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Utilising genetic variability and diversity analysis as a tool to identify drought tolerant pre-breeding genetic materials in rice (*Oryza sativa* L.)

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Abstract
Rice (*Oryza sativa* L.) is the main cereal crop cultivated throughout the globe the importance of rice can be judged by finding that rice alone caters to around half of the world's population. Therefore, studying rice in different environments is a need of time because of climate change which severely hampers crop production. Hence the study was carried out in 50 rice landraces to observe their phenotypical variability and diversity under a drought environment. Analysis of variance shows that a wide range of variability is present among the genotypes so further analysis of PCV (phenotypic coefficient of variance) and GCV (Genotypic coefficient of variance) was calculated to show the environmental effect on traits which was maximum in leaf area (46.66 and 45.55) total leaves per plant (39.88 and 37.45) and number of panicles (38.39 and 35.40). Correlation studies revealed that the drought scores, tip drying score and leaf rolling scores are significantly correlated to each other as well as to total leaves per plant (0.491), leaf area (0.491), number of tillers (0.6244) and number of panicles (0.8003); which are in turn significantly correlated to single plant yield. By clustering, all the 50 genotypes were placed in 11 clusters. Among all clusters, the cluster three is major cluster which contains a total of 18 genotypes. Maximum intracluster distance was found in cluster IV (929.08). Cluster V (90.25) observed the highest cluster mean for single plant yield. Drought score ranking method revealed that the cluster number seven has a genotype which is tolerant to drought. Based on the study the variability and the diversity among the genotypes were assessed under drought environment. Cluster number seven contains a genotype IC 216378 which has superior in performance under drought situation and selected as a best pre-breeding material for drought breeding programme.

Keywords: Drought, PCV, GCV, clustering, correlation, ranking, pre-breeding

Introduction
Rice (*Oryza sativa* L.) is the staple food, supplementing about fifty per cent of people living on Earth. In addition, it serves as the valuable source of dietary energy (27%) and dietary protein (25%). In recorded history, rice is the backbone of Indian agriculture and source of revenue for around 120-150 million rural households. It occupies an area of 321.79 lakh ha contributing to the production of 121.46 million tonnes (Press Information Beuro, 2020).

Despite its excellence, the crop still faces enumerable abiotic stresses which restrain its production. The changing environmental scenario has negatively undermined the yield of prevalent crops like rice in many regions (IPCC, 2018). As an impact of climate change, World is running out of water day by day and it was appraised that the proportion of drought-affected area has doubled across the globe since, 1970 (Sabesan and Saravanan, 2016) [15]. It has become one of the most distressing environmental stresses stirring up food insecurity as it adversely affects agricultural production. On the other hand, the accelerating population is creating a burning need for national food security. This persuades the need for breeding of rice cultivars with improved drought tolerance and enhanced yield.

Landraces are the outstanding source of genetic variation for higher adaptability and drought tolerance (Sitaresmi *et al*., 2019). Genetic variations form the base of breeding programme which helps the breeder to select a pre-breeding material (Palaniyappan *et al*., 2020) [12]. The preliminary step in breeding is the identification of such variants for drought tolerance from the available germplasm. Genetic variations responsible for drought tolerance can be unveiled *via* the screening and characterization of rice germplasm for different agro-morphological traits under drought stress.

Thus, it sets off the need to understand the variability and genetic diversity prevailing in the existing germplasm by means of several statistical measures *viz.,* GCV, PCV, heritability genetic advance and D^2 analysis respectively. With this backdrop, the present investigation was undertaken with fifty traditional rice landraces was characterized for various agro-morphological traits under drought stress at reproductive stage.

Materials and Methods
Plant material: The experimental material comprised of fifty diverse rice landraces obtained from National Bureau of Plant Genetic Resources (NBPGR) New Delhi (Table 1) as indigenous collection (IC). The experiment was carried out during *Kharif* 2021 in a rainout shelter at Paddy Breeding Station (PBS) TNAU, Coimbatore, which is geographically located at 11^0N latitude and 77^0E longitude at the elevation of 426.75m. The experimental materials were subjected to reproductive stress before flower initiation.

Table 1: List of landraces studied

Sl. No.	Accession No.*	Sl. No.	Accession No.
1.	IC205988	26.	IC458407
2.	IC217818	27.	IC459854X
3.	IC208155	28.	IC458416
4.	IC458545	29.	IC514623
5.	IC248059	30.	IC135299
6.	IC99458	31.	IC458796
7.	IC67496	32.	IC516839
8.	IC555090	33.	IC458480X
9.	IC114610	34.	IC378202
10.	IC540621	35.	IC206810
11.	IC467267	36.	IC462181
12.	IC207562	37.	IC516792
13.	IC518720	38.	IC554943
14.	IC86337	39.	IC206999
15.	IC216378	40.	IC114751
16.	IC378170	41.	IC217501
17.	IC114628	42.	IC207596
18.	IC458677	43.	IC457996
19.	IC217294	44.	Ic377122
20.	IC135643	45.	IC206954
21.	IC207753	46.	IC301091
22.	IC380614	47.	IC323750
23.	IC282506	48.	IC377149
24.	IC389916	49.	IC594028
25.	IC207540	50.	IC599520

*IC= Indigenous collection of NBPGR, New Delhi.

