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Research Article

Revealing genetic variation and clustering pattern in upland rice using morpho-economic traits

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Abstract

A set of 36 upland genotypes comprising 24 popular short duration ruling rice varieties and 12 mutants derived from cv. Mandakini and Zhu 11-26 was characterized for eight morpho-economic traits including seed yield. The data were analysed using SAS software programme for estimation of Euclidian genetic distance and grouping of test genotypes. Cluster composition was set up for six clusters and the corresponding cluster means for eight morpho-economic traits were derived from mean performance of the test genotypes. Cluster I included all the four top yielding (3260-36kg/ha) test genotypes comprising one mutant of cv. Zhu 11-26 (ORT 39) and three mutants of cv. Mandakini (ORT 35, ORT 11, ORT 30). Besides, it was identified to be the most divergent cluster with high intra-cluster heterogeneity. Cluster II contained almost all popularly known drought tolerant cultivars e.g., Zhu 11-26, Saria, Vandana, Pathara and Vanaprava. Cluster V was highly distant from above clusters and included both the promising widely adaptable standard check varieties e.g., Khandagiri and Subhadra with average productivity more than 3000kg/ha. The above highly divergent upland genotypes with distinct morphological diversity may be combined in hybridization programme for recovery of desirable transgressive segregants that can serve as potential parents to facilitate high resolution QTL mapping and validate candidate genes responsible for quantitative characters.

Key words: Morpho-economic traits, genetic variation, genetic diversity, clustering pattern, upland rice.

Introduction

During the last century, breeding of high yielding varieties alone has contributed nearly 50% of global increase (32mt annually) in food production. It has been estimated that an additional annual increase of 12mt food grains will be needed to meet the global food demand in the coming decades. In this context, India needs to produce 120mt by 2030 to feed its one and a half billion plus population by then (Adhya, 2011). Genetic improvement of rice in India and many other rice growing countries has already achieved yield plateau for medium land irrigated rice ecosystems, but areas pertaining to rainfed rice ecosystems particularly upland situations are constrained with low productivity owing to ecological adversities e.g., erratic rain fall distribution, extremes of temperature or mineral supply either transient or lasting throughout the growing season. Globally, about 100 million people now depend on upland rice as their daily staple food. Almost two-third of the upland rice area is in Asia and in particular Bangladesh, Cambodia, China, India, Indonesia, Myanmar, Thailand, and Vietnam have major area under upland rice. In India, 62% of total area under rice is rain fed (Adhya, 2011). Drought is the predominant cause of yield reduction under rainfed rice production systems, Cultivation of drought tolerant rice varieties can reduce the demand for irrigation water by 50–70%. However, the ongoing breeding strategies have not been able to make any breakthrough to develop drought-tolerant cultivars. The complex nature of drought tolerance, genotype × environment interaction, and the difficulty of effective drought tolerance screening complicate the development of drought tolerant varieties. The existing genotypes are rarely adaptable to pre and post-monsoon drought situation. It has been contemplated that climatic change will compel rice breeders to reorient the breeding strategies and develop high yielding short duration rice varieties to combat the recurrent occurrence of drought in coming years.

Continued human selection and monoculture resulted loss of genes and narrowing of the genetic base of cultivated crops (Fu and Somers, 2009 and Wouw *et al.*, 2009) resulting increased vulnerability of crops to disease epidemics, pest infestation and abiotic stresses. Therefore, genetic resource with broad genetic diversity is a pre-requisite for accelerated genetic improvement of crops. This helps to distinguish the genotypes into genetically close and divergent types. Morphological, biochemical, cytogenetic and molecular markers have been reported to unveil the extent of genetic diversity in crop plants (Mohammadi and Prasanna, 2003). However, many workers have analysed genetic diversity of upland rice based on morpho-economic traits (Chauhan *et al.*, 1994; Patra and Dhua, 2003; Pradhan *et al.*, 2007; Yadav and Sharma, 2010 and Nascimento *et al.,* 2011). Various statistical techniques including numerical taxonomic approaches have been found quite efficient to assess genetic diversity in a set of germplasm lines. Researchers can use this information on genetic dissimilarity to make decisions on selection of superior genotypes for genetic improvement or for use as parents in hybridization programme. In addition, it helps in design of populations for genome mapping experiments. Success rate will improve with the increase of genetic variability. Therefore, an attempt has been made to quantify the magnitude of *inter se* genetic divergence between each pair of test genotypes and identify highly divergent upland genotypes to tailor desirable gene combinations through recombination breeding.

