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GENETIC ANALYSIS OF DROUGHT TOLERANCE TRAITS IN RICE (*Oryza sativa* L.) UNDER CONTRASTING MOISTURE ENVIRONMENTS

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ABSTRACT

The present investigation was carried out to estimate genetic variability, character association, path coefficients and drought tolerance indices in rice under irrigated and drought stress environments in a two-replicated Randomized Block Design during *Kharif* 2025 at the Research Farm of Narain College, Shikohabad, Uttar Pradesh. Analysis of variance revealed significant genetic variation among the genotypes for all the studied characters under both environments. High broad-sense heritability coupled with high genetic advance was observed for effective tillers per plant, fertile grains per panicle, total tillers per plant and biomass, indicating the predominance of additive gene action. Grain yield per plant exhibited significant positive genotypic and phenotypic correlations with effective tillers per plant, fertile grains per panicle, panicle length, test weight and biomass. Path coefficient analysis identified effective tillers per plant, fertile grains per panicle and biomass as the major direct positive contributors to grain yield. Evaluation of drought tolerance indices identified HURS-21-D-M-10, GAR-13, Prabhat, HURS-21-D-M-4 and HURS-21-D-M-5 as promising drought-tolerant genotypes. Therefore, selection based on effective tillers per plant, fertile grains per panicle and biomass would be an effective strategy for improving grain yield and drought tolerance in rice.

Key words : Rice, Drought stress, Genetic variability, Heritability, Correlation, Path analysis, Drought tolerance indices.

Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops and serves as the staple food for more than half of the world's population. It belongs to the family *Poaceae* ($2n = 2x = 24$) and is cultivated across diverse agro-climatic regions of the world. Rice contributes significantly to global food security and plays a vital role in the agricultural economy of many Asian countries, particularly India (FAOSTAT, 2022). It is grown under a wide range of ecosystems, ranging from irrigated lowlands to rainfed uplands and occupies the largest cultivated area among food crops in India (Ministry of Agriculture and Farmers Welfare, 2023).

Despite its wide adaptability and economic importance, rice productivity is severely affected by

drought, which is considered one of the most destructive abiotic stresses limiting crop production worldwide (Samal *et al.*, 2018). Moisture stress during the reproductive stage adversely affects flowering, grain filling and grain yield, resulting in substantial yield losses. The increasing frequency and severity of drought due to climate change have further emphasized the need for developing drought-tolerant rice cultivars (Pathak *et al.*, 2018).

Grain yield is a complex quantitative trait controlled by several component characters and is greatly influenced by environmental conditions. Therefore, improving grain yield under drought stress requires a thorough understanding of the genetic variability present in the breeding material. Effective selection strategies depend upon the estimation of genetic parameters such as genotypic and phenotypic coefficients of variation (GCV

and PCV), heritability and genetic advance, which provide useful information regarding the nature of gene action and the effectiveness of selection (Burton and De Vane, 1953; Johnson *et al.*, 1955).

Furthermore, grain yield is influenced by several component traits through direct and indirect effects. Therefore, correlation and path coefficient analyses are important tools for understanding the relationship among different quantitative characters and identifying the major yield-contributing traits (Dewey and Lu, 1959). In addition, drought tolerance indices have been widely used to identify stable and superior genotypes under contrasting moisture environments (Rosielle and Hamblin, 1981; Fernandez, 1992). Therefore, the present investigation was undertaken to estimate genetic variability, heritability, genetic advance, character association, path coefficient and drought tolerance indices for identifying superior rice genotypes under irrigated and drought stress environments.

