

## Assessing the genetic diversity for yield traits in rice (*Oryza sativa* L.) genotypes using multivariate analysis under controlled and water stress conditions

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### ABSTRACT

The genetic diversity of yield and yield attributing characteristics was explored in this research. In the topical study, fifty-two rice genotypes including four checks were used under three environmental conditions i.e. irrigated (IR), rainfed (RF) and terminal stage drought (TSD) conditions. The prevalence of genetic divergence was evaluated using clustering and Principal component analysis (PCA) was used to determine the relative contribution of various traits. To fulfill the aim of the study, fifty-two genotypes were grouped into three distinct and non-overlapping clusters among these 3 clusters, cluster-I was the largest with the highest number of genotypes i.e. 47, 49 and 49 under IR, RF and TSD conditions, respectively. The highest average intra-cluster distance was observed in cluster-I, also the genotypes showed high variability under all three conditions. The highest inter-cluster distance between the cluster-II and cluster-III (IR and TSD) and cluster-I and cluster-II (RF) was observed, indicated that genotypes from the group should be considered for direct use as parents in hybridization programme to produce high yield. Only five of the 13 principal components (PCs) have been considered in the study based on the Eigen values and variability criteria. From the complex matrix it was revealed that the first-PC accounted for the highest variability. Genotypes which fall under a common PC were observed to be the most important factor for grain yield.

### Introduction

Rice (*Oryza sativa* L.) is a major staple crop that feeds more than half of the world's population (Ricepedia, 2020; USDA, 2020). Rice genotypes from Chhattisgarh are critical for preserving and maintaining rice biodiversity. Rice germplasm is a valuable resource that must be protected. In order to produce superior hybrid and desirable transgressive segregants, genetic diversity plays a critical role in selecting suitable parents for the hybridization programme (Burman *et al.*, 2019). Cluster analysis is a numerical approach used for

measuring genetic divergence in the germplasm lines. Although yield is a complex trait that is influenced by a variety of factors and the environment, principal component analysis was used to discover and minimize the number of traits for effective selection (Gaur *et al.*, 2019). Because it is a simple, non-parametric method for extracting crucial data from confusing data sets, PCA has become a standard tool in modern data analysis. It is a mathematical process that converts a set of (potentially) correlated variables into a set of

(smaller) uncorrelated variables known as principal components. It decreases the data's dimensionality while preserving the majority of data set variation. The first principal component accounts for as much variability as possible. Multivariate analysis (PCA) has been widely used in the selection of diverse parents in any hybridization programme. The main advantage of PCA is that it quantifies the value of each dimension in characterizing the variability of a data set (Raj *et al.*, 2020). The current study was conducted to assess genetic divergence and PCA in 52 rice germplasm lines to discover yield related characteristics whose selection would result in an increase in rice grain yield.

### Material and Methods

The current research was conducted at the Research Farm, Department of Genetics and Plant Breeding, Indira Gandhi Agricultural University, Raipur (Chhattisgarh) during *kharif* 2018 and *kharif* 2019 using Randomized Block Design (RBD) with two replications. The experimental material consists of 52 germplasm lines which were grown in two rows with row to row and plant to plant spacing of 20 × 20 cm maintained under three environmental conditions (IR, RF and TSD). In IR and TSD conditions, seeds were sown in nurseries and seedlings were transplanted as a single plant after twenty-one days and under RF condition, seeds were sown directly in both the seasons. The collected data were pooled over the season and the data recorded for thirteen yield traits were days to 50% flowering, plant height in cm, flag leaf length in cm, flag leaf width in cm, number of tillers per m<sup>2</sup>, panicle length in cm, biological yield per plot in g, grain yield per plot in g, harvest index in per cent, thousand grain weight in g, number of filled grains per panicle, number of unfilled grains per panicle and total number of grains per panicle. Cluster analyses for the above characters were done by following Agglomerative hierarchical clustering (AHC) using XLSTAT. The Hierarchical clustering method's structure is represented by a dendrogram. For the traits, intra and inter cluster distances, as well as mean cluster performance were calculated (Sudeepthi *et al.*, 2020). Similarly, Multivariate Analysis (PCA) was performed by following Pearson correlation type (Kumari *et al.*, 2019) using

XLSTAT. For the traits, Eigen values, factor loading and principal component scores were calculated.