Methodology
The present investigation was carried to study the variability available among the yield and drought related traits and to assess the diversity among the different landraces. Each genotype was replicated twice in RBD in a row length of 170 cm with a spacing of 20 x 15 cm. Reproductive stage in rice is one of the critical stages of life cycle which determines yield and it is highly sensitive to drought stress. Therefore the drought was imposed in reproductive stage and the observations are recorded on five randomly selected plants for traits *viz.,* plant height, days to 50 per cent flowering, number of tillers, leaf length, leaf breadth, leaf area, number of leaves per tiller, number of panicles, panicle length, total number of leaves per plant, 100 seed weight, seed length, seed breadth and hulling percentage and single plant yield, was recorded on

plot basis. Drought parameters viz., drought score, tip drying score, leaf rolling score,

Statistical analysis: All the statistical analyses were carried out using TNAU STAT software.

- **Analysis of variance:** The observed data were subjected to analysis of variance to test the significance of genotypes for each trait.
- **Variability analysis:** Genetic parameters *viz.,* genotypic and phenotypic variances, genotypic and phenotypic coefficient of variations (GCV and PCV) were calculated based on formulae given by Burton (1952) [4]. Heritability and genetic advance (GA) as per cent mean based on Lush (1940) [10] and Johnson *et al.,* (1955) [8] respectively.
- **Diversity analysis:** Mahalnobis D^2 statistics (1936) [11].
- **Correlation:** Correlation analysis was performed in software SPSS version (16).

A ranking procedure was followed to group the drought tolerant genotypes using the three drought traits recorded viz., drought score, tip drying score and leaf rolling score. The pooled values were taken for ranking the genotype. The genotype which ranked one is considered most tolerant followed by rank two. The maximum genotypes in this rank occupying cluster is considered for selection of drought tolerant genotypes.

Result and Discussion
The analysis of variance for all the fifteen characters studied showed highly significant difference between the genotypes representing the presence of appropriate heterogeneity table-2, satisfying the requirement of variability and diversity analysis table. The magnitude of variability and heritability are the two factors determining the effectiveness of selection in any successful breeding programme. Variability parameters estimated for fifteen traits were presented in table 3. The PCV ranges from (6.4-46.66) and GCV ranges from (6.3-45.55), On comparison of estimated variability, PCV is higher than GCV for all traits with minimum difference in values between them indicating the less influence of environment as the crops are grown inside the rainout shelter. The major environmental stress given in the study is by way of imposing reproductive drought stress. Studies of Singh *et al.,* 2021, Divya *et al.,* 2018 and Dhurai *et al.,* 2014 [16, 6, 7] showed similar results. High estimates of PCV and GCV for traits viz., leaf area (46.66 and 45.55), total leaves per plant (39.88 and 37.45) and number of panicles (38.39 and 35.40) respectively. Similar findings were reported by Singh *et al.,* 2021 and Ahmad *et al.,* 2021 [16, 3]. Moderate PCV and GCV were recorded for plant height (10.05 and 9.88), No. of. leaves per tiller (16.8 and 11.5), Panicle length (17.5 and 16.72) Lowest PCV and GCV were observed in hulling percentage (6.47 and 6.35), Days to 50% flowering (7.4879 and 6.1701) and seed length (8.4729 and 7.7978). Presence of high magnitude of genotypic variation is not the sole criterion for effectiveness of selection. Moreover, heritability and GAM estimates are required to arrive at a more reliable conclusion.

Heritability describes the contribution of genetic variability to the total variability. In other words, it reveals the extent to which a particular trait passes from its parents to progeny. In the evaluated material all the traits recorded high heritability ranging from 67.89 to 97.71 except for number of leaves per tiller (47.23). Genetic advance in per cent of mean (GAM) was high for twelve traits ranging from 10.47 to 91.61.

Moderate GAM was recorded for number of leaves per tiller (16.35), seed length (14.78) and hulling percentage (12.86). Traits with high heritability without high GAM holds no practical importance in selection. In the present study, all the traits except number of leaves per tiller, seed length and hulling percentage recorded high heritability coupled with high GAM indicating the influence of additive gene action and the effectiveness of selection for improvement of these traits. The obtained results were in line with the findings of Singh *et al*., (2021) [16], Perwedeen *et al*., (2020) [14] and Kurmanchali *et al*., (2019) [9] for plant height and days to fifty percent flowering. Seed length and hulling percentage recorded high heritability with moderate GAM, which stated the possibility of a reasonable response to selection in these two traits owing to their high transmissibility even if their GAM is moderate. The results find co-linearity with the findings of Kurmanchali *et al*., 2019 [9] for some of the yield attributing and quality traits in basmati rice.