Materials and Methods

The present investigation was carried out at the Research Farm of the Department of Genetics and Plant Breeding, Narain College, Shikohabad, Dr. Bhim Rao Ambedkar University, Agra (Uttar Pradesh), India. The experimental material comprised 28 diverse rice genotypes collected from different research institutes for the evaluation of drought tolerance under irrigated and drought stress environments. The experiment was conducted during the *kharif* season of 2025 under two environments, viz., irrigated and drought stress. The experiment was laid out in a Randomized Block Design (RBD) with two replications in each environment. Each genotype was grown in two rows of 3.0 m length by maintaining a spacing of 20 cm between rows and 15 cm between plants. The recommended package of practices was followed to raise a healthy crop under both environments. In the drought stress environment, irrigation was withheld at the reproductive stage to impose moisture stress. The observations were recorded for 10 quantitative characters, viz., days to 50 per cent flowering, days to maturity, plant height (cm), effective tillers per plant, panicle length (cm), fertile grains per panicle, test weight (g), grain yield per plant (g), total tillers per plant and biomass (g). Observations on days to 50 per cent flowering and days to maturity were recorded on plot basis, whereas observations for the remaining characters were recorded on five randomly selected competitive plants from each genotype in each replication, and the mean values were used for statistical analysis. The analysis of variance was carried out for all the characters following the standard

statistical procedure given by Panse and Sukhatme (1985). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated according to Burton and De Vane (1953). Broad-sense heritability and genetic advance as per cent of mean were estimated following the method suggested by Johnson *et al.* (1955). Genotypic and phenotypic correlation coefficients were computed according to Johnson *et al.* (1955). Path coefficient analysis was carried out considering grain yield per plant as the dependent variable following the method proposed by Wright (1921) and Dewey and Lu (1959). Drought tolerance indices, namely Tolerance Index (TOL), Mean Productivity (MP), Geometric Mean Productivity (GMP), Harmonic Mean (HM), Stress Susceptibility Index (SSI), Stress Tolerance Index (STI), Yield Index (YI), Yield Stability Index (YSI) and Relative Stress Index (RSI) were estimated using the standard procedures suggested by Rosielle and Hamblin (1981) and Fernandez (1992).

Results and Discussion

Analysis of variance

Analysis of variance showed highly significant differences among the genotypes for all the studied traits under both irrigated and drought stress environments, except plant height under drought stress, which was significant at 5% level (Table 1). The observed variability indicated the presence of sufficient genetic diversity among the genotypes, providing ample scope for effective selection in rice breeding programmes.

Genetic Variability Parameters

The magnitude of the phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the studied characters under both irrigated and drought stress environments, indicating the influence of environmental factors on the expression of these traits (Table 2).

Under the irrigated environment, effective tillers per plant, total tillers per plant, fertile grains per panicle and biomass exhibited high genotypic and phenotypic coefficients of variation. Similar findings were reported by Kandel *et al.* (2022) and Hussain *et al.* (2023) for productive tillers, fertile grains per panicle and grain yield. Plant height, panicle length, days to 50 per cent flowering and grain yield per plant showed moderate GCV and PCV, whereas days to maturity and test weight exhibited low genotypic and phenotypic coefficients of variation.

Similarly, under the drought stress environment, biomass, fertile grains per panicle and total tillers per plant recorded high GCV and PCV, while effective tillers per

Table 1 : Analysis of variance of 28 rice genotypes under both irrigated and drought stress environments for all traits.

Source	df	DFF	DM	PH	ET	PL	FG/P	TW	GY/P	TT/P	BM
Irrigated environment											
Replication	1	27.16	1.45	7.88	1.28	1.59	0.16	1.02	0.15	3.34	0.01
Genotypes	27	302.83**	293.16**	447.3**	23.99**	21.87**	2960.02**	5.61**	10.74**	21.76**	0.257**
Error	27	34.98	59.82	89.84	0.60	3.68	106.83	1.84	3.10	1.71	0.02
SEm±		4.18	5.47	6.70	0.55	1.36	7.31	0.96	1.24	0.93	0.10
CD at 5%		12.14	15.87	19.45	1.59	3.94	21.21	2.79	3.61	2.68	0.29
CV (%)		6.08	6.01	7.62	6.03	7.72	5.38	6.98	8.77	10.07	8.03
Drought stress environment											
Replication	1	189.45	15.02	0.88	0.03	1.87	62.16	1.58	0.15	0.06	0.01
Genotypes	27	241.12**	358.49**	166*	2.822**	22.97**	4027.52**	10.01**	10.68**	5.634**	0.205**
Error	27	42.11	56.05	74.32	0.40	2.17	330.35	2.02	1.43	0.41	0.01
SEm±		4.59	5.29	6.10	0.45	1.04	12.85	1.00	0.85	0.46	0.07
CD at 5%		13.32	15.36	17.69	1.30	3.02	37.30	2.92	2.46	1.32	0.21
CV (%)		6.43	5.52	8.34	8.45	6.80	9.57	8.17	8.02	8.61	8.02

*, ** Significant at 5 and 1 per cent level, respectively.

