

Genetic Diversity Analysis for Economic Traits in Advance Breeding Lines of Upland Rice (*Oryza sativa* L.) Germplasm

Reddy Pavankumar¹, Gera Roopa Lavanaya¹, Shaik Ayesha Taranum¹, Ruchi Bishnoi² and Bestha Jaya Sai Krishna¹

¹Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (Allahabad), U.P.

²Department of Genetics and Plant Breeding, Agriculture University, Kota, Rajasthan

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*Corresponding author:

E-mail: pavan7253@gmail.com

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Abstract

The present investigation was conducted on 48 genotypes and 2 check varieties of upland rice (*Oryza sativa* L.) grown in Randomized block design with three replications during *Kharif* 2020, to estimate genetic variability and genetic diversity. Based on the mean performance high grain yield per hill was identified for the genotype SHUATS UPR-48 followed by SHUATS UPR-45. High phenotypic and genotypic coefficient of variation were observed for grain yield per hill and biological yield. High heritability coupled with high genetic advance as percent of mean was observed for plant height, spikelets per panicle, days to maturity, days to 50% flowering, panicle length and flag leaf length indicating that these traits are most probably under the control of additive gene action and hence these traits can be fixed by proper selection. Fifty genotypes were grouped into seven different clusters. Cluster I was the largest consisting of 29 genotypes followed by Cluster III with 9 genotypes and Cluster II consists of 7 genotypes. Clusters IV, VI, VII were monotypic with a single genotype in each cluster. Clusters VII (27.45) and IV (16.16) had significant and high Cluster mean for grain yield per hill. Grain yield per hill (15%) had maximum contribution to genetic divergence followed by test weight (11%). Maximum inter cluster distance was obtained between cluster IV & cluster V (198.51) followed by cluster III and cluster V (124.2). The divergent genotypes from clusters IV and V are SHUATS UPR-38, NDR-97 and SHABHAGIDHAN. Hence, these genotypes can be used as parents for further hybridization to develop new cultivars with broad genetic base.

Key words: D² analysis, Genetic variability, Upland Rice (*Oryza sativa* L.)

1. Introduction

Rice (*Oryza sativa* L.) is the staple food in many parts of the world including many developing countries and considered as a second most important cereal crop after Wheat around the globe. (Akinola *et al.*, 2019). More than 90% of the world's rice is grown and consumed in Asia, where 60% of the world's population lives (Alka and Pandey 2019). Upland rice cultivated in an area of

14 million hectares and share 11% across the globe (FAO, 2019). A major area of upland rice is concentrated in the Eastern states of Orissa, Jharkhand, West Bengal and Assam besides North Eastern states.

In future, cultivation of rice under traditional flooded conditions will not be possible because global agriculture



is now witnessing a severe scarcity of water availability and water resources are depleting at a very rapid pace. Acres of cultivated rice area is diminishing because of low availability of water in order to overcome this situation the most feasible alternative is cultivation of upland rice. It involves growing of rice under non-flooded and non-puddled conditions with the use of external inputs such as supplementary irrigation and fertilizers and aiming at high yields (Maliha *et al.* 2020). This method of growing rice requires approximately 73% less water during land preparation and 56% less during crop growth as compared to lowland system. water limitation in upland rice cultivation approach results in reduction of yield ranging between 15% - 40% which is not acceptable as consumer demand for rice increasing with increasing population. In such circumstances, genetic diversity present among the genotypes acts as very powerful tool for the selection of desired genotypes in breeding programs for increasing yield with low availability of water.

The success of upland rice cultivation is majorly decided by selection of appropriate cultivars. Several biometrical approaches have been shown to be useful in selecting parents for successful hybridization programme. D² analysis has been found most effective and therefore, widely used for the classification of parental lines and it evaluates large number of germplasm lines for genetic diversity. The present study is aimed to identify genetically divergent genotypes for their exploitation in hybridization programmes.