Estimates of genetic diversity is a prerequisite for parental selection to recover transgressive segregants. To quantify the degree of divergence in the fifty genotypes and grouping them into different cluster, the mean data of the observed traits were subjected to multivariate analysis developed by Mahalnobis (1936) [11]. Based on the D^2 values the genotypes were grouped into eleven clusters. (Table 4). This indicated that the materials used for the study is quite diverse for yield and drought traits. Ahmad *et al*., 2021, Khatun *et al*., 2015 and Worede *et al*., 2014 [3, 18, 20] also observed a similar clustering pattern for 54, 43 and 24 upland rice genotypes, respectively. Detailed insight into clustering pattern pointed out that 18 out of 50 genotypes belong to the same cluster i.e., cluster III. On the other hand, 14 genotypes belong to cluster I, 5 belongs to cluster VIII, 4 in cluster II, 2 in cluster IV and V, whereas clusters VI, VII, IX, X, XI contained one genotype. The genotypes in the above solitary clusters were found to be highly divergent from other genotypes used in the study.

The average inter and intra-cluster distance was presented in Table 5. Maximum intra-cluster distance was found in cluster IV (929.08) which comprised of two genotypes which were genetically diverse within the same cluster. It was followed by cluster V (878.88) and cluster II (764.33). The maximum inter-cluster distance of 6335.18 was observed between cluster X and cluster X1 indicating hybridization between genotypes of these clusters may be expected to result in better recombinant with the accumulation of favourable genes in segregating generations. Similar findings from Ahmad *et al*., 2021 and Singh *et al*., 2021 [3, 16]. also suggested that hybridization between the genotypes from clusters with maximum inter- cluster distance helps in achieving heterotic recombinants.

Analysis of cluster mean values were presented in table 6. The highest mean value for hulling percentage and single plant yield was noticed in cluster XI. The genotypes included in this cluster also recorded lowest mean value for days to fifty per cent flowering and seed breadth which denotes earliness and slender grains respectively. The cluster V grouped genotypes with highest mean value for plant height and leaf area. The cluster VI grouped genotypes with highest mean values for number of tillers, number of leaves per plant, flag leaf breadth and number of panicles. The cluster X

displayed the highest mean value for seed weight. Hence, the genotypes included in clusters VI, X and XI seems to be promising for various traits under study.

As a component of genetic diversity studies, per cent contribution of the traits towards diversity was estimated and depicted as a pie chart in Figure 1. Hulling percentage contributed most to the maximum diversity of 40% among the landraces studied. The landraces are having broad genetic base for hulling percentage as the kernel size, lemma and palea volume differs widely among the genotypes studied. Total number of leaves per plant ranked second in the contribution for diversity with the value of 20% followed by, flag leaf length (19%) and single plant yield (11%). The other traits viz., plant height, seed weight and number of tillers contributed 4%, 1% and 0.25% respectively.

The ranking procedure based on the three drought parameters scores *viz*, drought score, tip drying score and leaf rolling score revealed IC 378202, IC 206999, IC 208155, IC 207562, IC 467267, IC 86337 (table 7) and IC 216378 with a rank of one as a drought tolerant genotype. The fitment of these drought tolerant genotypes in their respective clusters revealed the presence of drought tolerant genotypes in the clusters I, II, III, V, VI and VII are predominant.

With respect to the ranking given to the clusters on the basis of drought score, leaf rolling and tip drying score cluster number seven contains a tolerant genotype therefore considered as a tolerant cluster. Members of cluster IV, VIII, IX, X and XI shows susceptibility towards drought therefore this clusters are considered as susceptible clusters.

The association of dependent and independent variables were depicted in Table 8. The traits viz., number of panicles (0.80), number of tillers (0.62), total leaves per plant (0.49) and leaf area (0.49) observed significant and positive correlation with single plant yield. Drought-responsive traits i.e. Drought score had a significant and positive correlation with leaf tip drying (0.91) and leaf rolling (0.58). Correlation between flag leaf length and leaf area was found perfectly significant and positive (1.00). A number of leaves per tillers (0.64) are significantly correlated with number of leaves per plant. Total leaves per plant are significantly correlated to number of tillers (0.89) and number of panicles (0.66). Leaf area showed a significant and positive correlation with number of tillers (0.89) and number of panicles (0.66). Number of tillers was significantly correlated with number of panicles (0.78). Hundred seed weight was significantly correlated with hulling percentage (0.40). Correlation between number of panicles and single plant yield was also observed by Abhilash *et al*., (2018) [1].

Correlation between number of tillers and single plant yield was also found by Panigrahi *et al*., (2018) [13]. Vengatesh *et al*., 2018 [19] also studied correlation between yield and yield component in rice. Dhanuja *et al*., (2021) [5] studied the correlation between 13 agro-morphological trait in Indian rice landraces. Most of the final yield related characters are deviated because on plant interaction with environment therefore correlation coefficient plays a key role while selecting any character of genotypes for breeders in crop improvement programmes Ahmadikhan *et al*., 2008. The prevalence of considerable genetic diversity among the lines used in the study showed that this material forms a source for parental selection in drought breeding programme.