DFF- Days to 50 % flowering, DM- Days to maturity, PH- Plant height, ET- Effective tillers, PL- Panicle length, FG/P- Fertile grains per panicle, TW- Test weight, GY/P – Grain yield per plant, TT/P – Total number of tillers per plant, BM - Biomass.

Table 2 : Genetic variability parameters of 28 rice genotypes under both irrigated and drought stress environments for all traits.

Character	Mean	Range	GCV (%)	PCV (%)	h ² (%)	GA	GAM (%)
Irrigated environment							
DFF	97.23	75.00-120.00	11.9	13.37	79.29	21.23	21.83
DM	128.7	105.00-150.00	8.39	10.32	66.11	18.09	14.06
PH	124.34	95.00-150.00	10.75	13.18	66.55	22.47	18.07
ET	12.82	6.96-20.00	26.68	27.35	95.13	6.87	53.6
PL	24.87	18.62-32.00	12.13	14.37	71.16	5.24	21.07
FG/P	192.27	123.00-263.00	19.64	20.37	93.03	75.05	39.03
TW	19.45	16.00-23.00	7.06	9.93	50.53	2.01	10.33
GY/P	20.06	15.00-25.00	9.75	13.12	55.25	2.99	14.93
TT/P	12.99	6.86-19.96	24.37	26.36	85.42	6.03	46.39
BM	1.75	1.09-2.49	19.71	21.28	85.76	0.66	37.6
Drought stress environment							
DFF	100.95	78.00-125.00	9.88	11.79	70.26	17.22	17.06
DM	135.7	110.00-160.00	9.06	10.61	72.96	21.64	15.95
PH	103.41	85.00-120.00	6.55	10.6	38.15	8.61	8.33
ET	7.5	5.04-10.00	14.68	16.94	75.09	1.96	26.2
PL	21.66	15.60-28.00	14.89	16.37	82.77	6.04	27.91
FG/P	189.91	106.00-282.00	22.64	24.58	84.84	81.58	42.96
TW	17.38	13.10-22.00	11.5	14.1	66.44	3.36	19.31
GY/P	14.92	10.32-19.79	14.42	16.5	76.36	3.87	25.95
TT/P	7.47	4.82-10.89	21.62	23.27	86.3	3.09	41.37
BM	1.26	0.73-1.88	24.83	26.1	90.55	0.61	48.68

GCV – Genotypic coefficient of variation, PCV – Phenotypic coefficient of variation, h² – Heritability as broad sense, GA – Genetic advance, GAM – Genetic advance as percent of mean, DFF- Days to 50 % flowering, DM- Days to maturity, PH- Plant height, ET- Effective tillers, PL- Panicle length, FG/P- Fertile grains per panicle, TW- Test weight, GY/P – Grain yield per plant, TT/P – Total number of tillers per plant, BM - Biomass

plant, panicle length, grain yield per plant and test weight exhibited moderate coefficients of variation. Plant height, days to 50 per cent flowering and days to maturity showed comparatively low GCV and PCV. The narrow differences between GCV and PCV observed for most of the characters indicated comparatively less environmental influence on their expression and suggested that phenotypic selection would be effective for their improvement.

The ability to select superior genotypes based on phenotypic performance is enhanced by high heritability estimates (Johnson *et al.*, 1955). In the present investigation, effective tillers per plant, fertile grains per panicle, total tillers per plant and biomass exhibited high heritability under both irrigated and drought stress environments. Panicle length, days to 50 per cent flowering and days to maturity also recorded high to moderately high heritability, whereas test weight, plant height and grain yield per plant showed moderate heritability under one or both environments. Similar findings were reported by Anis *et al.* (2016) and Bhor *et al.* (2020) for productive tillers, fertile grains and grain yield in rice.