2. Materials and Methods

The present experiment was carried out at Field Experimentation Centre of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology & Sciences, Prayagraj (UP), during *Kharif* - 2020. The

experimental materials comprising of 48 genotypes were grown under Randomized Block Design (RBD) with three replications along with 2 Checks. The experimental field was divided into 3 blocks of equal size with each line containing single genotype which were randomly arranged in each of three replications. The data recorded with 14 characters on the 50 Upland Rice genotypes were subjected to Analysis of Variance (Fisher, 1921), Genetic variability (Burton, 1952), Heritability (Broad sense) (Burton and Devane, 1953), Genetic advance (Lush, 1940 and Johnson *et al.*, 1955), D² Analysis (Mahalanobis, 1928).

In the present study, GCV and PCV were classified according to Sivasubrahmanian and Menon (1973), wherein if coefficient of variation is less than 10%, it is considered low, if it is between 10 and 20 %, it is moderate and at more than 20% it is high.

The study of heritability and GAM was done accordance to the Johnson *et al.*, (1955) classification; as low if (<30%), medium for (30-60%) and high for (>60%).

3. Results and Discussion

The Analysis of Variance for different characters are presented in Table 1. The mean sum of squares for fourteen quantitative traits of 50 upland rice genotypes in the season *Kharif* 2020 showed high significant differences among the genotypes for all the traits at 1% level of significance. This indicates that there was an ample scope for selection of promising lines from the present gene pool for yield and its components. It was observed that most of the traits in advance breeding lines possessed a large amount of genetic variability which gives the surety of these genotypes for being used for the breeding purposes so as to improve the grain yield and its linked attributes. These findings are in accordance with similar findings reported by Mamata *et al.* (2017) and Longjam and Singh (2019).

Table 1: Analysis of Variance For 14 Quantitative Characters of Upland Rice.

Characters	Mean Sum of Squares		
	Replication	Treatments	Error
	(df=02)	(df= 49)	(df=98)
Days to 50% flowering	4.58	48.07**	2.00
Plant height	15.85	696.04**	17.30
Number of tillers per hill	0.26	3.60**	0.60
Number of panicles per hill	0.58	2.78**	0.53
Panicle length	0.51	15.46**	1.06
Flag leaf length	0.27	100.93**	10.78



Flag leaf width	0.00	0.04**	0.00
Spikelets per panicle	0.40	2831.6**	71.81
Spikelet fertility percentage	13.31	77.27**	44.31
Days to maturity	0.98	43.48**	1.73
Biological yield per hill	29.99	231.28**	30.15
Harvest index	1.17	67.30**	18.44
Test weight	0.44	9.81**	1.37
Grain yield per hill	4.85	52.25**	6.54

** indicates 1% level of significance

On the basis of mean performance, the highest grain yield per hill was observed for the Rice genotypes SHUATS UPR-48 (27.45g) followed by SHUATS UPR-45 (21.64g), SHUATS UPR-46 (20.58g), SHUATS UPR-23 (19.64g) and SHUATS UPR-28 (18.49g) as furnished in Table 2. Variation was observed within the mean performance of genotypes which enables the scope for selection for further improvement.

From Table 3, it is evident that phenotypic coefficient of variation values were higher than genotypic coefficient of variation for all the traits under study indicating the influence of environment on studied characters. On an average high phenotypic and genotypic coefficient of variation were recorded for grain yield per hill, biological yield, number of spikelets per panicles suggesting sufficient variability among these characters and thus offer scope for genetic improvement through effective selection. The results are in confirmity with the findings of Anjaneyulu *et al.* (2010), Tiwari *et al.* (2015) and Longjam and Singh (2019).

In the present study estimates of broad sense heritability are computed which includes both additive and non-additive gene effects. Higher values of broad sense heritability for the traits plant height, spikelets per panicle, Days to maturity, days to 50% flowering, Panicle length, flag leaf length, grain yield per plant indicate that these characters are less influenced by environment effect and selection on the basis of phenotypic performance of genotypes would be more efficient in further improvement of these traits. High to moderate heritability for most of the traits in the present study indicated considerable potential for the development of high yielding varieties through desirable selection in succeeding generations. Similar results in rice have been reported by Pratap *et al.* (2018). In the present investigation, High Heritability coupled with high genetic advance as percent mean was

recorded for characters like grain yield per hill followed by number of spikelets per panicle, biological yield indicating that these traits are mostly under the control of additive gene action. Hence, these traits can be fixed by proper selection. Similar results in rice have been reported by Jahan *et al.* (2020).

