The minimum difference between GCV and PCV values were estimated for all the characters except protein, NR, starch upper and lower root under E_1 and SOD 3 and 1 day under both the conditions indicated minimum environmental influence and this was supported by higher values of heritability. Girish *et al.* (2006) also reported that that the PCV was higher than GCV indicating the influence of environment on the characters. Blum (1988) reported the reduction in genetic variance under severe stress condition. The high degree of heritability and genetic advance for all most all the characters has an edge over improvement as a guiding factor to breeders in selection program except for SOD at 3, and 0 days and protein under both the environments while starch lower root in E_1; starch upper root and NR in E_2. Starch at maturity, leaf starch, soluble sugar upper root and lower root under both the conditions and proline in E_1 and grain yield in E_2 were the only traits which possessed very high estimates of PCV, GCV, h^2b and Ga. Thus, these characters emerged as ideal traits for improvement through selection owing to their transmissibility and variability under irrigated and drought conditions. Selection procedures like mass selection (selection will only be effective for highly heritable traits), family selection (used when hereditary of selected characteristics is low) would be effective for improvement of these characters.

Valliyodan and Nguyen, 2006 reported that high proline accumulation under stress may be used as tolerant trait for drought. The tested genotypes showed wide range of genetic variation for proline in E_1 only consequently, simple selection will not be good enough to improve drought tolerance and additional gain is achieved by using sophisticated models. Sophisticated model must be developed to monitor phenotype expression at the crop level to characterize variation among genotypes across a range of environments. Valliyodan and Nguyen, 2006 found genotypic differences in stress induced proline accumulation and reported positive correlation with osmotic adjustment. In this way, benefits of large osmotic adjustment are expected in earlier stages of drought periods in rice (Fukai and Inthapan, 1988). The low estimates for heritability resulting of the high error variance due to drought and weed competition with some genotypes in 1 or 2 replication. In general, the character that shows high h^2b and Ga is genetically controlled by additive gene action and can be improved through simple or progeny selection methods. Whereas, the character showing high heritability along with moderate or low genetic advance, can be improved by intermitting superior genotypes of segregating population developed from combination breeding (Samadia, 2005).

Drought Resistance Parameters

Drought susceptible index with high yield potential can be used to identify parents to improve the performance of rice under variable moisture conditions (Raman *et al*., 2012). The genotypes with high DTE and low DSI recorded minimum yield reduction (Puri *et al*., 2010). The mean values of DSI for most of the characters were close to or below 1, indicating the relative tolerance of these characters to drought and higher DSI values observed for shoot starch (DSI = 1.06) and yield (DSI = 1.13) indicted that these characteristics are relatively more prone to drought stress. In parallel, most of findings (Ouk *et al*., 2006) showed that lowest DSI values were more tolerant than with the highest DSI. In this study, statistically significant correlations were obtained between yield and DSI under both the conditions. Thus, positive correlation (r = 0.511**) was shown between yield under irrigated and DSI while negative correlation (r = -0.771**, $P < 0.05$) between yield under drought and DSI. Results of this study were consistent with Ouk *et al*. (2006). Similarly, yield under drought significantly correlated with DTE (0.757**) while, negative and significant correlation (-0.903**) was found between DSI and DTE. These results are similar with that of Bahar and Yildirim (2010). Similar trends with correlation between *per se* performance and drought resistance parameters (DSI & DTE) were found for most of the characters under study. Plant breeders must select varieties capable of producing relatively high yields in both favorable and unfavorable years (Bernier *et al*., 2008). According to this, the genotypes *viz*., DSU 18-6, NDR 359, DGI 138, Vandana, Moroberekan and TN 1 with low DSI (<1.0) significantly yielded more than drought tolerant check (Azucena) under stress condition, thereby indicating that these genotypes were drought-tolerant. Bernier *et al*. (2008) also used Vandana as reproductive stage drought tolerant genotypes for developing mapping population to identify QTL's for grain yield under drought stress.

Test genotypes with drought tolerance traits are known to produce high seed yield under drought condition (Chauhan *et al*., 2007). Nguyen *et al*. (1997) reported the consistent differences in osmotic adjustment among rice genotypes at a RWC of 75%. Strong positive regression coefficient were obtained between grain yield and RWC (r = 0.52) and almost all the genotypes recorded low DSI for RWC in present investigation. On the basis of several results, it appeared that maintenance of RWC was necessary but not sufficient to ensure good yield while, similar results was reported by Lafitte (2002). In above view, genotypes selected as drought resistance with low DSI (<1) for grain yield *viz*., NDR 359, DSU 18-6, Vandana, Moroberekan were considered as the best among the top genotypes with low DSI for all other biochemical and physiological traits under study.

Plant water status and proline accumulation

Grain yield correlated positively and significantly (*r* = 0.78) with proline accumulation under water stress. It is also observed that genotypes TN 1 Vandana, Azucena, NDR 359, DS 18-6 and Morobreken recorded highest RWC, accumulated more proline (in per cent) and had a lower DSI values for yield whereas, the genotypes recorded lowest RWC, had vice versa results. Similar results were reported by Bayoumi *et al*. (2008). In present study, leaf water potential was positively associated with accumulation of proline and grain yield under drought stress. Similarly, we found strong negative correlation between RWC vs sterility and LWP *vs* sterility (data not present in manuscript). Thus, studies indicated that capacity to maintain high LWP is promising traits for selection to improve tolerance against late season drought in rainfed upland rice.

CONCLUSION

Starch at maturity, soluble carbohydrate upper root, leaf starch, proline content and CHO lower root emerged as ideal traits for improvement through selection in respective environments. The test entries namely, NDR 359, DSU 18-6, Vandana, Moroberekan were considered as the best among the top genotypes with low DSI for all other biochemical and physiological traits under study. The establishment of managed drought conditions by rainout shelter allows rice research workers to select drought tolerant genotypes. Drought susceptibility index is the most important parameters to evaluate the genotypes under drought stress and can be easily used to find drought tolerant lines in rice breeding programs.

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