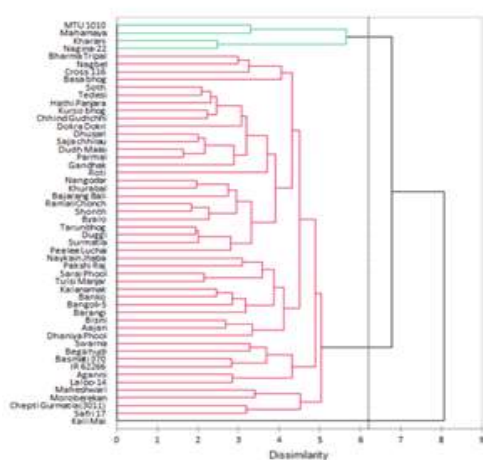
## Results and Discussion

### Cluster analysis

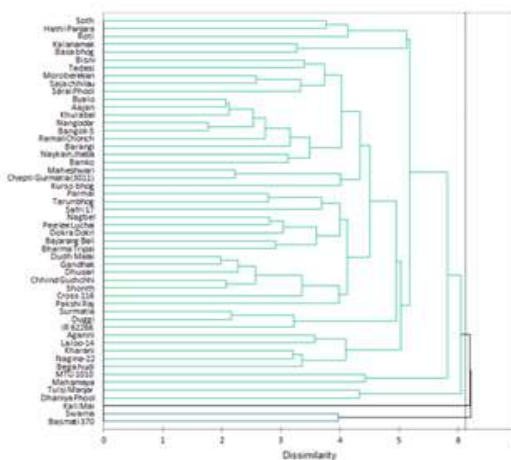
Cluster analysis divides the fifty-two rice genotypes into 3 clusters under three conditions (Table 1) and dendrogram showed in Figure 1. Cluster-I with 47 genotypes was the biggest cluster followed by cluster-II with 2 genotypes, while cluster-III was mono-genotypic under irrigated condition. Cluster-I with 49 genotypes had the most genotypes under rainfed and TSD conditions, followed by cluster-II, which had 2 genotypes and cluster-III was mono-genotypic. As per the topical study the intra and inter cluster under irrigated, rainfed and TSD conditions are shown in Table 2. The highest intra-cluster distance under all three conditions were found in cluster-I (IR-14.41), (RF-8.23), (TSD-8.18), and crossing between the genotypes of cluster-I produces better segregants with greater genetic diversity and genetic advance. The highest inter-cluster distance between the clusters-II and cluster-III under irrigated (30.56) and TSD (12.46) conditions and between the cluster-I and cluster-II under rainfed (13.38) condition, followed by cluster-I and cluster-II (26.96), cluster-I and cluster-III (15.87) under irrigated condition; cluster-II and cluster-III (10.87), cluster-I and cluster-III (9.91) under rainfed condition; cluster-I and cluster-III (10.53), cluster-I and cluster-II (8.21) under TSD condition, revealed greater diversity among these clusters and may be used in hybridization for the development of germplasm lines. Based on mean performance of three clusters (Table 3), the traits which showed high mean values were biological yield per plot, grain yield per plot, number of tillers per m<sup>2</sup> and total number of grains per panicle in all conditions. The highest percent contribution (Table 4) were showed by the traits, harvest index under irrigated (16.104) and rainfed (13.598) conditions and thousand grain weight under TSD (11.800) condition. Kali Mai was the only genotype commonly observed in all three clusters. The genotypes falling in the same cluster (intra-cluster) are more closely related and less divergent than those which are placed in different clusters (inter-cluster).

**Table 1: Pooled clustering pattern of fifty two rice genotypes in different water regimes during *Kharif* 2018 and 2019.**

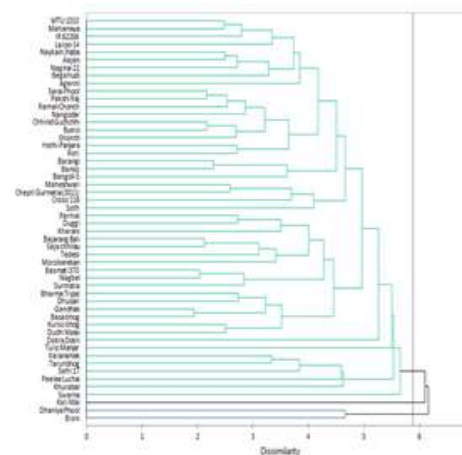
Cluster No.	No. of genotypes	Name of genotypes	No. of genotypes	Name of genotypes	No. of genotypes	Name of genotypes
			<b>Rainfed (Pooled)</b>		<b>Terminal Stage Drought (Pooled)</b>	
I	47	Bega hudi, Aajan, Banko, Barangi, Khurabal, Peelee Luchai, Nagbel, Bangoli-5, Byalo, Duggi, Saja chhilau, Surmatia, Basa bhog, Dhusari, Gandhak, Cross 116, IR 62266, Laloo-14, Aganni, Safri 17, Tarunbhog, Chepti Gurmatia (3011), Basmati 370, Kalanamak, Moroberekan, Pakshi Raj, Dokra Dokri, Parmal, Tedesi, Bisni, Dhaniya Phool, Tulsi Manjar, Sarai Phool, Bharna Tripal, Dudh Malai, Shonth, Chhind Guchchhi, Naykain Jhaba, Ramali Chonch, Roti, Hathi Panjara, Nangodar, Soth, Bajarang Bali, Kurso bhog, Swarna, Maheshwari	49	Bega hudi, Aajan, Banko, Barangi, Khurabal, Peelee Luchai, Nagbel, Bangoli-5, Byalo, Duggi, Saja chhilau, Surmatia, Basa bhog, Dhusari, Gandhak, Cross 116, IR 62266, Laloo-14, Aganni, Safri 17, Tarunbhog, Chepti Gurmatia (3011), Kalanamak, Moroberekan, Nagina-22, Pakshi Raj, Dokra Dokri, Parmal, Tedesi, Bisni, Dhaniya Phool, Tulsi Manjar, Sarai Phool, Kharani, Bharna Tripal, Dudh Malai, Shonth, Chhind Guchchhi, Naykain Jhaba, Ramali Chonch, Roti, Hathi Panjara, Nangodar, Shoth, Bajarang Bali, Kurso bhog, Maheshwari, Mahamaya, MTU 1010	49	Bega hudi, Aajan, Banko, Barangi, Khurabal, Peelee Luchai, Nagbel, Bangoli-5, Byalo, Duggi, Saja chhilau, Surmatia, Basa bhog, Dhusari, Gandhak, Cross 116, IR 62266, Laloo-14, Aganni, Safri 17, Tarunbhog, Chepti Gurmatia (3011), Basmati 370, Kalanamak, Moroberekan, Nagina-22, Pakshi Raj, Dokra Dokri, Parmal, Tedesi, Tulsi Manjar, Sarai Phool, Kharani, Bharna Tripal, Dudh Malai, Shonth, Chhind Guchchhi, Naykain Jhaba, Ramali Chonch, Roti, Hathi Panjara, Nangodar, Soth, Bajarang Bali, Kurso bhog, Swarna, Maheshwari, Mahamaya, MTU 1010
II	4	Nagina-22, Kharani, Mahamaya, MTU 1010	2	Basmati 370, Swarna	2	Bisni, Dhaniya Phool
III	1	Kali Mai	1	Kali Mai	1	Kali Mai