Diversity analysis carried out for 50 Upland Rice genotypes to understand the degree of divergence in stress environments. It was observed that 50 genotypes were grouped into 7 different clusters based on Mahalanobis D² statistics are presented in Table 4 and Figure 1 (Dendrogram). Among 7 clusters, cluster I had highest number of genotypes (29) followed by cluster III (9 genotypes), cluster II (7 genotypes), cluster V (2 genotypes) On the other hand, cluster IV, VI, VII was monotypic with a single genotype. Guru *et al.* (2017).

Inter and intra cluster distances are furnished in Table 5 and Figure 2. The intra cluster values ranged from 0 to 26.52. The maximum intra cluster distance was observed in cluster III (26.52) followed by cluster I (22.96), cluster II (19.2) and cluster V (9.65). The minimum intra cluster distance for cluster IV, VI and VII exhibited zero. The inter cluster distance differ from 33.72 (between I and IV) to 198.51 (between IV and V). The highest inter cluster distance observed between cluster IV & cluster V (198.51) followed by cluster III and cluster V (124.2), cluster II and cluster V (122.53), cluster I and cluster V (121.29), cluster V and cluster VI (116.83), cluster II and cluster VI (89.51), cluster IV and cluster VII (85.97), cluster V and cluster VII (84.83). Similar results were reported by Shafina *et al.* (2014), Khokhar and Sarial (2016) and Anyoha *et al.* (2018). Clusters VII (27.45) and IV (16.16) had significant and high Cluster mean for grain yield per hill. The percent contribution of 15 biometrical traits of 50 rice genotypes towards genetic divergence was estimated and given in Table 7. The trait grain yield per hill (15%) had maximum