Materials and Methods

A set of 24 popular short duration ruling rice varieties and 12 high yielding mutants derived from cv. Mandakini and Zhu 11-26 (Table 1) was characterized based on eight morpho-economic traits.. The test genotypes were grown in upland condition following Randomized Block Design (RBD) with three replications to assess yield and ancillary traits over two seasons during Pre-Kharif 2013. The crop was raised following recommended package of practices. Observations were recorded on five randomly selected plants from middle row of each plot for all biometric traits except days to maturity and grain yield which were recorded on plot basis, and 100-grain weight, which was taken from random sample of seeds from each plot. The morphological data were subjected to SAS (Statistical Analysis System) software programme (SAS Institute, Inc. Cary. NC, USA, 2010, version 9.3) to estimate Euclidian genetic distance between paired genotypes and clustering of genotypes were done based on Root Mean Square tie distance values between succeeding clusters. Cluster composition was set up for six clusters and the corresponding cluster means for eight agro-economic traits were derived from mean performance of the test genotypes.

Results and Discussion

Rice can effectively survive and grow in a wide range of agro-climatic conditions (Kim *et al.,* 2012). Short duration rice varieties are suitable to combat frequent drought spell spread over seasons. The varieties so far developed are not up to the mark in terms of productivity. The available ruling rice varieties e.g., Khandagiri, Parijat, Udaygiri, Naveen and Nilagiri have practically poor genetic potential for seed yield (<20q/ha) and lack abiotic stress tolerance. However, the local land races e.g., Sathiapia, Kalapank, Saria etc and some of the germplasm lines e.g., Jhu 11-26 and N 22 to name a few, harbour very high degree of tolerance to drought stress. Keeping in view, a number of breeding lines have been developed to recombine desirable genes from diverse sources through hybridization. Besides, several mutant lines of a few popular high yielding short duration rice varieties have been bred at the Dept. of Plant Breeding & Genetics, College of Agriculture, OUAT, Bhubaneswar (Odisha, INDIA) to test the level of genetic potential for productivity under drought stress. In the present pursuit, a detailed study of the phenotypic performance and genetic relationship among 12 mutant lines and 24 popular short duration ruling rice varieties have been carried out based on morpho-economic traits.

Genetic distance: The genotypes which are genetically distant enough with regard to traits contributing sizeable genetic divergence are expected to generate wide range of genetic variation in recombination breeding and pave the way for greater scope for recovery of transgressive segregants (Kole, 2000; Shukla *et al.*, 2006; Sharma *et al.,* 2008). The estimated Euclidian genetic distances (root mean square distance) between all possible paired genotypes involving a set of 36 short duration rice genotypes are presented in Table 2. The genetic distances represented as root mean square (RMS) distance provide a quantified genetic diversity which ranged from 37.2 between var. Sankar and Keshari to as high as 1822.2 in between Vanaprabha and ORT 39 (a mutant of Zhu 11-26). An attempt was taken to identify divergent genotype combinations having RMS distance > 1500.0 (arbitrary limit). ORT 39 maintained very high degree of genetic divergence with most of the test genotypes and it happens to be maximum with Vanaprabha followed by Vandana, Pathara, Zhu 11-26, Saria and Lalitgiri. Besides, ORT 30 (a mutant of Mandakini) was shown to be genetically distant from. Zhu 11-26, Vandana, Vanaprabha, Pathara as well as Saria. Similarly, ORT 11 exhibited appreciably high genetic distance with Vandana, Vanaprabha and Pathara. Zhu 11-26, Pathara, Vandana and Saria are popular for their genetic potentiality to combat drought stresses, but poor in yield performance. Hybridization of so called high yielding divergent mutants (ORT 39, ORT 30 and ORT 11) with either of the above drought tolerant genotypes could be a valid approach for recovery of transgressive segregants with high yield potential and drought tolerance. Vivekanandan and Subramanian (1993) assessed genetic divergence in twenty-eight genotypes of rain fed rice and identified few highly divergent rice genotypes suitable for upland rice breeding.