Heritability estimates coupled with genetic advance provide a more reliable indication of the effectiveness of selection than heritability alone (Johnson *et al.*, 1955). In the present study, effective tillers per plant, total tillers per plant, fertile grains per panicle and biomass recorded high genetic advance as per cent of mean under both irrigated and drought stress environments. Panicle length and grain yield per plant exhibited moderate genetic advance, whereas days to 50 per cent flowering, days to maturity, plant height and test weight recorded comparatively low genetic advance. High heritability coupled with high genetic advance observed for effective tillers per plant, total tillers per plant, fertile grains per panicle and biomass indicated the predominance of

additive gene action and suggested that these characters could be effectively improved through direct selection. These findings are in close agreement with those reported by Ovung *et al.* (2012), Tuwar *et al.* (2013), Sawarkar and Senapati (2015) and Tuhina-Khatun (2015).

Character association

Genotypic and phenotypic correlation coefficients were determined for ten characters under irrigated and drought stress environments (Tables 3 and 4, respectively). In all cases, genotypic correlation coefficients were higher than their phenotypic counterparts, indicating that character expression was governed more by genetic inheritance than by environmental influences. Grain yield per plant exhibited positive and significant correlation at both genotypic and phenotypic levels with effective tillers per plant, panicle length, fertile grains per panicle, test weight and biomass. This indicated that grain yield could be improved through simultaneous selection for these traits.

Regarding intercorrelations among other traits, days to 50 per cent flowering showed a significant positive association with days to maturity at the genotypic level, whereas it exhibited a significant negative association with total tillers per plant under both genotypic and phenotypic levels. Days to maturity was negatively correlated with total tillers per plant, while plant height exhibited positive association with effective tillers per plant, panicle length, test weight and grain yield per plant. Furthermore, effective tillers per plant showed positive association with panicle length, total tillers per plant and biomass. Panicle length displayed a significant positive correlation with test weight, whereas fertile grains per panicle showed significant positive association with biomass. Test weight exhibited a significant positive association with grain yield per plant and plant height. Under drought stress environment, grain yield per plant

Table 3 : Genotypic correlation coefficient of 28 rice genotypes in both irrigated (above diagonal) and drought stress (below diagonal) conditions for all traits.

Trait	DF	DM	PH	ET	PL	FG/P	TW	TT/P	BM	GY/P
DF	1.000	0.386*	0.047	-0.296	0.142	-0.047	0.016	-0.459*	-0.012	-0.079
DM	-0.080	1.000	0.253	0.008	-0.022	-0.030	-0.155	-0.456*	-0.093	-0.096
PH	0.030	0.046	1.000	0.234	0.294	-0.065	0.153	0.030	0.136	0.346
ET	-0.272	-0.011	0.313	1.000	0.276	-0.048	0.175	0.298	0.182	0.610**
PL	0.347	0.36*	0.225	-0.156	1.000	-0.046	0.374	-0.014	0.037	0.488**
FG/P	0.008	-0.073	-0.277	-0.031	-0.248	1.000	-0.171	0.189	0.361	0.406*
TW	0.245	-0.231	0.023	0.182	-0.074	0.354*	1.000	0.015	0.027	0.410*
TT/P	0.097	0.054	0.361*	-0.271	0.018	0.122	0.095	1.000	-0.083	0.355
BM	-0.201	0.294	0.293	-0.149	0.007	-0.014	-0.271	-0.145	1.000	0.591**
GY/P	0.192	-0.110	-0.017	0.613**	0.388	0.695**	0.428*	0.275	0.414*	1.000

Table 4 : Phenotypic correlation coefficient of 28 rice genotypes in both irrigated (above diagonal) and drought stress (below diagonal) conditions for all traits.

