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## Genetic Diversity Analysis for Yield and Yield Attributing Character in Upland Rice Germplasm (*Oryza sativa* L.)

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### ABSTRACT

The present investigation consists of 52 upland rice advanced breeding lines used for the experiment was conducted during *Kharif*-2018 in randomized block design with three replications at Field Experimentation Centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj (Allahabad). The data were recorded on fourteen quantitative characters to study genetic diversity. Based on the relative magnitude of  $D^2$  values, the genotypes were grouped into seven clusters by Euclidean methods of divergence study. Cluster I consist of a maximum of thirty-one advanced breeding lines, followed by cluster II with thirteen advanced breeding lines, cluster III with four breeding lines and cluster IV, V, VI, VII had one breeding line each. The maximum inter-cluster distance was observed between cluster VII and III followed by cluster VI and III. Thus, the breeding lines from the clusters having maximum inter cluster distance can be selected and used as parents for hybridization programme to develop desirable lines. Maximum genetic divergence was exhibited by panicle length followed by plant height, spikelets per panicle, harvest index and flag leaf length contributed to 95.11% of total divergence which is needed to be focused while selecting parents for hybridization programme.

**Key words:** Upland rice, Clusters, Genetic divergence, Yield, Rice germplasm

Rice is one of the most important food crops and primary source of food for more than one-third of world's population. Rice is a water-loving cereal crop that can grow for long periods of time in standing water as well as in diverse condition ranging from aerobic upland to permanently flooded land. It belongs to the family Poaceae and genus *Oryzae*. It is a self-pollinated crop normally grown as an annual plant. Upland rice is grown in rainfed, naturally well-drained soils without surface water accumulation. It is grown both level and slopy lands in around 15 million hectares globally out of total rice area of 156 million hectares [1]. Major upland rice is in Asia (8.9 million hectares), Africa (3 million hectares) and Latin America (3.1 million hectares). Upland rice comprises 11% of the total global rice production and is cultivated on about 14 million hectares. It is also important in cropping systems, because of the lack of irrigation facilities and lower cost of production [2-3]. Diversity analysis is a useful tool in

quantifying the degree of divergence between the biological population at the genotypic level and to assess the relative contribution of different components to the total divergence both at intra and intercluster levels [4-5]. It also permits to select the genetically diverged parents which can produce new recombinants with desirable traits when they are crossed together. Genetic diversity was very much an important factor for any hybridization program aiming at genetic improvement of yield, especially in self-pollinated crops [6]. Genetic diversity determines the genetic discrimination among the genotypes which is used to select appropriate plant genotypes for hybridization to develop high yielding potential variety [7]. The use of Mahalanobis  $D^2$  statistics for estimating genetic divergence has been emphasized by many workers [8-9].

### MATERIALS AND METHODS

The experiment was laid out in randomized block design with three replications in a plot size of 1×1m at Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (Allahabad), U.P during *Kharif*-2018 to identify genetic diversity for 52 advanced breeding lines. The trial was conducted in clay loam soils. All the

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recommended agronomic practices were followed to raise a normal crop. Data were recorded on five randomly selected plants in each treatment for fourteen characters viz., days to 50 per cent flowering, plant height, number of tillers per plant, number of panicles per plant, panicle length, flag leaf length, flag leaf width, number of spikelets per panicle, spikelet fertility, days to maturity, biological yield per plant, harvest index, test weight and grain yield per plant. The data collected were subjected to analysis of variance as suggested by Panse and Sukhatme [10].

RESULTS AND DISCUSSION

Analysis of variance showed significant differences for all the fourteen characters studied among the advanced breeding lines. Based on D<sup>2</sup> value, 52 genotypes were grouped into seven clusters by Euclidean methods of divergence study. Cluster I consist of a maximum of thirty-one advanced breeding lines, followed by cluster II with thirteen advanced breeding lines, cluster III with four breeding lines and cluster IV, V, VI, VII had one breeding line each. (Table 1).