Clustering pattern: The estimated values of Euclidian genetic distance (Root Mean Square distance) are in turn used to derive Norm RMS tie distance between each paired hierarchical genetic clusters. The details of the step-wise genetic clusters to be joined hierarchically based on RMS tie distance are given in Table 3. The first logical step to construct a dendrogram is to select the paired genotypic combination which has the lowest tie distance. The next follow up step is to choose a genotype which has bit higher value of tie distance with the preceding two variety cluster. This process will continue hierarchically until all genotypes are positioned in the dendrogram (Fig. 1).

In the present investigation, 36 upland test genotypes of rice were distinctly grouped into six broad genetic clusters. Selection of parents should be done from two clusters having wide genetic distance to get more variability and high heterotic effect (Pradhan and Roy, 1990; De and Rao 1987). Cluster-I included four test genotypes e.g., ORT 30,ORT 39, ORT 11 and ORT 35 which were initially separated from rest of the 32 genotypes at a inter cluster tie distance 1.5801 (Table 2). Cluster-II contained six genotypes e.g., Zhu 11-26, Lalitgiri, Saria, Vandana, Pathara and Vanaprabha which are separated at inter cluster tie distance 1.1302. These two highly divergent groups/clusters have high *inter se* divergence as well as either group’s maintained appreciable genetic distance with rest 26 test genotypes. These 26 test genotypes were subsequently clearly distributed into four genetic clusters e.g., Cluster-III, Cluster-IV, Cluster-V and Cluster-VI containing 4, 11, 4 and 7 genotypes respectively at < 0.5 tie distance. Chuahan *et al*. (1994) studied genetic divergence among 44 breeding lines of rain fed upland rice employing Mahalanobis D^2 analysis based on eleven characters; the genotypes were grouped into twelve clusters. Pradhan *et. al.* (2007) assessed nature and magnitude of genetic divergence in 57 genotypes of rice germplasm lines based on 14 agro morphological traits. They showed three multi genotypic and two mono-genotypic clusters using Tocher’s method.

The genotypes in each of the above six genetic clusters had shown high *inter se* genotypic homology; and between any paired genotypes, the tie distance varied from 0.0561 (between Sankar and Keshari in Cluster-IV) to 0.4349 (between ORT 35 with rest of the genotypes in Cluster- I). Among the above six genetic clusters, Cluster III had shown lowest intra cluster tie distance (0.1013), whereas Cluster I exhibited maximum tie distance (0.4349) between its paired genotypes indicating high heterogeneity in its cluster composition.

Cluster mean performance: An effort was made to note agronomic performance of the test genotypes in relation to their distribution in the dendrogram based on agro-economic traits (Table 4). The order of occurrence of the genotypes in the dendrogram was used as a reference for arranging performance values of the accessions for eight agro-morphological traits that were observed in the field. For better clarity, the significantly lower performance values for days to maturity and plant height; and for rest of the morpho-economic traits significantly higher mean values compared to the experimental grand mean are marked astrick (**), as such plant types are of special consideration for rice genetic improvement.

Plant types with early heading, low tillering and heavy panicle are suitable for upland condition (Fukuta *et al*., 2012). The test genotypes had shown wide variation in morpho-economic traits e.g., maturity duration (68-115days), plant height (56-96cm.), tiller number (410-685/m2), panicle length (16-25), number of seeds per panicle (42-115), grain fertility percentage (58.05-95.35%), 100-grain weight (1.75-2.65), and overall seed yield (1780-3600kg/ha). Among the rulling varieties and land races; Subhadra and Khandagiri had shown seed yield to the tune of around 3000kg/ha and found statistically significant over the grand mean. Hence, these two ruling varieties could be considered as the best check varieties to compare yield performance of the mutants.