Trait	DFE	DM	PH	ET	PL	FG/P	TW	TT/P	BM	GY/P
DFE	1.000	0.351**	0.018	-0.260	0.128	-0.038	-0.010	-0.412**	0.001	-0.084
DM	0.173	1.000	0.225	0.017	-0.007	-0.023	-0.100	-0.411**	-0.082	-0.127
PH	-0.257	0.228	1.000	0.216	0.220	-0.090	0.092	-0.010	0.129	0.285*
ET	0.297	-0.012	0.101	1.000	0.240	-0.046	0.140	0.268*	0.184	0.536**
PL	-0.259	0.325	-0.276	0.225	1.000	-0.042	0.277*	0.025	0.046	0.393**
FG/P	0.062	0.236	-0.114	0.036	-0.050	1.000	-0.123	0.201	0.345**	0.342**
TW	0.270	0.047	0.181	0.149	0.050	0.297	1.000	0.007	0.005	0.305*
TT/P	-0.124	0.212	0.378*	-0.112	-0.276	0.009	-0.179	1.000	-0.067	0.396
BM	0.144	-0.035	-0.155	-0.054	-0.030	-0.257	-0.137	0.285	1.000	0.749**
GY/P	0.011	0.193	0.239	0.598**	0.511*	0.782**	0.467*	0.236	0.354**	1.000

Note: Irrigated condition values are presented above diagonal and drought stress values below diagonal.

*, ** Significant at 5 and 1 per cent level, respectively.

Table 5 : Genotypic path coefficient analysis under irrigated environment for yield and yield contributing traits.

Character	DFE	DM	PH	ET	PL	FG/P	TW	TT/P	BM	r with GY/P
DFE	0.103	-0.028	0.007	-0.141	0.029	-0.021	0.005	-0.032	-0.002	-0.079
DM	0.040	-0.072	0.039	0.004	-0.005	-0.013	-0.044	-0.032	-0.012	-0.096
PH	0.005	-0.018	0.153	0.111	0.061	-0.028	0.043	0.002	0.018	0.346
ET	-0.030	-0.001	0.036	0.475	0.057	-0.021	0.050	0.021	0.024	0.610**
PL	0.015	0.002	0.045	0.131	0.206	-0.020	0.106	-0.001	0.005	0.488**
FG/P	-0.005	0.002	-0.010	-0.023	-0.009	0.438	-0.049	0.013	0.048	0.406*
TW	0.002	0.011	0.023	0.083	0.077	-0.075	0.284	0.001	0.004	0.410*
TT/P	-0.047	0.033	0.005	0.142	-0.003	0.083	0.004	0.070	-0.011	0.275
BM	-0.001	0.007	0.021	0.086	0.008	0.158	0.008	-0.006	0.133	0.414*

Residual effect = 0.436; $R^2 = 0.810$

also exhibited significant positive association with effective tillers per plant, fertile grains per panicle, biomass and test weight, indicating the importance of these traits under moisture stress conditions. These findings are in close agreement with the reports of Ashfaq *et al.* (2012), Sawarkar and Senapati (2015), Kahani and Hittalmani (2015), Singh *et al.* (2016), Bhor *et al.* (2020), Kandel *et al.* (2022) and El-Agoury *et al.* (2023), who also reported positive association of grain yield with productive tillers, panicle length, fertile grains per panicle, biomass and test weight in rice. Therefore, simultaneous selection for these characters would be an effective strategy for improving grain yield under both irrigated and drought stress environments.

Path coefficient analysis

Relying on correlation alone can be misleading due to the mutual cancellation of component traits. Therefore, path coefficient analysis was carried out to partition the correlation coefficients into direct and indirect effects

and to identify the most important yield contributing characters. In the present study, genotypic and phenotypic path coefficients were estimated for ten characters, considering grain yield per plant as the dependent variable and the remaining traits as independent variables (Tables 4 to 8).

Under the irrigated environment, the maximum positive direct effects on grain yield per plant were exerted by effective tillers per plant, fertile grains per panicle, test weight, panicle length and plant height at both genotypic and phenotypic levels. In contrast, days to maturity exhibited a negative direct effect on grain yield, while days to 50 per cent flowering showed a comparatively low positive direct effect. Similarly, desirable positive indirect effects on grain yield were exerted by effective tillers per plant through panicle length and test weight, fertile grains per panicle through biomass, and panicle length through test weight. These results confirmed the important role of these traits in determining grain yield under irrigated conditions and, therefore, their

Table 6 : Genotypic path coefficient analysis under drought stress environment for yield and yield contributing traits.