**IRRIGATED**



**RAINFED**



**TSD**

**Figure 1: Dendrogram of fifty-two rice genotypes in different conditions.**

**Table 2: Average intra (diagonal and bold) and inter cluster distance for irrigated, rainfed and terminal stage drought**

Cluster	Irrigated			Rainfed			TSD		
	I	II	III	I	II	III	I	II	III
I	14.41	26.96	15.87	8.23	13.38	9.91	8.18	8.21	10.53
II		13.25	30.56		5.35	10.87		7.62	12.46
III			0.00			0.00			0.00

**Table 3: Cluster mean value for different traits under different conditions.**

	Class	DTF	PH	FLL	FLW	NT	PL	BY	GY	HI	TGW	NFG	NUFG	TNG
Irrigated	I	108.388	133.421	32.352	1.528	185.213	25.808	1691.862	279.351	17.071	28.502	98.156	29.537	127.693
	II	91.938	101.738	28.986	1.375	217.188	20.929	876.870	313.800	39.121	27.878	86.705	30.963	117.668
	III	118.000	128.450	36.885	1.450	217.500	27.668	1890.800	361.600	19.238	38.971	143.810	72.710	216.520
Rainfed	I	97.776	103.423	30.222	1.340	122.742	24.435	373.192	69.648	19.221	22.434	82.444	36.851	119.275
	II	104.125	80.550	27.995	1.285	146.250	23.048	206.100	74.264	37.205	19.576	75.020	41.803	116.823
	III	109.000	91.150	29.800	1.175	103.750	25.550	322.900	75.300	23.347	37.250	110.380	45.050	155.430
TSD	I	92.939	109.473	32.428	1.412	174.834	23.741	542.895	110.371	20.828	27.727	85.212	24.757	109.969
	II	80.625	130.100	29.768	1.178	181.875	26.148	434.325	124.215	30.013	19.926	79.962	32.645	112.606
	III	103.000	110.850	33.555	1.345	108.750	27.000	617.400	102.000	18.016	27.813	91.647	11.680	103.327

Note: DTF= days to 50% flowering, PH= plant height (cm), FLL= flag leaf length (cm), FLW= flag leaf width (cm), NT= number of tillers m<sup>2</sup>, PL= panicle length (cm), BY= biological yield/plot (g), GY= grain yields per plot (g), HI= harvest index (%), TGW=thousand grain weight (g), NFG= number of filled grains per panicle, NUFG= number of unfilled grains per panicle, TNG= total number of grains per panicle

**Table 4: Percent contribution of each character under various conditions**

Traits	% contribution of each character		
	IRRIGATED	RAINFED	TSD
DTF	3.771	3.530	4.192
PH	6.353	5.837	6.292
FLL	5.715	6.231	7.054
FLW	5.945	3.126	6.519
NT	5.118	8.958	6.128
PL	5.087	4.440	3.554
BY	8.364	8.789	6.356
GY	5.620	9.902	9.803
HI	16.104	13.598	11.733
TGW	6.730	9.298	11.800
NFG	9.749	10.531	9.238
NUFG	12.187	8.145	10.107
TNG	9.256	7.615	7.225

Note: DTF= days to 50% flowering, PH= plant height (cm), FLL= flag leaf length (cm), FLW= flag leaf width (cm), NT= number of tillers m<sup>2</sup>, PL= panicle length (cm), BY= biological yield/plot (g), GY= grain yields per plot (g), HI= harvest index (%), TGW=thousand grain weight (g), NFG= number of filled grains per panicle, NUFG= number of unfilled grains per panicle, TNG= total number of grains per panicle

**Table 5: Eigen values of yield and yield related traits of 52 rice germplasm accessions under different conditions**

		PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
IR	Eigenvalue	3.877	2.924	1.171	1.088	0.911	0.714	0.651	0.546	0.412	0.380	0.271	0.057
	Variability (%)	29.820	22.489	9.008	8.366	7.007	5.489	5.009	4.197	3.171	2.920	2.087	0.438
	Cumulative %	29.820	52.309	61.317	69.683	76.690	82.178	87.187	91.384	94.555	97.475	99.562	100.000
RF	Eigenvalue	2.506	2.244	1.588	1.386	1.145	0.986	0.878	0.814	0.601	0.558	0.264	0.031
	Variability (%)	19.281	17.258	12.214	10.662	8.806	7.583	6.751	6.261	4.622	4.295	2.031	0.235
	Cumulative %	19.281	36.539	48.753	59.415	68.221	75.804	82.555	88.816	93.439	97.734	99.765	100.000
TSD	Eigenvalue	2.607	2.101	1.709	1.595	1.158	1.004	0.840	0.633	0.491	0.432	0.417	0.014
	Variability (%)	20.056	16.165	13.144	12.268	8.905	7.720	6.459	4.866	3.780	3.323	3.204	0.109
	Cumulative %	20.056	36.221	49.365	61.633	70.539	78.259	84.717	89.583	93.364	96.687	99.891	100.000