Cluster I included all the four promising high yielding mutants(ORT35, ORT 11, ORT 39 and ORT 30) which were the top yielders (3260-3600kg/ha) with significantly higher grain yield at even 1% level of significance as compared to the best standard check varieties as well as their respective parent varieties (Mandakini and Zhu-11-26). Besides productivity, the Cluster-I also exhibited invariably higher mean values for plant height, tillers/m^2, number of grains/panicle, 100-seed weight and fertility percentage compared to rest of the clusters (Table 4). Thus, the study of genetic diversity based on Euclidian genetic distance is effective enough to identify/isolate potential high yielding divergent genotypes from a set of test genotypes. Nascimento *et al.* (2011) observed polymorphism among 11 out of 14 quantitative characters. However, they found that most divergent group among 146 upland accessions showed a higher number of spikelet per plant. Joshi *et al*. (2008) and Pradhan *et.al.* (2007) observed importance of days to 50% flowering and plant height for genetic divergence. Bhardwaj *et al.* (2001) concluded that length: breadth ratio by 100-grain weight and grain yield per plant contributed 80% of total divergence. Osman *et al.* (2012) emphasized importance of plant height, number of tillers per plant and 1000 grain weight as compared to other traits in boosting yield performance of upland rice. Whereas, Sarhadi *et al.* (2009) had shown that cultivars showing more than 100 grains per panicle could be desirable for breeding programme.

Cluster II congregates almost all popularly known drought tolerance donors e.g., Zhu 11-26, Saria, Vandana, Pathara and Vanaprabha. Besides, these genotypes were separated from the rest of the varieties at erstwhile mentioned appreciably high Norm RMS tie distance indicating high genetic divergence with the above four high yielding genotypes as well as the rest of the genotypes included in Cluster III, Cluster IV, Cluster V and Cluster VI. Thus, the genotypes of Cluster II are of immense value for transfer of drought tolerance to the so called above high yielding mutants.

Genotypes under Cluster III, Cluster IV, Cluster V and Cluster VI maintained relatively high homology among themselves as indicated by the *inter se* tie distance discussed earlier. However, average productivity of more than 3000kg/ha was revealed in Cluster V that included both the promising standard check varieties e.g., Khandagiri and Subhadra. These two varieties are popular among the farming community owing to their high productivity *vis -a- vis* higher level of stability of performance over different environments. Such genotypes with stable and moderately high yield performance could serve as valuable genetic material for transfer of stability of performance and yield *per se*. These may be combined with the erstwhile mentioned top high yielding and highly divergent mutants (ORT35, ORT 11, ORT 39 and ORT 30) in hybridization programme for recovery of desirable transgressive segregants. Besides, identification of divergent genotypes with distinctly different morphological traits could be used as potential parents to facilitate high resolution QTL mapping and validate candidate genes responsible for quantitatively agronomic characters (Li *et al.*, 2010).

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Table 1. Details of short duration rice genotypes used in the study.