Character	DFE	DM	PH	ET	PL	FG/P	TW	TT/P	BM	r with GY/P
DFE	0.035	0.008	0.004	0.151	0.072	-0.091	-0.001	0.067	-0.005	0.068
DM	-0.003	0.104	0.013	0.122	0.063	-0.154	0.064	-0.038	0.099	-0.112
PH	0.001	0.005	0.093	-0.034	0.083	0.088	0.059	0.085	-0.041	0.028
ET	-0.010	-0.001	0.029	0.579	0.067	0.091	-0.013	-0.030	0.040	0.688**
PL	0.012	0.037	0.021	-0.090	0.239	-0.015	-0.032	0.080	0.053	0.449*
FG/P	0.000	-0.008	-0.026	-0.018	-0.059	0.574	-0.039	-0.037	-0.033	0.685**
TW	0.009	-0.024	0.002	0.105	-0.018	0.203	0.233	-0.031	-0.102	0.426*
TT/P	0.003	0.006	0.034	-0.157	0.004	0.070	0.022	0.302	0.003	0.363
BM	-0.007	0.031	0.027	-0.086	0.002	-0.008	-0.063	-0.044	0.517	0.697**

Note: Diagonal values (shaded) indicate direct effects; off-diagonal values indicate indirect effects via respective characters. * and ** indicate significance at 5% and 1% levels, respectively.

Genotypic Residual effect = 0.310; Phenotypic Residual effect = 0.770

Table 7 : Phenotypic path coefficient analysis under irrigated environment for yield and yield contributing traits.

Character	DFE	DM	PH	ET	PL	FG/P	TW	TT/P	BM	r with GY/P
DFE	0.081	-0.057	0.003	-0.115	0.024	-0.014	-0.002	-0.005	0.000	-0.084
DM	0.028	-0.161	0.042	0.008	-0.001	-0.009	-0.020	-0.005	-0.008	-0.127
PH	0.001	-0.036	0.186	0.095	0.042	-0.034	0.019	0.000	0.012	0.285*
ET	-0.021	-0.003	0.040	0.442	0.045	-0.017	0.029	0.003	0.018	0.536**
PL	0.010	0.001	0.041	0.106	0.189	-0.016	0.057	0.000	0.004	0.393**
FG/P	-0.003	0.004	-0.017	-0.020	-0.008	0.376	-0.025	0.002	0.033	0.342**
TW	-0.001	0.016	0.017	0.062	0.052	-0.046	0.204	0.000	0.000	0.305*
TT/P	-0.033	0.066	-0.002	0.118	0.005	0.076	0.001	0.012	-0.006	0.236
BM	0.000	0.013	0.024	0.081	0.009	0.130	0.001	-0.001	0.096	0.354**

Genotypic Residual effect = 0.628; Phenotypic Residual effect = 0.605

Table 8 : Phenotypic path coefficient analysis under drought stress environment for yield and yield contributing traits.

Character	DFE	DM	PH	ET	PL	FG/P	TW	TT/P	BM	r with GY/P
DFE	0.105	-0.014	-0.001	-0.014	-0.060	0.084	0.007	-0.035	0.012	0.043
DM	0.018	0.096	0.006	0.061	-0.060	0.111	0.007	-0.038	0.063	0.180
PH	-0.027	0.022	0.018	0.157	0.026	0.127	0.080	0.032	-0.045	0.035
ET	0.031	-0.001	0.002	0.473	-0.008	0.048	0.030	-0.036	-0.143	0.738**
PL	-0.027	0.031	-0.005	0.106	0.347	0.133	-0.036	-0.046	-0.032	0.387
FG/P	0.007	0.023	-0.002	0.017	-0.017	0.545	0.091	-0.038	0.144	0.592**
TW	0.028	0.005	0.003	0.070	0.017	0.162	0.249	0.066	-0.119	0.375
TT/P	-0.013	0.020	0.007	-0.053	-0.096	0.005	-0.045	0.184	-0.090	0.475*
BM	0.015	-0.003	-0.003	-0.026	-0.010	-0.140	-0.034	0.052	0.614	0.684**

Note: Diagonal values (shaded) indicate direct effects; off-diagonal values indicate indirect effects via respective characters. * and ** indicate significance at 5% and 1% levels, respectively.