**Table 6: Factor loading (Eigen vectors) of 52 rice germplasm accessions for yield traits under different conditions**

	PC1	PC2	PC3	PC4	PC5	PC1	PC2	PC3	PC4	PC5	PC1	PC2	PC3	PC4	PC5
	Irrigated					Rainfed					TSD				
DTF	<b>0.634</b>	0.233	-0.078	-0.002	-0.468	<b>0.653</b>	0.158	-0.150	0.243	0.282	<b>0.501</b>	-0.189	-0.469	0.336	0.177
PH	<b>0.788</b>	-0.186	-0.077	0.071	0.102	-0.271	<b>0.549</b>	-0.361	-0.128	0.404	-0.125	-0.002	<b>0.638</b>	0.314	0.323
FLL	0.532	0.110	<b>0.595</b>	0.092	-0.180	0.205	<b>0.475</b>	-0.188	0.371	-0.385	0.202	-0.394	0.292	0.063	<b>0.530</b>
FLW	<b>0.575</b>	0.056	-0.153	0.368	0.482	-0.027	0.396	-0.219	<b>0.642</b>	-0.127	0.028	-0.500	0.271	<b>0.593</b>	-0.090
NT	<b>-0.526</b>	0.278	-0.351	0.078	-0.452	0.157	-0.068	-0.089	<b>-0.442</b>	-0.033	-0.087	0.227	<b>0.523</b>	-0.429	-0.301
PL	<b>0.636</b>	-0.198	-0.112	0.401	-0.367	0.249	0.587	-0.280	-0.119	<b>0.590</b>	-0.225	-0.117	-0.127	-0.183	<b>0.678</b>
BY	<b>0.825</b>	0.090	0.183	-0.286	-0.039	-0.508	0.011	<b>-0.629</b>	-0.316	-0.174	0.396	<b>-0.644</b>	-0.075	0.012	-0.209
GY	-0.212	0.449	<b>0.681</b>	0.345	-0.005	0.264	<b>0.627</b>	0.188	-0.449	-0.178	<b>0.664</b>	0.491	-0.092	0.445	-0.061
HI	<b>-0.800</b>	0.176	0.106	0.477	0.022	0.570	0.401	<b>0.671</b>	-0.168	-0.042	0.346	<b>0.818</b>	-0.023	0.374	0.107
TGW	0.417	0.369	-0.341	<b>0.491</b>	0.129	0.085	-0.175	0.124	<b>0.453</b>	0.241	-0.286	-0.287	0.340	<b>0.536</b>	-0.318
NFG	0.108	<b>0.881</b>	-0.035	-0.254	0.173	<b>0.791</b>	-0.246	-0.450	-0.086	-0.206	<b>0.853</b>	-0.209	0.182	-0.308	-0.042
NUFG	0.010	<b>0.796</b>	-0.123	0.060	-0.144	0.039	<b>-0.593</b>	0.134	-0.021	0.471	-0.002	0.369	<b>0.581</b>	0.021	0.147
TNG	0.090	<b>0.957</b>	-0.067	-0.185	0.094	<b>0.768</b>	-0.433	-0.385	-0.090	-0.044	<b>0.844</b>	-0.090	0.363	-0.298	0.005

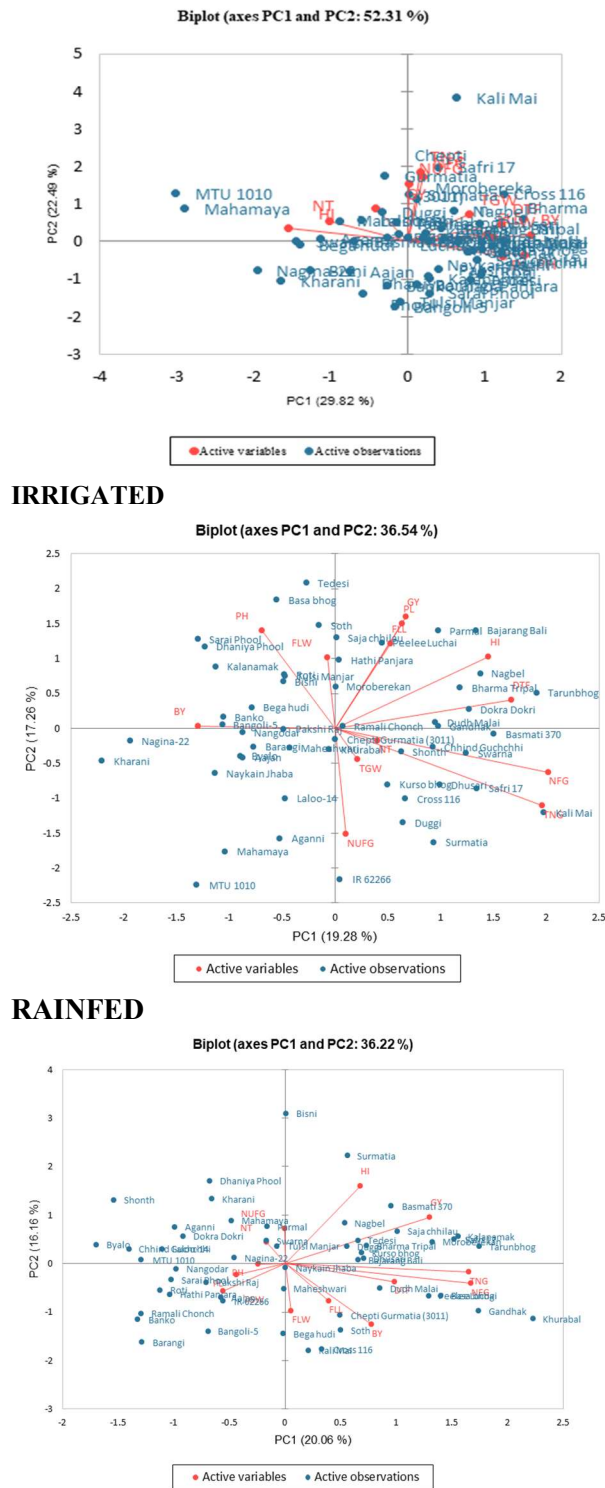
Note: DTF= days to 50% flowering, PH= plant height (cm), FLL= flag leaf length (cm), FLW= flag leaf width (cm), NT= number of tillers m<sup>2</sup>, PL= panicle length (cm), BY= biological yield/plot (g), GY= grain yields per plot (g), HI= harvest index (%), TGW=thousand grain weight (g), NFG= number of filled grains per panicle, NUGF= number of unfilled grains per panicle, TNF= total number of grains per panicle