Table 2: Analysis of variance for the morphological traits studied

Characters	Mean sum of squares	
	Replication	Treatment
Days to 50% flowering	0.8976	5.23[**]
Plant height	62.5	57.88[**]
Number of tillers	35.7	11.29[**]
Number of leaves per tillers	0.0577	2.7903[**]
Total leaf on plants	33.77	19.07[**]
Flag leaf length	85	112.26[**]
Leaf breadth	14.03	31.24[**]
Leaf area	41.53	41.64[**]
Number of Panicles	16.17	12.33[**]
Panicle length	17.58	22.1[**]
Seed length	16.93	12.07[**]
Seed breath	15.9	14.3[**]
Hundred seed weight	11.34	34.4[**]
Hulling percentage	10.36	54.78[**]
Single plant yield	0.86	86.45[**]

**Significance at 1% level.

Table 3: Analysis of variability parameters of agro morphological characters

Characters	PV	GV	EV	PCV	GCV	h² %	GAM%
Days to 50% flowering	29.1871	19.818	9.3692	7.4879	6.1701	67.8996	10.4736
Plant height	175.45	169.49	5.9594	10.0568	9.8845	96.6034	20.0132
Number of tillers	7.7267	6.4694	1.2573	32.0611	29.3368	83.7273	55.2985
Number of leaves per tillers	0.3284	0.1551	0.1733	16.8045	11.5493	47.2343	16.3512
Total leaf on plants	142.5398	128.338	14.2018	39.8898	37.8504	90.0366	73.9857
Flag leaf length	179.19	176.0306	3.1641	31.9789	31.6953	98.2343	64.7133
Leaf breadth	0.2276	0.2134	0.0141	33.9163	32.8477	93.7982	65.5345
Leaf area	729.89	695.6582	34.2319	46.6602	45.5529	95.31	91.6119
Number of Panicles	7.6214	6.4784	1.1431	38.3963	35.4001	85.002	67.2335
Panicle length	11.4496	10.4584	0.9912	17.501	16.7263	91.343	32.9309
Seed length	0.0029	0.0024	0.0004	8.4729	7.7978	84.6988	14.7835
Seed breath	0.0011	0.001	0.0001	14.313	13.3453	86.9343	25.6325
Hundred seed weight	0.1075	0.1015	0.0061	17.8625	17.3506	94.3508	34.718
Hulling percentage	24.199	23.3319	0.868	6.4761	6.3589	96.4131	12.8623
Single plant yield	426.6337	416.8767	9.7569	27.7511	27.4319	97.713	55.8598

PV-Phenotypic variation, GV-Genotypic variation, EV-Environmental variation, PCV-Phenotypic coefficient of variation, GCV-Genotypic coefficient of variation, h²-broad-sense heritability, GAM-Genetic advance percent mean.

Table 4: Distribution of genotypes in seven different clusters

Cluster Number	Total genotypes	Accessions Numbers
Cluster-1	14	IC205988, IC518720, IC114628, IC540621, IC207753, IC380614, IC458480X, IC378202, IC206810, IC516792, IC206999, IC207596, IC377149
Cluster-2	4	IC217818, IC206954, IC208155, IC323750
Cluster-3	18	IC458545, IC135643, IC99458, IC458416, IC594028, IC458677, IC378170, IC248059, IC207562, IC555090, IC282506, IC389916, IC207540, IC514623, IC516839, IC462181, IC554943
Cluster-4	2	IC67496, IC114610
Cluster-5	2	IC467267, IC377122
Cluster-6	1	IC86337
Cluster-7	1	IC216378
Cluster-8	5	IC217294, IC458407, IC459854X, IC457996, IC301091
Cluster-9	1	IC135299
Cluster-10	1	IC540621
Cluster-11	1	IC207562

Table 5: Intra and inter cluster distance matrix based on Toucher value

	Cluster - 1	Cluster - 2	Cluster - 3	Cluster - 4	Cluster - 5	Cluster - 6	Cluster - 7	Cluster - 8	Cluster - 9	Cluster - 10	Cluster - 11
Cluster-1	600.3252	1231.38	905.23	12.99.41	1614.548	1712.16	3188.78	867.31	1617.85	5550.45	832.72
Cluster-2		764.33	1098.76	1937.17	783.57	1042.34	1605.27	1388	1329	3394.14	2126.24
Cluster-3			695.15	1297.47	1154.56	1894.42	2251.97	903.18	881.97	3888.66	1089.87
Cluster-4				929.08	2276.21	2222.21	2961.51	1829.63	973.24	4657.93	1266.57
Cluster-5					878.88	1764.69	1923.93	1524.54	1375.78	2690.87	2172.99
Cluster-6						0	1350.21	2494.77	2184.45	3819.08	3386.8