Genotypic Residual effect = 0.310; Phenotypic Residual effect = 0.615

usefulness in formulating selection criteria. The residual effect was 0.436 at the genotypic level and 0.628 at the phenotypic level, indicating that a major proportion of the

variability in grain yield was explained by the characters included in the present investigation.

Under the drought stress environment, the maximum

Table 9 : Abiotic stress tolerance indices and ranks of 28 rice genotypes evaluated under irrigated and drought stress environments.

Genotype	Yp	Ys	TOL	MP	GMP	HM	SSI	STI	YI	YSI	RSI	Rank
Satabdi	15.48	16.32	-0.85	15.90	15.89	15.89	-0.21	0.63	1.09	1.06	1.42	22
Prabhat	22.18	17.39	4.80	19.79	19.64	19.50	0.84	0.96	1.17	0.78	1.05	3
Ratnagiri-4	17.95	12.94	5.01	15.45	15.25	15.04	1.09	0.58	0.87	0.72	0.97	25
S-172	23.36	14.44	8.92	18.90	18.36	17.84	1.49	0.84	0.97	0.62	0.83	8
Rajendra Dhan-102	19.41	16.68	2.73	18.04	17.99	17.94	0.55	0.81	1.12	0.86	1.16	10
HPR-2143	21.92	11.08	10.85	16.50	15.58	14.72	1.93	0.60	0.74	0.51	0.68	24
Himalaya-1	19.10	14.43	4.68	16.77	16.60	16.44	0.96	0.69	0.97	0.76	1.02	18
Dandi	20.42	16.96	3.46	18.69	18.61	18.53	0.66	0.86	1.14	0.83	1.12	7
Khamong	15.00	14.80	0.20	14.90	14.90	14.90	0.05	0.55	0.99	0.99	1.33	26
BD-202	21.68	16.33	5.36	19.01	18.82	18.63	0.96	0.88	1.10	0.75	1.01	6
BUD-110	17.85	18.05	-0.20	17.95	17.95	17.95	-0.04	0.80	1.21	1.01	1.36	11
GAR-13	22.74	17.68	5.06	20.21	20.05	19.89	0.87	1.00	1.19	0.78	1.05	2
NCS-348	22.60	12.27	10.32	17.43	16.65	15.90	1.78	0.69	0.82	0.54	0.73	17
HURS-21-D-M-1	19.73	11.19	8.54	15.46	14.86	14.28	1.69	0.55	0.75	0.57	0.76	27
HURS-21-D-M-2	18.65	15.94	2.71	17.29	17.24	17.19	0.57	0.74	1.07	0.86	1.15	13
HURS-21-D-M-3	18.71	13.68	5.04	16.19	16.00	15.80	1.05	0.64	0.92	0.73	0.98	21
HURS-21-D-M-4	20.47	18.36	2.11	19.42	19.39	19.36	0.40	0.93	1.23	0.90	1.21	4
HURS-21-D-M-5	19.94	18.49	1.45	19.22	19.20	19.19	0.28	0.92	1.24	0.93	1.25	5
HURS-21-D-M-6	21.64	13.92	7.72	17.78	17.36	16.95	1.39	0.75	0.93	0.64	0.87	12
HURS-21-D-M-7	18.60	10.86	7.74	14.73	14.21	13.71	1.62	0.50	0.73	0.58	0.79	28
HURS-21-D-M-8	24.18	11.76	12.42	17.97	16.87	15.83	2.00	0.71	0.79	0.49	0.65	15
HURS-21-D-M-9	19.37	14.86	4.51	17.12	16.97	16.82	0.91	0.72	1.00	0.77	1.03	14
HURS-21-D-M-10	23.52	17.54	5.98	20.52	20.31	20.09	0.99	1.03	1.18	0.75	1.00	1
HURS-21-D-M-11	21.55	15.17	6.38	18.36	18.08	17.81	1.16	0.81	1.02	0.70	0.95	9
HURS-21-D-M-12	16.87	15.81	1.06	16.34	16.33	16.32	0.25	0.66	1.06	0.94	1.26	19
HURS-21-D-M-13	18.87	13.06	5.81	15.97	15.70	15.44	1.20	0.61	0.88	0.69	0.93	23
HURS-21-D-M-14	20.43	13.02	7.41	16.73	16.31	15.91	1.42	0.66	0.87	0.64	0.86	20
HURS-21-D-M-15	19.37	14.64	4.74	17.00	16.84	16.67	0.95	0.71	0.98	0.76	1.02	16