Table 1 Distribution of 52 Upland Rice Germplasm into Different Clusters

Cluster No.	No. of genotypes	Genotypes included
I	31	SHUATS UPR-37, SHUATS UPR-49, SHUATS UPR-31, SHUATS UPR-48, SHUATS UPR-14, SHUATS UPR-29, SHUATS UPR-20, SHUATS UPR-16, SHUATS UPR-11, SHUATS UPR-6, SHUATS UPR-25, SHUATS UPR-2, SHUATS UPR-8, SHUATS UPR-10, SHUATS UPR-18, SHUATS UPR-32, SHUATS UPR-50, SHUATS UPR-34, SHUATS UPR-47, SHUATS UPR-27, SHUATS UPR-15, SHUATS UPR-19, SHUATS UPR-3, SHUATS UPR-13, SHUATS UPR-1, SHUATS UPR-5, SHUATS UPR-7, SHUATS UPR-9, SHUATS UPR-24, SHUATS UPR-4, SHUATS UPR-51
II	13	SHUATS UPR-45, SHUATS UPR-46, SHUATS UPR-44, SHUATS UPR-43, SHUATS UPR-41, SHUATS UPR-40, SHUATS UPR-39, SHUATS UPR-26, SHUATS UPR-23, SHUATS UPR-22, SHUATS UPR-21, SHUATS UPR-17, SHUATS UPR-35
III	4	SHUATS UPR-12, SHUATS UPR-36, SHUATS UPR-28, SHUATS UPR-52
IV	1	SHUATS UPR-30
V	1	SHUATS UPR-33
VI	1	SHUATS UPR-38
VII	1	SHUATS UPR-42

The intra- and inter-cluster distances are presented in (Table 2). Inter-cluster distance was higher than intra-cluster distance indicating wider genetic diversity among the genotypes. The greater distance between the two clusters indicated wider the genetic diversity between genotypes. The maximum inter-cluster distance was observed between cluster VII and III (1708.70), followed by cluster VI and III (1098.53) and Cluster VII and I (1087.39), indicating wider genetic diversity among the genotypes between these groups

[11]. Therefore, the breeding lines from the clusters having maximum intercluster distance can be selected and used as parents for hybridization programme to develop desirable lines. The minimum inter-cluster distance (D<sup>2</sup>) was observed between cluster IV and I (293.14), followed by cluster VII and VI (308.86) and cluster IV and II (312.49). The breeding lines in these clusters are genetically very close and hence, hybridization among the varieties will not give fruitful results.

Table 2 Intra and intercluster average distances in upland rice germplasm

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	168.82	466.44	347.36	293.14	361.77	367.59	1087.39
Cluster II		208.93	1026.40	312.49	407.46	345.05	493.31
Cluster III			177.88	713.79	580.44	1098.53	1708.70
Cluster IV				0.000	450.45	410.69	623.18
Cluster V					0.000	406.03	641.11
Cluster VI						0.000	308.86
Cluster VII							0.000

Hence, the breeding lines in the cluster VII (SHUATS UPR-42) had wider diversity with cluster III (SHUATS UPR-12, SHUATS UPR-36, SHUATS UPR-28, SHUATS UPR-52) and the breeding lines in the cluster VI (SHUATS UPR-38) had wider diversity with cluster III (SHUATS UPR-12, SHUATS UPR-36, SHUATS UPR-28, SHUATS UPR-52) and these lines may be utilized in further breeding programme for the exploitation of hybrid vigour.

The maximum intra-cluster distance (D<sup>2</sup>) was registered for cluster II (208.93), followed by cluster III (177.88) and cluster I (168.82) indicating hybridization involving genotypes within the same clusters may result in good cross combinations. Hence, selection within these

clusters which would be made use in improvement through inter varietal hybridization [12]. While, the minimum intracluster distance (D<sup>2</sup>) was registered in cluster IV, cluster V, cluster VI and cluster VII (0.000). These genotypes in these clusters are genetically very close and hence, hybridization among the breeding lines will not give productive results.