									0	3485.96	1472.89	1815.71	4844.8
Cluster-7									0	3485.96	1472.89	1815.71	4844.8
Cluster-8										54.71	1470.44	5504.42	939.85
Cluster-9											0	2769.59	1830.33
Cluster-10												0	6335.18
Cluster-11													0

Table 6: Cluster mean differences for each character

| Cluster Number	Days to 50% flowering	Plant height	Number of tillers	Number of leaves per tiller	Number of leaves per plant	Flag leaf length	Flag leaf breath	Leaf area	Number of panicles	Panicle length	Seed length	Seed breath	100 seed weight	Hulling percentage	Single plant yield
1.	72.03	129.67	10.46	19.38	37.5	40.64	1.4	58.95	8.78	19.38	0.61	0.21	1.6	77.27	82.89
2.	68.5	151.25	9.25	20.47	35.125	49.87	1.63	84.1	7.75	20.47	0.65	0.23	1.9	73.3	87.12
3.	72.66	127.77	7.555	18.86	24.75	39.75	1.28	51.12	6.02	18.86	0.61	0.24	1.9	76.94	66.75
4.	73.5	123.5	7.5	19.76	26.25	16	2.05	32.87	8.75	19.76	0.71	0.21	1.3	71.27	78.5
5.	74.75	148.25	8.5	16.8	25.5	56.25	1.5	92.32	7.75	16.8	0.7	0.24	1.6	67.57	90.25
6.	70.5	128	12.5	15	62.5	37	2.4	91.82	11	15	0.61	0.22	2.1	76.04	88
7.	83.5	134	9.5	20	47.5	16.5	1.6	26.4	4.5	20	0.55	0.27	2.5	73.09	49
8.	72.3	136.8	7.1	20.52	21.3	60.2	1.04	62.05	5.8	20.52	0.65	0.22	1.8	78.47	62.5
9.	68.5	133.5	4.5	22.87	13.5	29	2.05	59.45	4	22.87	0.69	0.24	2.05	73.77	40
10.	68.5	110.5	12	22	36	37.5	0.9	33.9	8	22.075	0.63	0.24	2.2	63.63	87
11.	68	131	8	17.75	16	43.5	0.95	41.2	7.5	17.75	0.66	0.2	1.7	81.36	97
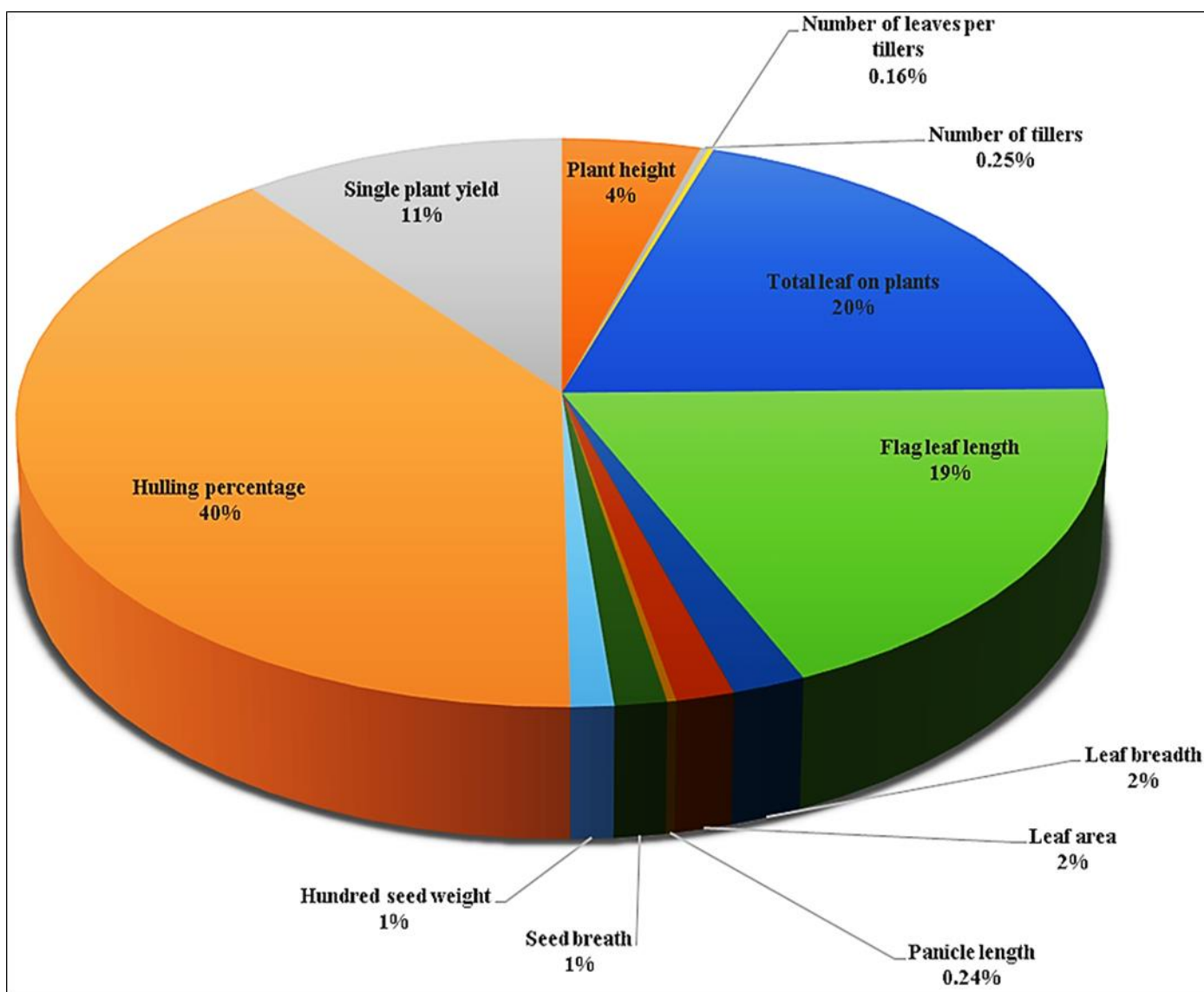
Fig 1: Contribution of traits for divergence