Sl. No	Genotype	Pedigree	Source
1.	Rudra	Parijat / IET 3225	Rice Res. Station, OUAT, BBSR
2.	Sankar	-do-	-do-
3.	Subhadra	T(N-1) / SR 26B	DLAP, Phulbani(OUAT),Odisha
4.	Heera	CR 404-48 / CR289-1208	Rice Res. Station, OUAT, BBSR
5.	Zhu 11-26	-	DLAP, Phulbani(OUAT),Odisha
6.	Kalinga III	AC 540 / Ratna	Rice Res. Station, OUAT, BBSR
7.	Vandana	C22 / Kalakeri	-do-
8.	ORT 39	Mutant of Zhu 11-26	Deptt. of PB &G, OUAT, BBSR
9.	Sneha	Annada / CR 143-2-2	Rice Res. Station, OUAT, BBSR
10.	Anjali	Sneha / RR 149-1129	-do-
11.	Suphala	T 141 / TN 1	-do-
12.	Khandagiri	Parijat / IR 13429-196-1-20	-do-
13.	Udayagiri	IRAT 138 / IR 13543-66	-do-
14.	Sidhyanta	Jajati / Annapurna	-do-
15.	Jogesh	CR 544-1-3-4 / NDR 1008	-do-
16.	Pathara	CO 18 / Hema	-do-
17.	Lalitgiri	OR 164-5 / IR19661-364	-do-
18.	Annada	MTU 15 / Waikoku	-do-
19.	Ghanteswari	IR 2061-628-1-6-4-3 / N22	-do-
20.	Keshari	Kumar/ Jagannath	-do-
21.	Badami	Suphala / Annapurna	-do-
22.	Nilagiri	Suphala / DZ 192	-do-
23.	Mandakini	Ghanteswari / IR 27069	-do-
24.	Saria	Local upland rice of Odisha	DLAP, Phulbani (OUAT), Odisha
25.	ORT30	Mutant of Mandakini	Deptt. of PB &G, OUAT, BBSR
26.	ORT11	-do-	-do-
27.	ORT 5	Mutant of Mandakini	-do-
28.	ORT 32	Mutant of Zhu 11-26	-do-
29.	ORT 22	-do-	-do-
30.	ORT28	Mutant of Zhu 11-26	-do-
31.	ORT 36	Mutant of Mandakini	-do-
32.	ORT 38	-do-	-do-
33.	Vanaprava	ARC 12422 / ARC 12751	Rice Res. Station, OUAT, BBSR
34.	ORT 8	Mutant of Mandakini	-do-
35.	ORT 35	-do-	-do-
36.	ORT 10	Mutant of Zhu 11-26	-do-

Table 2. Euclidian genetic distance (Root mean square distance) between paired test genotypes

Genotypes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	0.0	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
2	309.4	0.000	.	.	.	.	.	.	.	.	.	.	.	.	.	.
3	260.6	402.8	0.00	.	.	.	.	.	.	.	.	.	.	.	.	.
4	263.0	66.0	344.4	0.000	.	.	.	.	.	.	.	.	.	.	.	.
5	907.0	643.6	1045.7	703.4	0.00	.	.	.	.	.	.	.	.	.	.	.
6	687.5	414.6	816.8	475.1	233.8	0.00	.	.	.	.	.	.	.	.	.	.
7	1036.0	787.1	1189.3	847.8	163.0	378.7	0.00	.	.	.	.	.	.	.	.	.
8	1106.4	840.9	1242.5	901.8	204.5	429.3	113.8	0.00	.	.	.	.	.	.	.	.
9	426.8	138.6	538.8	199.1	508.2	280.3	652.2	704.8	0.00	.	.	.	.	.	.	.
10	116.4	234.4	340.8	204.7	799.0	582.1	925.4	997.9	331.6	0.00	.	.	.	.	.	.
11	185.6	149.9	346.5	123.7	738.1	514.7	870.7	936.1	250.1	99.8	0.0	.	.	.	.	.
12	137.6	439.4	246.8	389.0	1043.7	824.1	1170.3	1242.0	561.1	246.8	316.9	0.0	.	.	.	.
13	168.5	162.5	255.9	110.2	799.4	572.3	939.1	997.7	295.8	147.5	107.9	284.9	0.0	.	.	.
14	414.7	171.0	562.4	227.7	497.7	275.0	631.6	695.3	79.0	309.7	242.4	550.4	309.1	0.0	.	.
15	486.5	281.6	662.4	334.7	430.1	234.3	550.1	625.6	182.1	375.6	328.4	620.2	406.8	114.5	0.00	.
16	1001.6	736.8	1138.9	797.2	98.2	323.7	96.5	109.5	601.0	893.0	831.7	1137.6	893.5	590.8	522.1	0.0
17	807.9	543.0	945.0	603.8	114.4	134.3	250.2	300.9	406.6	700.1	635.8	943.7	698.5	395.1	333.4	198.4