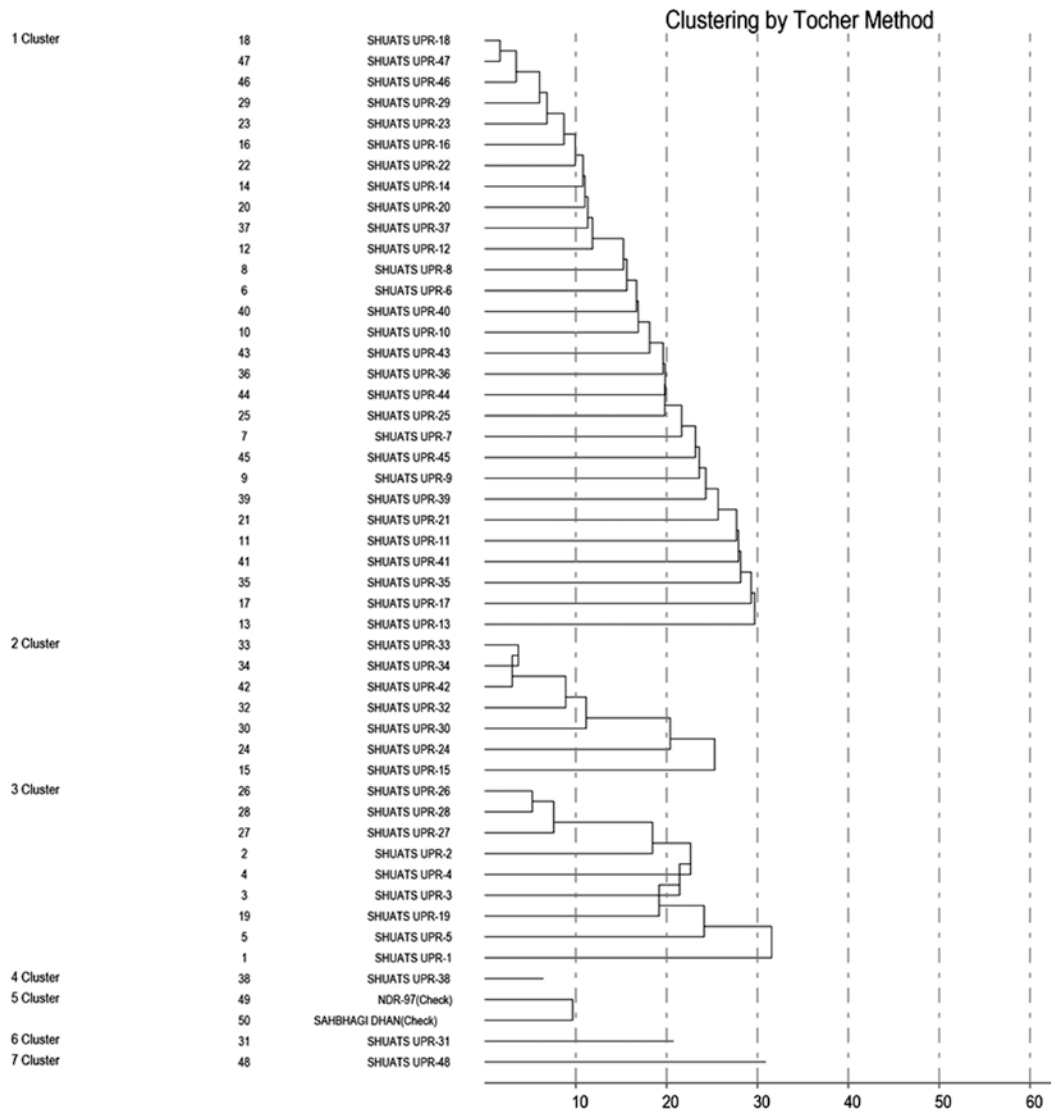


Fig. 1 Clustering by Tocher method

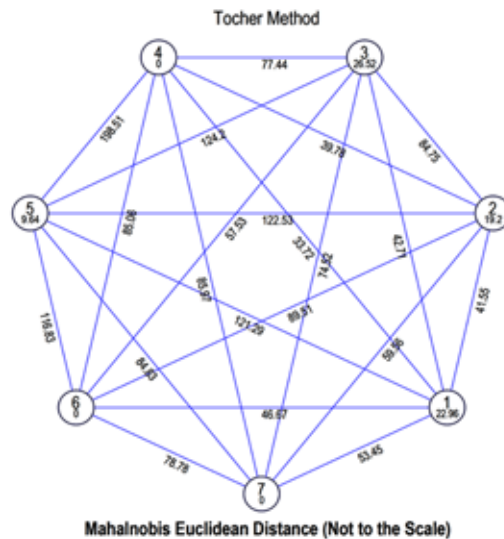


Fig. 2 Cluster diagram for 50 Upland Rice genotypes



Table 2: Mean Performance of 50 Genotypes For 14 Quantitative Characters in Upland Rice