**Table 7: Principal component score of rice genotypes under irrigated, rainfed and TSD conditions**

Accessions	Score														
	PC1	PC2	PC3	PC4	PC5	PC1	PC2	PC3	PC4	PC5	PC1	PC2	PC3	PC4	PC5
	IRRIGATED					RAINFED					TSD				
Bega hudi	-2.766	-0.138	0.021	-1.135	-1.501	-1.242	0.448	<b>1.119</b>	0.398	-1.603	-0.031	-2.095	-0.309	-1.262	-1.695
Aajan	-1.475	-1.374	<b>1.305</b>	-1.770	0.734	-1.383	-0.625	0.431	-0.125	0.303	-0.930	-1.021	-0.140	-0.588	0.108
Banko	-0.526	-2.000	0.272	<b>1.221</b>	-1.274	-1.674	0.241	-0.256	<b>0.922</b>	0.562	-2.134	-1.669	<b>1.318</b>	-1.122	<b>1.117</b>
Barangi	0.233	-1.948	<b>1.292</b>	<b>2.254</b>	0.233	-1.216	-0.396	-1.055	<b>1.240</b>	<b>1.613</b>	-2.073	-2.352	<b>1.690</b>	-2.071	<b>2.484</b>
Khurabal	0.478	0.376	-0.364	-1.077	0.556	-0.086	-0.447	0.116	0.820	0.370	<b>3.598</b>	-1.654	<b>2.183</b>	-0.345	-0.778
Peelee Luchai	-0.217	0.333	0.774	-0.672	-0.354	0.706	<b>1.837</b>	-1.062	-0.159	-1.139	<b>2.085</b>	-0.963	1.165	-0.639	0.405
Nagbel	1.190	<b>1.397</b>	<b>1.176</b>	-0.190	0.535	<b>2.179</b>	1.174	-0.217	0.484	-1.742	0.865	<b>1.207</b>	-0.398	0.107	0.408
Bangoli-5	-0.314	-2.955	0.771	0.713	0.490	-1.687	0.077	-0.707	-0.103	0.068	-1.118	-2.025	0.459	0.220	0.530