18	158.1		206.4	208.9	150.4	846.2	618.1	986.1	1043.3	340.3	168.1	142.5	257.0	50.1	355.9	454.1	939.8
19	661.7		390.5	792.1	451.3	255.5	60.0	402.4	452.4	256.1	557.8	491.2	798.0	546.5	251.5	212.4	349.2
20	336.3		37.2	432.2	98.4	614.8	386.3	758.0	810.9	107.5	255.2	167.5	466.7	191.8	145.8	258.7	707.6
21	445.7	143.5	533.0	203.7	520.7	291.4	666.1	712.4	55.7	357.1	269.7	576.6	302.0	126.4	227.0	610.5
22	369.7	179.5	557.3	223.7	602.9	374.0	738.8	814.3	154.5	253.0	199.7	513.7	284.8	91.2	153.6	702.9
23	73.0	290.2	325.2	255.3	856.3	641.4	980.4	1054.3	391.6	64.8	154.1	191.8	178.6	368.7	430.4	950.2
24	861.0	635.8	1032.5	693.3	157.5	261.8	194.3	293.3	505.5	749.3	702.8	993.8	778.3	471.8	377.3	208.0
25	689.4	947.2	561.7	888.8	1584.1	1357.1	1718.0	1782.1	1081.0	799.6	849.2	560.8	786.7	1087.9	1171.0	1678.0
26	57.4	264.4	292.4	223.8	852.3	633.3	980.7	1051.5	375.4	59.7	134.7	191.4	141.1	360.2	431.0	946.7
27	481.5	250.0	635.7	302.5	435.1	227.4	567.5	634.6	139.1	370.8	312.7	616.1	384.7	98.9	87.9	528.9
28	584.5	810.1	411.6	750.9	1452.8	1223.6	1592.5	1650.0	945.6	692.3	727.9	472.8	654.4	961.3	1053.3	1546.2
29	675.3	394.2	793.6	455.5	261.8	62.3	407.9	450.0	257.7	571.9	498.8	810.8	552.6	262.8	238.7	349.3
30	630.2	355.5	755.9	416.7	296.9	78.1	438.6	488.8	218.0	525.1	453.5	765.7	511.8	216.4	192.3	386.3
31	234.5	423.7	86.1	366.2	1064.1	834.2	1202.2	1260.6	557.3	323.5	341.3	196.7	269.1	571.6	666.3	1156.8
32	498.9	224.7	623.4	285.9	429.7	202.5	568.7	623.4	89.9	396.6	320.4	633.6	378.0	93.3	139.9	520.6
33	729.2	987.2	601.1	928.7	1624.2	1397.0	1758.0	1822.2	1121.1	839.3	889.1	600.3	826.9	1127.9	1211.1	1718.1
34	126.1	339.8	140.2	283.3	972.6	746.1	1108.7	1171.3	471.1	213.2	242.3	142.4	178.4	477.6	566.1	1066.7
35	391.4	647.7	281.4	589.7	1282.8	1055.8	1416.9	1481.2	781.2	501.4	548.7	271.6	486.9	786.6	870.8	1376.7
36	374.7	181.1	547.2	226.1	533.7	321.1	662.5	733.0	134.7	265.6	216.5	510.1	291.9	70.5	118.2	627.9