Table 7: Ranking of genotypes basis of drought characters and their position in clusters

Sl. No.	Accession No.	Drought score	leaf rolling	leaf tip drying	Mean	Ranking	Cluster
1.	IC 205988	6	6	4	5.3	6	I
2.	IC 217818	8	6	6	6.6	10	II
3.	IC 208155	4	4	4	4.0	2	II
4.	IC 458545	5	8	6	6.3	9	III
5.	IC 248059	4	8	6	6.0	8	III
6.	IC 99458	4	6	5	5.0	5	III
7.	IC 467496	4	8	5	5.6	7	IV
8.	IC 55090	5	8	6	6.3	9	III
9.	IC 114610	6	8	6	6.6	10	IV
10.	IC 540621	4	6	4	4.6	4	I
11.	IC 467267	5	4	4	4.3	3	V
12.	IC 207562	4	4	4	4.0	2	III
13.	IC 518720	5	6	5	5.3	6	I
14.	IC 86337	3	6	4	4.3	3	VI
15.	IC 216378	3	3	3	3.0	1	VII
16.	IC 378170	4	7	5	5.3	6	III
17.	IC 114628	6	7	5	6.0	8	I
18.	IC 458677	8	8	7	7.6	13	III
19.	IC 217294	6	6	4	5.3	6	VIII
20.	IC 135643	6	4	4	4.6	4	III
21.	IC 207753	6	6	4	5.3	6	I
22.	IC 380614	6	8	5	6.3	9	I
23.	IC 282506	7	8	6	7.0	11	III
24.	IC 389916	7	6	6	6.3	9	III
25.	IC 207540	6	9	6	7.0	11	III
26.	IC 458407	6	9	5	6.6	10	VIII
27.	IC 459854	8	9	6	7.6	13	VIII
28.	IC 458416	6	9	5	6.6	10	III
29.	IC 514623	4	8	4	5.3	6	III
30.	IC 35299	8	6	7	7.0	11	IX
31.	IC 458796	6	9	5	6.6	10	III
32.	IC 516839	7	8	7	7.3	12	III
33.	IC 458480	8	8	7	7.6	13	I
34.	IC 378202	6	8	6	6.6	10	I
35.	IC 206810	9	8	9	8.6	14	I
36.	IC 462181	7	8	8	7.6	13	III
37.	IC 516792	4	8	4	5.3	6	I
38.	IC 554943	6	8	6	6.6	10	III
39.	IC 206999	4	4	4	4.0	2	I
40.	IC 217501	4	6	5	5.0	5	I
41.	IC 457996	6	8	6	6.6	10	X
42.	IC 377122	6	8	6	6.6	10	I
43.	IC 206954	6	8	6	6.6	10	VIII
44.	IC 301091	6	9	6	7.0	11	V
45.	IC 323750	6	9	6	7.0	11	II
46.	IC 377149	6	9	6	7.0	11	VIII
47.	IC 594028	6	9	6	7.0	11	II
48.	IC 59920	7	9	7	7.6	13	I
49.	IC 386140	8	9	9	7.0	11	III
50.	IC 216827	6	9	6	8.6	14	XI