S. NO.	GENOTYPES	DF50	PH	NT/H	NP/H	PL	FLL	FLW	SP	SF%	DM	BY/H	HI	TW	GY/H	GY/H
1	SHUATS UPR-1	68.33	118.16	4.80	4.27	24.51	33.59	1.47	79.33	93.66	98.33	14.96	34.43	21.38	5.13	1.69
2	SHUATS UPR-2	64.33	130.36	5.87	5.27	24.24	47.42	1.41	92.33	93.27	96.33	24.88	48.04	20.89	11.91	3.93
3	SHUATS UPR-3	66.33	125.57	6.93	6.60	21.79	43.35	1.32	108.66	93.43	95.67	31.52	41.56	21.38	12.93	4.27
4	SHUATS UPR-4	68.33	126.38	5.20	4.87	22.50	41.04	1.19	88.93	95.03	98.67	20.85	36.76	19.48	7.55	2.49
5	SHUATS UPR-5	67.00	131.27	4.73	4.47	21.55	43.84	1.22	118.64	92.22	98.33	19.95	33.75	23.18	6.64	2.19
6	SHUATS UPR-6	68.33	158.39	8.07	7.67	23.17	48.88	1.21	104.53	92.13	97.33	39.42	41.88	22.89	16.53	5.46
7	SHUATS UPR-7	67.33	153.58	6.33	5.53	22.20	45.83	1.21	97.26	91.81	96.67	37.07	35.82	21.54	13.28	4.38
8	SHUATS UPR-8	68.33	148.51	5.47	5.27	20.69	51.35	1.13	120.46	91.66	97.00	23.26	49.12	23.80	11.30	3.73
9	SHUATS UPR-9	70.00	155.41	6.27	5.80	22.81	52.49	1.40	101.66	92.56	99.67	36.62	39.26	21.20	14.59	4.81
10	SHUATS UPR-10	71.33	152.24	6.33	6.07	19.93	50.67	1.21	125.33	91.13	102.67	23.27	45.03	22.00	10.53	3.47
11	SHUATS UPR-11	69.33	162.45	6.53	6.33	22.22	46.95	1.18	169.66	90.79	100.67	28.11	42.42	20.94	11.95	3.94
12	SHUATS UPR-12	71.00	151.15	6.47	6.13	22.33	42.81	1.16	112.00	92.39	100.33	30.60	41.64	23.58	12.73	4.20
13	SHUATS UPR-13	66.67	131.51	7.33	6.87	19.45	39.59	1.01	126.56	93.54	97.67	19.11	42.66	24.97	8.18	2.70
14	SHUATS UPR-14	70.33	157.36	6.47	6.20	23.01	41.86	1.05	138.33	92.66	101.33	26.74	38.78	22.90	10.38	3.43
15	SHUATS UPR-15	68.67	138.39	5.87	5.53	22.33	39.23	1.05	189.66	91.00	99.33	19.87	38.54	22.10	7.61	2.51
16	SHUATS UPR-16	67.33	151.23	7.67	7.33	19.97	47.35	1.02	136.56	92.88	98.67	28.63	42.84	24.85	12.68	4.19
17	SHUATS UPR-17	62.33	147.31	7.07	6.07	20.38	46.62	1.03	146.26	91.09	92.33	25.54	39.97	25.14	10.29	3.40
18	SHUATS UPR-18	68.33	147.20	7.53	6.73	22.37	40.63	1.12	151.60	90.87	97.67	34.03	44.13	24.84	15.56	5.14
19	SHUATS UPR-19	67.00	126.56	6.87	6.20	21.91	36.81	1.14	109.66	91.00	96.33	34.37	37.79	21.11	13.04	4.30
20	SHUATS UPR-20	69.33	150.29	7.87	6.93	25.09	45.78	1.04	122.33	88.94	99.33	24.17	47.83	24.16	11.52	3.80
21	SHUATS UPR-21	63.67	156.00	7.13	6.73	22.78	44.73	1.10	131.53	92.35	93.67	44.39	37.95	25.13	16.82	5.55
22	SHUATS UPR-22	64.67	142.67	7.20	6.17	22.97	45.18	1.04	162.46	91.92	96.33	27.34	40.35	21.06	11.16	3.68
23	SHUATS UPR-23	68.00	155.57	8.87	7.93	22.43	46.01	1.15	128.33	92.85	98.00	45.16	43.52	24.72	19.65	6.49
24	SHUATS UPR-24	69.33	150.66	6.80	6.07	27.91	50.91	1.35	146.66	92.68	100.33	23.80	38.87	22.17	9.27	3.06
25	SHUATS UPR-25	66.00	145.02	7.93	6.73	25.53	40.73	1.11	106.66	82.22	94.67	25.00	41.75	21.42	10.44	3.45
26	SHUATS UPR-26	64.33	148.71	7.87	7.27	27.21	45.35	1.18	95.60	91.78	94.00	33.55	40.85	20.57	13.79	4.55
27	SHUATS UPR-27	68.33	152.04	8.33	7.47	27.85	49.89	1.19	78.46	87.24	98.33	46.26	38.55	23.26	17.87	5.90
28	SHUATS UPR-28	65.00	155.07	8.40	7.53	28.55	44.70	1.32	91.00	89.98	95.33	43.54	43.05	19.36	18.49	6.11