Assessing the genetic diversity for yield traits in rice

Byalo	0.004	0.162	-0.226	-0.633	0.614	-1.417	-0.590	-0.440	0.348	0.165	-2.737	0.560	0.155	0.462	0.812
Duggi	-0.638	<b>1.343</b>	0.524	-0.929	-0.414	1.017	-2.027	-0.411	0.210	-0.290	0.896	0.515	-0.916	<b>1.348</b>	-1.576
Saja chhilau	1.792	-0.848	0.757	0.814	-0.392	0.021	<b>1.949</b>	-1.553	-0.360	-0.610	<b>1.625</b>	0.961	<b>1.419</b>	1.173	-0.048
Surmatia	0.033	<b>2.131</b>	0.509	-0.888	0.144	1.484	-2.445	0.985	0.640	-0.951	0.906	<b>3.225</b>	0.104	0.265	-0.053
Basa bhog	<b>1.917</b>	-0.346	<b>2.824</b>	0.031	-1.235	-0.870	<b>2.753</b>	0.329	-0.220	-1.547	<b>2.257</b>	-0.967	-1.274	0.411	1.023
Dhusari	<b>1.856</b>	0.821	0.440	0.350	-0.160	<b>1.567</b>	-1.209	-1.819	-0.635	-0.679	1.138	0.148	-2.765	0.643	<b>1.328</b>
Gandhak	1.557	-0.460	<b>1.756</b>	0.244	-0.301	1.546	0.049	-1.179	0.485	-0.405	<b>2.802</b>	-1.419	-1.692	0.417	0.086
Cross 116	<b>2.456</b>	<b>2.158</b>	<b>1.898</b>	0.101	<b>1.495</b>	1.046	-1.512	-2.679	0.095	0.133	0.536	-2.565	<b>1.636</b>	-0.611	0.543
IR 62266	-0.525	0.182	0.981	0.087	-0.874	0.070	-3.237	<b>1.264</b>	0.549	-0.231	-0.904	-1.120	-1.597	-1.257	-0.710
Laloo-14	-1.187	0.956	-0.770	-1.215	<b>1.579</b>	-0.744	-1.500	<b>1.141</b>	<b>1.056</b>	0.126	-1.787	0.437	-1.864	-1.114	-0.922
Aganni	-2.217	0.124	-0.032	-1.255	0.128	-0.824	-2.363	-0.184	-1.384	-1.158	-1.598	<b>1.092</b>	<b>1.299</b>	-2.369	-0.728
Safri 17	0.799	<b>3.387</b>	-0.344	-0.502	-0.917	<b>2.128</b>	-1.286	-0.198	-1.682	<b>0.639</b>	<b>2.448</b>	0.718	0.118	-1.035	-0.366
Tarunbhog	-0.305	0.845	<b>1.202</b>	-1.836	-0.506	<b>3.029</b>	0.764	0.292	-1.674	-0.012	<b>2.819</b>	0.503	<b>1.322</b>	-1.748	-0.184
Chepti Gurmatia (3011)	-0.584	<b>2.981</b>	-1.161	-0.649	<b>1.274</b>	0.006	-0.234	0.606	-1.154	-0.369	0.795	-1.554	0.258	-0.366	-1.690
Basmati 370	-1.371	0.005	0.114	-1.240	-1.373	<b>2.374</b>	-0.125	<b>3.519</b>	-1.280	-0.237	<b>1.536</b>	<b>1.714</b>	-1.627	-0.580	0.370
Kalanamak	0.564	-1.692	<b>1.081</b>	0.579	-0.680	-1.787	1.325	0.647	0.579	-1.318	<b>2.513</b>	0.808	1.020	-1.925	<b>1.403</b>
Moroberekan	0.241	<b>1.956</b>	0.450	<b>1.422</b>	<b>2.053</b>	0.009	0.896	-0.816	-0.560	0.385	<b>2.136</b>	0.650	0.796	<b>2.497</b>	-1.025
Nagina-22	-3.853	-1.331	0.353	<b>1.598</b>	<b>1.585</b>	-3.063	-0.268	<b>1.314</b>	-0.012	-2.660	-0.737	0.172	1.120	-0.975	-1.036
Pakshi Raj	0.794	-1.255	-0.691	-0.232	0.522	-0.767	-0.015	-2.264	-1.049	-1.922	-1.141	-0.561	0.914	0.283	-0.189
Dokra Dokri	<b>2.480</b>	-0.029	-1.553	<b>1.322</b>	-0.506	<b>2.013</b>	0.405	0.517	0.845	-0.802	-1.478	0.814	0.814	<b>1.999</b>	<b>1.828</b>
Parmal	1.279	-0.034	-0.752	0.378	-0.842	1.543	<b>2.090</b>	0.049	-1.707	0.119	-0.260	<b>1.098</b>	-0.105	<b>1.559</b>	0.145
Tedesai	1.610	-1.743	-1.953	0.681	0.559	-0.424	<b>3.120</b>	0.218	-1.021	<b>1.273</b>	1.061	0.689	1.061	<b>1.940</b>	-1.594
Bisni	-2.480	-1.333	<b>1.421</b>	-0.302	-0.051	-0.771	1.003	-0.661	-1.290	<b>1.195</b>	0.014	<b>4.482</b>	0.960	-1.082	<b>1.264</b>
Dhaniya Phool	-1.132	-2.382	-0.242	-0.591	-0.404	-1.945	<b>1.755</b>	0.517	-2.997	<b>2.558</b>	-1.088	<b>2.474</b>	<b>1.780</b>	-0.337	<b>2.400</b>
Tulsi Manjar	-0.183	-2.768	-0.730	-1.445	-1.440	-0.746	1.121	<b>1.607</b>	-2.769	0.496	-0.117	0.519	-2.168	-1.467	0.054
Sarai Phool	0.573	-2.362	-0.576	-1.177	-0.775	-2.048	<b>1.914</b>	-1.636	0.354	-0.254	-1.655	-0.487	0.376	0.268	-0.523
Kharani	-3.243	-1.785	0.771	0.608	0.703	-3.489	-0.697	<b>1.134</b>	0.137	-0.403	-1.058	<b>1.925</b>	0.812	0.556	-1.512
Bharma Tripal	<b>2.976</b>	1.046	<b>1.080</b>	0.565	-0.720	<b>1.875</b>	0.867	-0.396	<b>1.193</b>	0.408	1.183	0.530	-1.401	<b>1.620</b>	<b>1.600</b>
Dudh Malai	<b>1.912</b>	-0.006	0.175	0.054	-0.838	1.505	0.127	-1.522	0.259	0.225	1.374	-0.747	-0.810	-0.649	<b>1.321</b>
Shonth	0.526	0.027	0.614	-0.097	<b>0.947</b>	0.993	-0.505	-2.261	0.076	0.462	-2.488	<b>1.896</b>	-0.162	<b>1.225</b>	-0.448
Chhind Guchchhi	<b>2.394</b>	-0.453	-1.100	-0.058	0.736	1.462	-0.402	-1.076	0.207	0.565	-2.261	0.435	0.162	0.584	0.673
Naykain Jhaba	0.547	-1.558	0.011	-1.043	<b>1.457</b>	-1.797	-0.968	0.460	<b>2.083</b>	-0.073	0.007	-0.129	0.808	0.026	-0.816
Ramali Chonch	0.931	0.101	-0.172	-0.723	<b>1.091</b>	0.120	0.047	-0.795	<b>1.008</b>	0.268	-2.088	-1.491	<b>1.503</b>	0.608	-0.339
Roti	<b>1.903</b>	-1.379	-1.714	<b>1.600</b>	-0.446	-0.760	1.146	0.215	<b>2.056</b>	<b>3.435</b>	-1.812	-0.793	-0.507	<b>3.186</b>	-0.012
Hathi Panjara	<b>1.878</b>	-1.538	-0.746	<b>0.977</b>	-0.128	0.057	<b>1.467</b>	<b>1.133</b>	<b>3.260</b>	<b>0.638</b>	-1.668	-0.923	-0.848	<b>1.346</b>	0.045
Nangodar	0.388	0.167	-0.622	-1.184	<b>1.380</b>	-1.380	-0.088	-0.222	<b>1.042</b>	0.048	-1.580	-0.157	-0.709	0.954	-1.235
Soth	1.674	-0.412	-0.942	<b>1.014</b>	0.629	-0.237	<b>2.214</b>	<b>1.638</b>	<b>1.067</b>	0.401	0.802	-2.000	<b>2.102</b>	<b>2.232</b>	-0.623
Bajarang Bali	0.852	0.608	-1.815	-0.813	-0.723	<b>2.111</b>	<b>2.102</b>	0.384	0.621	-1.364	1.060	0.104	0.744	0.038	-0.539
Kurso bhog	<b>2.189</b>	-0.178	-1.958	0.289	0.202	0.792	-1.201	0.158	0.643	<b>0.913</b>	1.108	0.314	-0.697	0.524	1.066
Kali Mai	1.268	<b>6.564</b>	0.004	<b>1.157</b>	-1.616	<b>3.131</b>	-1.802	0.394	0.595	<b>1.550</b>	0.334	-2.601	-3.262	0.703	<b>1.836</b>
Swarna	-2.848	0.001	-2.308	-0.381	-1.867	<b>1.968</b>	-0.534	<b>3.872</b>	0.116	0.092	-0.272	0.674	-2.756	-1.561	-1.365
Maheshwari	-1.749	0.941	-1.199	0.281	<b>1.346</b>	-0.674	-0.414	-0.429	-0.067	-0.439	-0.019	-0.752	-0.228	-0.883	-0.470
Mahamaya	-5.725	<b>1.486</b>	0.069	<b>3.118</b>	-0.655	-1.650	-2.639	0.901	-1.955	<b>1.071</b>	-0.781	<b>1.280</b>	-0.739	-1.629	-1.366
MTU 1010	-5.956	<b>2.207</b>	-0.678	0.576	0.002	-2.071	-3.361	-1.122	-1.182	0.127	-2.083	0.100	-1.124	-1.579	-1.007