Table 8: Correlation between the characters

	D.F.F.	P.H.	N.L.T.	T.L.P.	F.L.L.	F.L.B.	L.A.	N.T.	N.P.	P.L.	S.L.	S.B.	H.S.W.	H.P.	D.S.	L.R.	L.T.D.	S.P.Y.
D.F.F.	1	0.0416	0.1566	-0.0812	-0.2066	0.1307	-0.0812	-0.1955	-0.3338**	-0.0789	-0.176	-0.1742	-0.2528	-0.1044	-0.4606**	-0.4368**	-0.4467**	-0.2847
P.H.		1	-0.0184	0.102	0.2617	0.0526	0.102	0.0795	0.0963	0.0579	0.2841*	0.1603	-0.1696	-0.3112*	0.1121	-0.0544	0.0099	0.1626
N.L.T.			1	0.6446**	-0.3801**	0.2072	0.6446**	0.2491	0.1363	-0.0991	-0.2848*	0.0391	0.1997	0.0132	-0.1509	-0.241	-0.2035	0.0431
T.L.P.				1	-0.1071	0.1073	1**	0.8916**	0.6687**	-0.0172	-0.0541	-0.0531	-0.0216	-0.0428	0.1221	-0.1666	-0.0103	0.491**
F.L.L.					1	-0.0997	-0.1071	0.0812	0.1385	0.1074	0.1433	-0.0385	-0.009	0.0953	0.2382	0.3751**	0.274	0.2355
F.L.B.						1	0.1073	-0.0239	-0.1539	-0.0601	0.2123	-0.0502	-0.0138	-0.2008	-0.4067**	-0.375**	-0.3797**	0.0119
L.A.							1	0.8916**	0.6687**	-0.0172	-0.0541	-0.0531	-0.0216	-0.0428	0.1221	-0.1666	-0.0103	0.491**
N.T.								1	0.7884**	0.0457	0.0708	-0.1031	-0.1474	-0.0706	0.231	-0.0636	0.1054	0.6244**
N.P.									1	0.0121	0.0157	-0.2538	-0.1625	0.0263	0.3097*	0.1261	0.2555	0.8003**
P.L.										1	0.2075	-0.0324	0.062	0.041	0.1152	0.3*	0.1216	0.0098
S.L.											1	-0.0634	-0.268	-0.3969**	0.0992	0.1384	0.0217	0.1274
S.B.												1	0.1501	-0.1842	0.1555	0.1117	0.2012	-0.2021
H.S.W.													1	0.4029**	0.0762	0.0996	0.1399	-0.1153

															1	0.1243	0.2196	0.1214	-0.117
H.P.																1	0.1243	0.2196	0.1214	-0.117
D.S.																	1	0.5834**	0.9198**	0.1027
L.R.																		1	0.7012**	0.1182
L.T.D.																			1	0.1071
S.P.Y.																				1

S.L.-Seed length, S.B.-Seed breath, H.S.W.-hundred seed weight, H.P.-Hulling percentage, D.F.F.-Days to fifty Percent flowering, N.T.-Number of tillers. N.P-Number of panicle, F.L.L.-Flag leaf lengtsh, F.L.B.-Flag leaf breath, P.H.-Plant height, L.A.-Leaf area, N.L.T.-Number of leaves per tiller, P.L.-Panicle length, N.L.P.-Number of leaves per plant.

Conclusion

From the present investigation it was found that all the 50 landraces of rice studied are diverse both phenotypically and genetically. ANOVA revealed that there is significant variability among traits of the genotypes. PCV and GCV were highest in traits of leaf area and the total number of leaves per plant. High heritability coupled with GAM is found in traits flag leaf length (98.23 and 64%) and plant height (96.60 and 20.01%). Plant height have positive significant correlation with seed length (0.2841) and flag leaf length has significant positive correlation with leaf rolling score (0.3751). The 50 genotypes have been grouped in 11 clusters of which cluster number three has a maximum number of genotypes i.e. 18 followed by cluster number one which has 14 genotypes. Drought parameters recorded were utilised in identifying the clusters with drought tolerant genotypes. The genotypes number IC 378202, IC 206999, IC 208155, IC 207562, IC 467267, IC 86337 and IC 216378 found drought tolerant in terms of leaf rolling, tip drying and rejuvenating ability under drought environment and they are the members of the clusters numbers I, II, III, V, V and VII. Cluster number seven contains a genotype IC 216378 which has superior in performance under drought situation. Hence, this cluster is considered as drought tolerant cluster based on ranking studies. Apart from cluster seven; members of cluster number I (3), II(2), III (12), V(1), VI(1) and VII(1) shows drought tolerance therefore this clusters can be consider as the clusters of moderately tolerant genotypes and cluster number IV, VIII, IX, X, XI contains all the susceptible genotypes hence this clusters will considered as susceptible clusters. Maximum contribution for divergence showed by hulling percentage (40%) followed by total leaf on plant (20%), flag leaf length (19%) and single plant yield (11%).