29	SHUATS UPB-29	67.00	157.78	8.53	7.93	23.51	45.99	1.06	150.33	93.60	97.33	35.34	45.55	23.89	16.09	5.31
30	SHUATS UPB-30	72.33	160.75	8.87	8.13	25.69	42.15	1.23	188.33	91.10	99.67	44.24	36.67	23.75	16.51	5.45
31	SHUATS UPB-31	74.33	149.62	5.67	4.93	19.05	45.25	1.02	78.66	88.82	103.67	19.47	33.32	18.51	6.61	2.18
32	SHUATS UPB-32	74.67	160.18	8.87	8.33	28.57	47.55	1.12	183.23	91.86	102.67	44.46	41.86	23.41	18.20	6.01
33	SHUATS UPB-33	72.33	164.09	7.73	7.07	26.18	49.07	1.03	179.53	95.73	102.33	36.76	37.19	22.13	13.75	4.54
34	SHUATS UPB-34	72.33	164.29	7.13	6.53	25.05	50.81	1.04	167.46	94.15	102.33	30.87	42.16	23.66	13.06	4.31
35	SHUATS UPB-35	65.67	158.19	7.27	6.47	24.80	49.31	0.96	158.46	89.42	95.33	30.05	50.63	19.85	14.98	4.94
36	SHUATS UPB-36	72.00	139.01	8.07	7.47	24.64	40.43	1.18	121.00	91.75	101.00	24.20	38.27	23.60	9.33	3.08
37	SHUATS UPB-37	72.33	153.35	7.67	6.93	22.66	48.08	1.12	147.66	90.11	101.67	30.63	37.82	24.93	11.60	3.83
38	SHUATS UPB-38	64.00	169.78	8.93	7.67	24.35	49.54	1.07	160.26	92.76	93.67	35.72	45.08	20.98	16.16	5.33
39	SHUATS UPB-39	71.67	166.74	5.93	5.27	25.85	48.59	1.21	121.46	91.78	101.67	30.26	41.96	18.95	12.63	4.17
40	SHUATS UPB-40	72.67	154.24	7.53	6.53	25.12	48.29	1.01	117.66	90.95	102.67	38.28	40.30	21.38	15.42	5.09
41	SHUATS UPB-41	64.00	171.04	7.73	6.47	22.67	48.33	1.05	149.89	98.09	95.33	30.16	39.05	23.15	11.82	3.90
42	SHUATS UPB-42	72.33	170.39	6.93	6.13	25.49	46.01	1.13	177.42	95.31	102.67	36.23	43.79	23.73	15.93	5.26
43	SHUATS UPB-43	70.00	152.34	6.47	5.33	23.08	42.86	1.03	94.62	78.78	100.33	28.99	41.17	22.91	11.97	3.95
44	SHUATS UPB-44	71.67	144.23	7.07	5.93	23.99	34.65	1.01	101.69	86.84	102.33	25.66	43.73	20.06	11.26	3.72
45	SHUATS UPB-45	72.67	155.51	8.80	7.53	25.25	45.04	1.09	98.42	84.07	101.33	45.84	47.32	23.31	21.64	7.15
46	SHUATS UPB-46	67.33	149.61	8.27	6.93	24.51	42.20	1.06	160.96	91.03	97.33	45.56	45.29	24.72	20.58	6.79
47	SHUATS UPB-47	69.67	147.27	7.47	6.67	23.29	38.83	1.07	152.42	93.53	98.67	33.93	46.62	23.90	15.82	5.22
48	SHUATS UPB-48	75.33	135.27	9.07	7.93	25.19	42.85	1.03	149.62	98.91	103.67	53.10	51.79	25.68	27.45	9.06
49	NDR-97(Check)	79.33	106.86	7.33	6.47	21.98	28.30	1.08	126.96	71.38	109.33	23.08	53.80	21.43	12.36	4.08
50	SAHBHAGI DHAN (Check)	83.33	99.68	6.67	6.37	22.46	22.34	1.03	147.29	73.26	113.00	25.70	52.26	22.24	13.26	4.38
	Mean	69.33	147.99	7.20	6.50	23.62	44.20	1.13	130.28	90.73	99.26	31.61	42.06	22.52	13.37	4.41
	C.V.	2.04	2.81	10.7	11.2	4.36	7.43	6.80	6.51	7.34	1.33	17.37	10.21	5.21	19.14	19.1
	S.E.	0.82	2.40	0.45	0.42	0.60	1.90	0.04	4.89	3.84	0.76	3.17	2.48	0.68	1.48	0.49
	C.D. 5%	2.29	6.74	1.26	1.18	1.67	5.32	0.12	13.73	10.79	2.13	8.90	6.96	1.90	4.14	1.37
	Range Lowest	62.33	99.68	4.73	4.27	19.05	22.34	0.96	78.46	71.38	92.33	14.96	33.32	18.51	5.13	1.69
	Range Highest	83.33	171.04	9.07	8.33	28.57	52.49	1.47	189.66	98.91	113.00	53.10	53.80	25.68	27.45	9.06