**TSD**

**Figure 2: Biplot graph representing the active variables and observations taking PC<sub>1</sub> and PC<sub>2</sub> under different conditions**

The greater the distance between two clusters, greater is the divergence (Singh and Narayanan, 2013). If crossing takes place among genotypes between clusters, they produce more diverse and better progenies when compared to the crossing of genotypes within the same cluster. Those genotypes can be used as parents in future crossing programmes. The results were found in agreement with Amegan *et al.*, 2020; according to Bekis *et al.*, 2021 the highest inter-cluster distance was recorded between cluster II & III. The results depicted that cross-genotype from cluster II & III, cluster I & III to get genotypes of rice with high grain yield and early maturing genotypes; Burman *et al.*, 2019; Iqbal *et al.*, 2018 and Shrestha *et al.*, 2021 revealed that cluster II & cluster IV showed the highest distance between cluster centroids. The genotypes in cluster II would be grown for higher grain yield. Genotypes in clusters of different conditions with high cluster mean value may be directly used for adaptation, or intercrossing may be recommended to produce the wide spectrum of variability, followed by effective selection for those traits according to the results.

**Principal Component Analysis (PCA)**

PCA was used in the topical study to analyze thirteen yield and yield-related parameters in 52 rice germplasm accessions (Table 5). Biplot graph representing the active variables and observations taking PC<sub>1</sub> and PC<sub>2</sub> under different conditions presented in Figure 2. The PC with Eigen value >1 that described at least 5% of the fluctuations in the data was evaluated in the current investigation, according to the criteria provided by Brejda *et al.* (2000) and Dhakal *et al.* (2020). The PC with the highest Eigen values and variables with the highest factor loading was deemed to be the most representational of system characteristics. Only five of the 13 principal components (PCs) had an Eigen value greater or nearer to 1. As a result, these five PCs were given due consideration for additional explanation. For the variables under research, the PC-1, PC-2, PC-3, PC-4, and PC-5 genotypes showed 29.82%, 22.489%, 9.008%, 8.366%, and 7.007% variability, in irrigated; variability 19.281%, 17.258%, 12.214%, 10.662% and 8.806% in rainfed; variability 20.056%,

16.165%, 13.144%, 12.268% and 8.905% in TSD conditions respectively. Each subsequent component accounts for as much of the remaining variability in the data as possible, with the first and second PCs accounting for as much as possible in all three conditions.

The factor loading for thirteen yield-related traits showed in Table 6. Only the most highly loaded factors were retained for further analysis within each PC. From the complex matrix it was revealed that the PC-1 (first PC) accounted for the highest variability (29.82%) was mainly related to traits like biological yield per plot and plant height in irrigated condition; variability in rainfed (19.281%) and TSD (20.056%) was mainly related to traits like total number of grains per panicle and number of filled grains per panicle in both rainfed and TSD conditions. Table 7 showed the top ten (bold values).

Principal Component scores for all genotypes, split down into five principal components. These scores can be used to develop exact selection indices, the intensity of which is determined by the variability described by each principal component. A high PC score for a given accession in a certain component indicates that the variables in that genotype have high values. It was revealed in the results that Bhurma tripal (2.976), Kali Mai (3.131) and Khurabal (3.598) had the best PC score in PC-1; Kali Mai (6.564), Tedesi (3.120) and Bisni (4.482) in PC-2; Basa bhog (2.824), Swarna (13.872) and Khurabal (2.183) in PC-3; Mahamaya (3.118), Hathi panjara (3.260) and Roti (3.186) in PC-4, and Moroberekan (2.053), Roti (3.435) and Barangi (2.484) in PC-5 under irrigated, rainfed and TSD conditions respectively.