Correlation studies discloses that traits total leaves per plant, leaf area, number of tillers, and number of panicles are positively significant for the single plant yield and all the three drought-related traits (leaf rolling score, tip drying score, and drought score) are positively correlated with each other. Panicle length (0.3) was positively correlated to leaf rolling score with heritability and GAM (84.69 And 14.78). Flag leaf length has a positive correlation with leaf rolling (0.3751) with heritability (98.23) and GAM (64.71). Days to fifty percent flowering a have negative correlation with leaf rolling (-0.43), tip drying (-0.46) and drought scores (-0.44). Flag leaf breadth has a negative correlation with drought score (-0.40) From the above variability, correlation and diversity studies, the characters *viz.* Days to fifty percent flowering, Flag leaf length, Panicle length, single plant yield, hulling percentage, Tip drying score, Leaf rolling score and drought score are the selectable characteristics for identification of genotypes under drought stress.

References

1. Abhilash R, Thirumurugan T, Sassikumar D, Chitra S. Genetic studies in F2 for biometrical traits in Rice (*Oryza sativa* L). Electronic Journal of Plant Breeding. 2018;9(3):1067-76.
2. Ahmadikhah A, Karlov GI, Nematzadeh GH, Ghasemi Bezdi K. Inheritance of the fertility restoration and genotyping of rice lines at the restoring fertility (Rf) loci using molecular markers. International Journal of Plant Production. 2007 Mar;1(1):13-21.
3. Ahmad MS, Wu B, Wang H, Kang D. Identification of Drought Tolerance on the Main Agronomic Traits for Rice (*Oryza sativa* L. ssp. *japonica*) Germplasm in China. Agronomy. 2021 Aug;11(9):17-40.
4. Burton GW. Quantitative inheritance in grasses. Proceedings: 6th Int. Grassland Cong. 1952;1:277-283.
5. Dhanuja N, Ganesamurthy K, Pushpam R, Amudha K, Uma D. Studies on genetic diversity in selected rice (*Oryza sativa* L.) landraces of Tamil Nadu. Electronic Journal of Plant Breeding. 2021 Sep;12(3):990-997.
6. Divya K, Rani TS, Babu TK, Padmaja D. Assessment of genetic variability, heritability and genetic gain in advanced mutant breeding lines of sesame (*Sesamum indicum* L.). Int. J Curr. Microbiol. App. Sci. 2018;7(6):1565-1574.
7. Dhurai SY, Bhati PK, Saroj SK. Studies on genetic variability for yield and quality characters in rice (*Oryza sativa* L.) under integrated fertilizer management. The Bioscan. 2014;9(2):745-748.
8. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans 1. Agronomy journal. 1955 Jul;47(7):314-318.
9. Kurmanchali M, Kurmanchali N, Kukreti A, Sihag N, Chaudhary H, Karnwal MK. Study of genetic variability, heritability and genetic advance for various yield attributing and quality traits in basmati rice (*Oryza sativa* L.). International Journal of Chemical Sciences. 2019;7(1):2486-2489.
10. Lush JL. Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. Journal of animal science. 1940 Dec;1940(1):293-301.
11. Mahalnobis PC. On the generalized distance in statistics. Proceeding Natural Institute Science India. 1936;2(1):49-55.
12. Palaniyappan S, Arunachalam P, Banumathy S, Mini ML, Muthuramu S. Genetic divergence and clustering studies in advanced breeding lines of rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding. 2020 Jul;11(02):499-504.
13. Panigrahi AK, Bharathi M, Kumaravadive N. Genetic variability and character association studies in advanced backcross generation of rice (*Oryza sativa* L.). Journal of pharmacognosy and phytochemistry. 2018;7(1):2397-2400.
14. Perween S, Kumar A, Prasad BD, Choudhary M. Assessment of Genetic Diversity in Rice (*Oryza sativa* L.) under Irrigated and Drought Stress Condition. Current

Journal of Applied Science and Technology. 2020;39(1):112-125.

15. Sabesan T, Saravanan K. *In vitro* screening of Indica rice genotypes for drought tolerance using polyethylene glycol. Int J Adv in Agric Environ Eng. 2016;3:2349-1531.

16. Singh B, Gauraha D, Sao A, Nair SK. Assessment of genetic variability, heritability and genetic advance for yield and quality traits in advanced breeding lines of rice (*Oryza sativa* L.). The Pharma Innovation. 2021;10(8):1627-1630.

17. Sitaresmi T, Wening RH, Rakhmi AT, Yunani N, Susanto U. Pemanfaatan plasma nutfah padi varietas lokal dalam perakitan varietas unggul. Iptek Tanaman Pangan. 2013;8(1):22-30.

18. Tuhina-Khatun M, Hanafi MM, Rafii Yusop M, Wong MY, Salleh FM, Ferdous J. Genetic variation, heritability, and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits. BioMed research international, 2015 Jun.

19. Vengatesh M. Studies on correlation and path analysis in rice (*Oryza sativa* L.) genotypes. Electronic Journal of Plant Breeding. 2018 Dec;9(4):1570-1576.

20. Worede F, Sreewongchai T, Phumichai C, Sripichitt P. Multivariate analysis of genetic diversity among some rice genotypes using morpho-agronomic traits. Journal of Plant Sciences. 2014 Jan;9(1):14.