DF50: Days to 50% flowering, PH: Plant height, NT/H: Number of tillers per hill, NP/H: Number of panicles per hill, PL: Panicle length, FLL: Flag leaf length, FLW: Flag leaf width, SP: Spikelets per panicle, SPW: Spikelet fertility percentage, DM: Days to maturity, BY/H: Biological yield per hill, HI: Harvest index, TW: Test weight, GY/H: Grain yield per hill



Table 3: Genetic Variability parameters for different quantitative characters in Upland Rice

Characteristics	GCV	PCV	h^2 (bs)	GA	GAM
Days to 50% flowering	5.653	6.01	88.5	7.593	10.953
Plant height (cm)	10.164	10.546	92.9	29.864	20.18
No. of tillers/hill	13.878	17.571	62.4	1.627	22.58
No. of Panicles hill	13.327	17.409	58.6	1.366	21.016
Panicle length (cm)	9.277	10.252	81.9	4.085	17.292
Flag leaf length (cm)	12.402	14.456	73.6	9.687	21.916
Flag leaf width (cm)	9.481	11.666	66	0.18	15.873
Spikelets per panicle	23.282	24.174	92.8	60.176	46.192
Spikelet fertility (%)	3.653	8.197	19.9	3.043	3.354
Days to maturity	3.758	3.986	88.9	7.247	7.301
Biological yield / hill	25.902	31.189	69	14.008	44.315
Harvest index	9.596	14.013	46.9	5.693	13.536
Test weight (g)	7.446	9.089	67.1	2.83	12.566
Grain yield/ hill	29.208	34.919	70	6.727	50.33
Grain yield/ hectore(tons)	29.224	34.929	70	2.222	50.36

Table 4: Distribution of 50 Upland Rice Genotypes into Different Clusters

S.NO.	CLUSTERS	NUMBER OF GENOTYPES	CLUSTER MEMBERS
1	Cluster I	29	SHUATS UPR-18, SHUATS UPR-47, SHUATS UPR-46, SHUATS UPR-29, SHUATS UPR-23, SHUATS UPR-16, SHUATS UPR-22, SHUATS UPR-14, SHUATS UPR-20, SHUATS UPR-37, SHUATS UPR-12, SHUATS UPR-8, SHUATS UPR-6, SHUATS UPR-40, SHUATS UPR-10, SHUATS UPR-43, SHUATS UPR-36, SHUATS UPR-44, SHUATS UPR-25, SHUATS UPR-7, SHUATS UPR-45, SHUATS UPR-9, SHUATS UPR-39, SHUATS UPR-21, SHUATS UPR-11, SHUATS UPR-41, SHUATS UPR-35, SHUATS UPR-17, SHUATS UPR-13
2	Cluster II	7	SHUATS UPR-33, SHUATS UPR-34, SHUATS UPR-42, SHUATS UPR-32, SHUATS UPR-30, SHUATS UPR-24, SHUATS UPR-15



3	Cluster III	9	SHUATS UPR-1, SHUATS UPR-2, SHUATS UPR-3, SHUATS UPR-4, SHUATS UPR-5, SHUATS UPR-26, SHUATS UPR-28, SHUATS UPR-27, SHUATS UPR-19
4	Cluster IV	1	SHUATS UPR-38
5	Cluster V	2	NDR-97, SAHBHAGIDHAN
6	Cluster VI	1	SHUATS UPR-31
7	Cluster VII	1	SHUATS UPR-48

Table 5: Intra (diagonal) and inter cluster average distances of 50 genotypes of Upland Rice

	Cluster Distances						
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	22.96	41.55	42.71	33.72	121.29	46.67	53.45
Cluster 2		19.2	84.75	39.78	122.53	89.51	59.56
Cluster 3			26.52	77.44	124.2	57.53	74.52
Cluster 4				0	198.51	85.06	85.97
Cluster 5					9.64	116.83	84.83
Cluster 6						0	78.78
Cluster 7							0

Table 6: Cluster mean values for grain yield and yield component characters in Upland Rice