The results were found in agreement with Raj *et al.*, 2020 and Burman *et al.*, 2021 revealed that first PC showed the most variability among the five principal components, all of the principal components contributed positively to yield and its contributing traits. As a result, Tarunbhog, Safri 17 and Basmati 370 are the common genotypes with high PC1 scores and highly correlated with yield component traits under RF and TSD conditions.

Hence, selecting these genotypes would result in higher yield and yield related traits under drought condition.

The PCA emphasizes the features with the maximum variability. As a result, intensive selection processes can be developed to improve yield and yield-related traits rapidly. PCA can also be used to rank genotypes based on PC scores in the corresponding component. The results showed that the selected accessions might be utilized as donors in a varietal development programme to improve yield attributes.

### Conclusion

Both multivariate statistical analysis tools showed the existence of the wide genetic diversity among the germplasm lines in the study. In accordance with the current findings, the cluster-I have more genetic variability in specific conditions. Hence, the genotypes present in this cluster could be selected as parents in future breeding programmes. The traits biological yield per plot, grain yield per plot, number of tillers per m<sup>2</sup> and total number of grains per panicle revealed that, they play a crucial role in genetic divergence among fifty-two rice genotypes and we would select these traits of rice lines for the diversity purpose. PCA revealed that, PC1 was dominated by the yield and yield contributing traits such as biological yield per plot and plant height under IR condition and the traits total number of grains per panicle and number of filled grains per panicle under both RF and TSD conditions. So, selecting the germplasm lines with a high score in PC1 could result in greater yield and yield related characters.

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### Conflict of interest

The authors declare that they have no conflict of interest.



## References

- Amegan, E., Efishure, A., Akoroda, M., Shittu, A., & Tonegnikes, F. (2020). Genetic Diversity of Korean Rice (*Oryza sativa* L.) Germplasm for Yield and Yield Related Traits for Adoption in Rice Farming System in Nigeria. *International Journal of Genetics and Genomics*, 8(1), 19-28.
- Bekis, D., Mohammed, H., & Belay, B. (2021). Genetic divergence and cluster analysis for yield and yield contributing traits in lowland rice (*Oryza sativa* L.) genotypes at Fogera, NorthWestern Ethiopia. *International Journal of Advanced Research in Biological Sciences*, 8(5), 1-11.
- Brejda, J. J., Karlen, D. L., Smith, J. L., & Allan, D. (2000). Identification of regional soil quality factors and indicators: II. Northern Mississippi Loess Hills and Palouse Prairie. *Soil Science Society of America Journal*, 64, 10.2136/sssaj2000.6462125x.
- Burman, M., Nair, S. K., & Sarawgi, A. K. (2019). Genetic Diversity Analysis in Unique Rice (*Oryza sativa* L.) of Chhattisgarh, India. *International Journal of Current Microbiology and Applied Sciences*, 8(11), 1096-1099.
- Burman, M., Nair, S.K., & Sarawgi, A.K. (2021). Principal Component Analysis for Yield and its Attributing Traits in Aromatic Landraces of Rice (*Oryza sativa* L.). *International Journal of Bio-resource and Stress Management*, 12(4), 303-308.
- Dhakal, A., Pokhrel, A., Sharma, S., & Poude, A. (2020). Multivariate Analysis of Phenotypic Diversity of Rice (*Oryza sativa* L.) Landraces from Lamjung and Tanahun Districts, Nepal. *International Journal of Agronomy*, 1-8.
- Gaur, A., Parray, G. A., Shikari, A. B., & Najeeb, S. (2019). Capturing the Genetic Diversity for Grain Quality Attributes in a Set of Temperate Rice (*Oryza sativa* L.) Germplasm by Cluster Analysis and the Assessment of Wx gene Polymorphism. *International Journal of Pure and Applied Bioscience*, 7(3), 67-73.
- Iqbal, T., Hussain, I., Ahmad, N., Nauman, M., Ali, M., Saeed, S., Zia, M., & Ali, F. (2018). Genetic Variability, Correlation and Cluster Analysis in Elite lines of Rice. *Journal of Scientific Agriculture*, 2, 85-91.
- Kumari, N., Kumar, R., Kumar, A., & Singh, U.K. (2019). Principal component analysis of morpho-physiological traits in mutants lines of rice under submerged condition. *The Pharma Innovation Journal*, 8(4), 402-407.
- Raj, P., Kumar, A., Satyendra., Singh, S. P., Kumar, M., Kumar, R. R., Prasad, B. D., & Kumar S. (2020). Principal Component Analysis for Assessment of Genetic Diversity in Rainfed Shallow Lowland Rice (*Oryza sativa* L.). *Current Journal of Applied Science and Technology*, 39(48), 256-261.
- Ricepedia, (2020). Rice as food. <http://ricepedia.org/rice-as-food>.
- Shrestha, J., Subedi, S., Kushwaha, U., & Maharjan, B. (2021). Evaluation of growth and yield traits in rice genotypes using multivariate analysis. *Heliyon*, 7.
- Singh, P., & Narayanan, S. S. (2013). Assessment of Polygenic Variation. *Biometrical Techniques in Plant Breeding*, 15-23.
- Sudeepthi, K., Srinivas, T., Kumar, B. R., Jyothula, D., & Umar, S. N. (2020). Genetic Divergence Studies for anaerobic Germination Traits in Rice (*Oryza sativa* L.). *Current Journal of Applied Science and Technology*, 39(1), 71-78.
- USDA, (2020). Rice Sector at a Glance. <https://www.ers.usda.gov/topics/crops/rice/rice-sector-at-a-glance/>.

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