The contribution of each trait to total divergence is presented in (Table 3). Among the traits studied, panicle length contributed maximum divergence (33.94%) followed by plant height (17.35%), spikelets per panicle (16.29%), harvest index (15.31%), flag leaf length (12.22%), biological yield per plant (2.49%), test weight (0.68%),

grain yield per plant (0.68%), days to 50% flowering (0.45%), flag leaf width (0.38%), days to maturity (0.15%) and tillers per plant (0.08%). The minimum percentage (0.00) of contribution was observed in number of panicles per plant and spikelet fertility. Ovung *et al.* [13] also reported a maximum contribution of plant height and spikelets per panicle. Devi [14] reported that number of spikelets per panicle had maximum contribution and also

reported that in contrast to our results panicle number had no contribution towards the genetic divergence. The traits viz., panicle length followed by plant height, spikelets per panicle, harvest index and flag leaf length contributed to 95.11% of total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population.

Table 3 Percent contribution of 14 characters to genetic divergence

Character	Contribution %	Number of times ranked first
Days to 50% flowering	0.45	6
Plant height	17.35	230
No. of tillers per plant	0.08	1
No. of panicles per plant	0.00	0
Panicle length	33.94	450
Flag leaf length	12.22	162
Flag leaf width	0.38	5
No. of Spikelets per panicle	16.29	216
Spikelet fertility	0.00	0
Days to maturity	0.15	2
Biological yield per plant	2.49	33
Harvest index	15.31	203

In cluster means cluster I showed lowest mean values for days to 50% flowering, number of tillers per plant, number of panicles per plant, biological yield per plant and grain yield per plant (Table 4). Whereas, cluster VII shows highest mean values for days to 50% flowering, plant height, number of tillers per plant, number of panicles per plant, panicle length, flag leaf width, days to maturity, biological yield per plant, test weight and harvest index. Cluster VI shows highest mean values for number of tillers per plant, harvest index and lowest mean value for test weight. Cluster V shows highest mean value for flag leaf length and spikelet fertility. Cluster IV shows high mean value for number of

spikelets per panicle and low mean values for panicle length, flag leaf length, flag leaf width and harvest index. Cluster III showed low mean value for plant height while the cluster II shows low mean values for number of spikelets per panicle and spikelet fertility.

However, clusters V, VI and VII recorded desirable mean value for maximum number of productive traits viz., total spikelets per panicle, spikelet fertility, biological yield per plant and grain yield per plant. Similar results were reported by [15-16] hybridization between the breeding lines of these clusters is useful for the development of the desirable lines.

Table 4 Cluster mean values for different component characters in Upland rice

Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Days to 50% flowering	72.74	78.95	81.25	74.00	77.00	74.33	83.67
Plant height	125.38	144.42	112.00	133.05	134.63	145.37	155.23
No. of tillers/ plant	5.45	5.76	5.90	5.67	5.93	6.20	6.33
No. of panicles/ plant	4.99	5.30	5.40	5.27	5.33	5.80	5.80
Panicle length	21.74	21.79	22.37	19.35	22.82	21.23	23.29
Flag leaf length	33.84	38.24	31.24	29.85	47.06	35.88	39.71
Flag leaf width	1.44	1.47	1.47	1.33	1.36	1.56	1.59
No. of Spikelets/ panicle	128.87	125.82	136.00	190.00	178.67	179.67	175.00
Spikelet fertility	91.70	91.06	91.46	91.10	95.73	92.76	92.53
Days to maturity	100.08	106.05	106.50	100.33	103.00	98.00	108.67
Biological yield per plant	24.80	28.93	30.04	28.98	39.58	31.00	73.45
Harvest index	37.61	38.83	42.39	32.42	43.35	58.62	38.22
Test weight	22.57	21.92	22.36	25.63	23.13	19.98	27.49
Grain yield per plant	9.23	11.12	12.79	9.38	17.14	18.13	28.07

CONCLUSION

The selection of divergent germplasm from the clusters having maximum inter-cluster distances i.e., cluster III and VII (1708.70) would produce a broad spectrum of variability for yield, which can be used for further selection and genetic improvement. So, hybridization between

germplasm of divergent cluster will lead to accumulation of favourable genes in a single variety.

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