Clusters	DF50	PH	NT/H	NP/H	PL	FLL	FLW	SP	SF%	DM	BY/H	HI	TW	GY/H
Cluster 1	68.59	152.25	7.29	6.55	22.99	45.17	1.1	129.52	90.75	98.59	31.63	42.51	22.96	13.47
Cluster 2	71.71	158.4	7.46	6.83	25.89	46.53	1.14	176.04	93.12	101.33	33.75	39.87	22.99	13.48
Cluster 3	66.56	134.9	6.56	5.99	24.46	42.89	1.27	95.84	91.96	96.81	29.99	39.42	21.18	11.93
Cluster 4	64	169.78	8.93	7.67	24.35	49.54	1.07	160.26	92.76	93.67	35.72	45.08	20.98	16.16
Cluster 5	81.33	103.27	7	6.42	22.22	25.32	1.06	137.12	72.32	111.17	24.39	53.03	21.84	12.81
Cluster 6	74.33	149.62	5.67	4.93	19.05	45.25	1.02	78.66	88.82	103.67	19.47	33.32	18.51	6.61
Cluster 7	75.33	135.27	9.07	7.93	25.19	42.85	1.03	149.62	98.91	103.67	53.1	51.79	25.68	27.45

DF50: Days to 50% flowering, PH: Plant Height, NT/H: Number of Tillers per Hill, NP/H: Number of Panicles per Hill, PL: Panicle Length, FLL: Flag Leaf Length, FLW: Flag Leaf Width, SP: Spikelets per Panicle, SF%: Spikelet Fertility Percentage, DM: Days to Maturity, BY/H: Biological Yield per Hill, HI: Harvest Index, TW: Test Weight, GY/H: Grain Yield per Hill

Table 7: Percent contribution of 14 Quantitative characters to divergence

S. No.	Traits	Character Contribution %
1	Days to 50% flowering	3
2	Plant height (cm)	5
3	No. of tillers/hill	1.39
4	No. of Panicles/hill	2
5	Panicle length (cm)	9.96
6	Flag leaf length (cm)	1.18
7	Flag leaf width (cm)	3.76
8	Spikelets per panicle	7
9	Spikelet fertility (%)	9
10	Days to maturity	1.5
11	Biological yield / hill	9
12	Harvest index	8
13	Test weight (g)	11
14	Grain yield/hill	15

contribution towards genetic divergence followed by test weight (11%), panicle length (10%), flag leaf length (1.18%) and spikelet fertility (8%), number of spikelets per panicle (7%), plant height (5%), flag leaf width (4%), biological yield (3%), days to maturity (2%), number of panicles per hill (2%), number of tillers per hill (1%), flag leaf length (1%). Similar results were reported by Umesh *et al.* (2016), Tripathi *et al.* (2017) and Tiruneh *et al.* (2019).

Conclusion

From the present investigation, it is concluded that among 50 genotypes of upland rice, SHUATS UPR – 48 was superior for grain yield per hectare followed by SHUATS UPR – 45 over the check variety NDR-97 a ruling variety of Upland Rice in Uttar Pradesh. Analysis of Variance for fourteen quantitative traits revealed that the mean sum of squares due to genotypes showed high significant differences for all the characters at 1% level of significance. The magnitude of Genotypic Coefficient of Variation and Phenotypic Coefficient of Variation were recorded high for grain yield per hill, biological yield, number of spikelets per panicle. High Heritability coupled with high genetic advance as percent mean was recorded for characters like grain yield per hill followed by number of spikelets per panicle, biological yield, indicating that these traits are mostly under the control of additive gene action. Hence, these traits can be fixed by proper selection. Fifty genotypes were grouped into seven clusters, cluster I was largest consisting of 29 genotypes. High inter cluster distance was found between cluster IV & cluster V (198.51)

followed by cluster III and cluster V (124.2). The divergent genotypes from clusters IV and V are SHUATS UPR-38, NDR-97 and SAHBHAGIDHAN. Therefore, crossing between genotypes with maximum genetic distance can be used in breeding programs to achieve maximum heterosis.

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Author contributions

Conceptualization of research (RP & GRL); Designing of the experiments (RP, SAT & RB); Contribution of experimental materials (RP & GRL); Execution of field/lab experiments and data collection (RP, SAT & BJSK); Analysis of data and interpretation (GRL & RB); Preparation of the manuscript (RP & GRL).

Conflict of interest: No

Declaration

The authors declare no conflict of interest.

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