positive direct effects on grain yield per plant were exerted by effective tillers per plant, fertile grains per panicle, biomass, total tillers per plant, panicle length and test weight at both genotypic and phenotypic levels. Furthermore, desirable positive indirect effects on grain yield were exerted by fertile grains per panicle through effective tillers per plant, biomass through fertile grains per panicle, and panicle length through effective tillers per plant. These findings indicated that these characters contributed substantially towards grain yield under drought stress and could therefore be considered as reliable selection criteria for the development of drought-tolerant rice genotypes. The residual effect was 0.310 at both the genotypic and phenotypic levels, suggesting that most of the variation in grain yield was accounted for by the characters included in the present study. These findings are in accordance with those reported by Pratap *et al.* (2012), Bhor *et al.* (2020), Singh *et al.* (2021) and Kandel *et al.* (2022), who also identified productive tillers, grains

per panicle and biomass as major contributors to grain yield through path coefficient analysis.

Drought tolerance indices

Different drought tolerance indices, namely tolerance index (TOL), mean productivity (MP), geometric mean productivity (GMP), harmonic mean (HM), stress susceptibility index (SSI), stress tolerance index (STI), yield index (YI), yield stability index (YSI) and relative stress index (RSI) were estimated to identify drought tolerant rice genotypes (Table 9). Considerable variation was observed among the genotypes for all the stress tolerance indices, indicating differential response of the genotypes under irrigated and drought stress environments.

Higher values of MP, GMP, HM, STI, YI and YSI together with lower values of TOL and SSI were considered desirable for identifying drought tolerant and stable genotypes. Among the twenty-eight genotypes,

HURS-21-D-M-10 recorded the highest stress tolerance index (STI = 1.03) and secured Rank 1, followed by GAR-13 (STI = 1.00; Rank 2), Prabhat (STI = 0.96; Rank 3), HURS-21-D-M-4 (STI = 0.93; Rank 4) and HURS-21-D-M-5 (STI = 0.92; Rank 5). These genotypes also exhibited comparatively higher values of MP, GMP and HM with lower SSI values, indicating their superior performance and greater stability under both irrigated and drought stress environments. On the other hand, HURS-21-D-M-7, HURS-21-D-M-1, Khamong, Ratnagiri-4 and HPR-2143 recorded comparatively lower STI, GMP and HM values together with higher SSI values, indicating their greater susceptibility to drought stress and poor yield stability. The results suggested that HURS-21-D-M-10, GAR-13, Prabhat, HURS-21-D-M-4 and HURS-21-D-M-5 may be considered as promising drought tolerant genotypes and could be effectively utilized in future breeding programmes for improving drought tolerance and grain yield in rice. The present findings are in close agreement with those reported by Kumar *et al.* (2014), Adhikari *et al.* (2019), Mau *et al.* (2019), Turin *et al.* (2021), Kandel *et al.* (2022) and El-Agoury *et al.* (2023), who identified drought tolerant rice genotypes using stress tolerance indices such as STI, SSI, GMP and MP.

Conclusion

The findings of the present study demonstrated that ample genetic variation existed among the studied rice genotypes under both irrigated and drought stress environments for all the characters. It can be stated that effective tillers per plant, fertile grains per panicle, panicle length, test weight and biomass had greater importance. Hence, due consideration should be given to these characters while planning selection criteria for grain yield improvement and drought tolerance in rice.

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