Genotypes	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
17	0.0	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
18	744.4	0.0	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
19	159.5	593.1	0.0	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
20	512.9	235.2	361.2	0.0	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
21	417.7	342.9	271.3	112.1	0.0	.	.	.	.	.	.	.	.	.	.	.	.	.	.
22	496.3	334.9	347.0	166.0	203.5	0.0	.	.	.	.	.	.	.	.	.	.	.	.	.
23	757.4	185.4	615.7	312.0	416.3	313.8	0.0	.	.	.	.	.	.	.	.	.	.	.	.
24	171.0	826.0	277.8	608.4	530.8	556.3	802.5	0.0	.	.	.	.	.	.	.	.	.	.	.
25	1481.8	741.3	1332.2	976.2	1081.7	1099.2	750.3	1547.5	0.0	.	.	.	.	.	.	.	.	.	.
26	753.1	145.9	608.1	289.2	396.6	310.4	42.8	805.8	743.0	0.0	.	.	.	.	.	.	.	.	.
27	339.7	431.0	207.6	225.0	183.3	157.7	431.0	401.9	1157.3	425.4	0.0	.	.	.	.	.	.	.	.
28	1350.8	607.0	1199.5	839.3	941.3	972.5	651.1	1429.0	176.7	635.6	1033.1	0.0	.	.	.	.	.	.	.
29	158.7	597.2	59.3	362.9	262.7	365.4	630.9	299.8	1337.3	621.6	223.9	1201.4	0.0	.	.	.	.	.	.
30	190.9	556.7	67.9	324.3	228.6	314.8	584.3	312.3	1295.4	575.9	176.2	1162.0	50.4	0.0	.	.	.	.	.
31	960.7	220.4	811.6	452.0	554.7	559.9	298.4	1040.7	528.7	272.4	645.3	391.7	812.8	772.2	0.0	.	.	.	.
32	323.8	422.5	181.7	192.8	110.5	189.5	456.1	425.3	1160.3	445.3	108.4	1027.7	179.3	135.4	637.5	0.0	.	.	.
33	1521.9	781.4	1372.5	1016.3	1121.6	1142.1	789.9	1587.4	41.5	782.9	1197.4	209.0	1377.3	1335.5	567.9	1200.3	0.0	.	.
34	871.1	136.6	721.5	368.5	476.8	451.6	189.4	941.8	611.6	160.9	548.2	487.7	727.6	685.2	114.4	550.6	651.7	0.0	.
35	1180.8	442.4	1031.6	677.1	783.9	777.9	455.4	1247.3	302.4	444.4	857.2	204.8	1037.5	995.2	236.6	860.2	342.0	311.1	0.0
36	436.3	339.7	296.1	166.4	185.0	39.4	323.4	491.5	1057.9	319.3	117.7	938.2	316.3	269.2	552.5	159.5	1098.0	450.9	757.0

*Average Root-Mean –Square (RMS) distance between genotypes = 664.3293, Range values and RMS distance >1500.0 are marked bold and underlined

Table 3. Details of cluster formation and relative cluster position based on Euclidian RMS tie distance using morpho-economic traits.

Sl. No. of heirarchical Clusters	Clusters joined with*		Frequency (No. of genotypes)	RMS Tie ditance
1	CL2	CL5	36	1.5801
2	CL3	CL7	32	1.1302
3	CL6	CL4	26	0.7422
4	CL8	CL26	15	0.4582
5	CL10	35	4	0.4349
6	CL13	CL9	11	0.3815
7	CL11	CL18	6	0.332
8	CL 24	CL 12	11	0.322
9	CL15	12	4	0.301
10	CL33	28	3	0.2914
11	CL17	24	3	0.2475
12	CL19	CL14	8	0.2393
13	CL23	CL16	7	0.2369
14	CL25	CL21	5	0.1936
15	CL22	34	3	0.1926
16	11	CL31	3	0.1903
17	5	17	2	0.1723
18	CL20	8	3	0.1681
19	CL29	32	3	0.1517
20	7	16	2	0.1453
21	15	27	2	0.1324
22	3	31	2	0.1296
23	1	CL27	4	0.1295
24	CL35	4	3	0.1262
25	14	CL34	3	0.1228
26	CL28	CL30	4	0.1013
27	10	CL32	3	0.0939
28	6	19	2	0.0904
29	9	21	2	0.0839
30	29	30	2	0.0759
31	13	18	2	0.0755
32	23	26	2	0.0645
33	25	33	2	0.0626
34	22	36	2	0.0594
35	2	20	2	0.0561

*Clusters denoted simply by numbers (i.e., the sl. No. of the varieties) indicate single variety clusters at noted RMS (root mean square) tie distance.

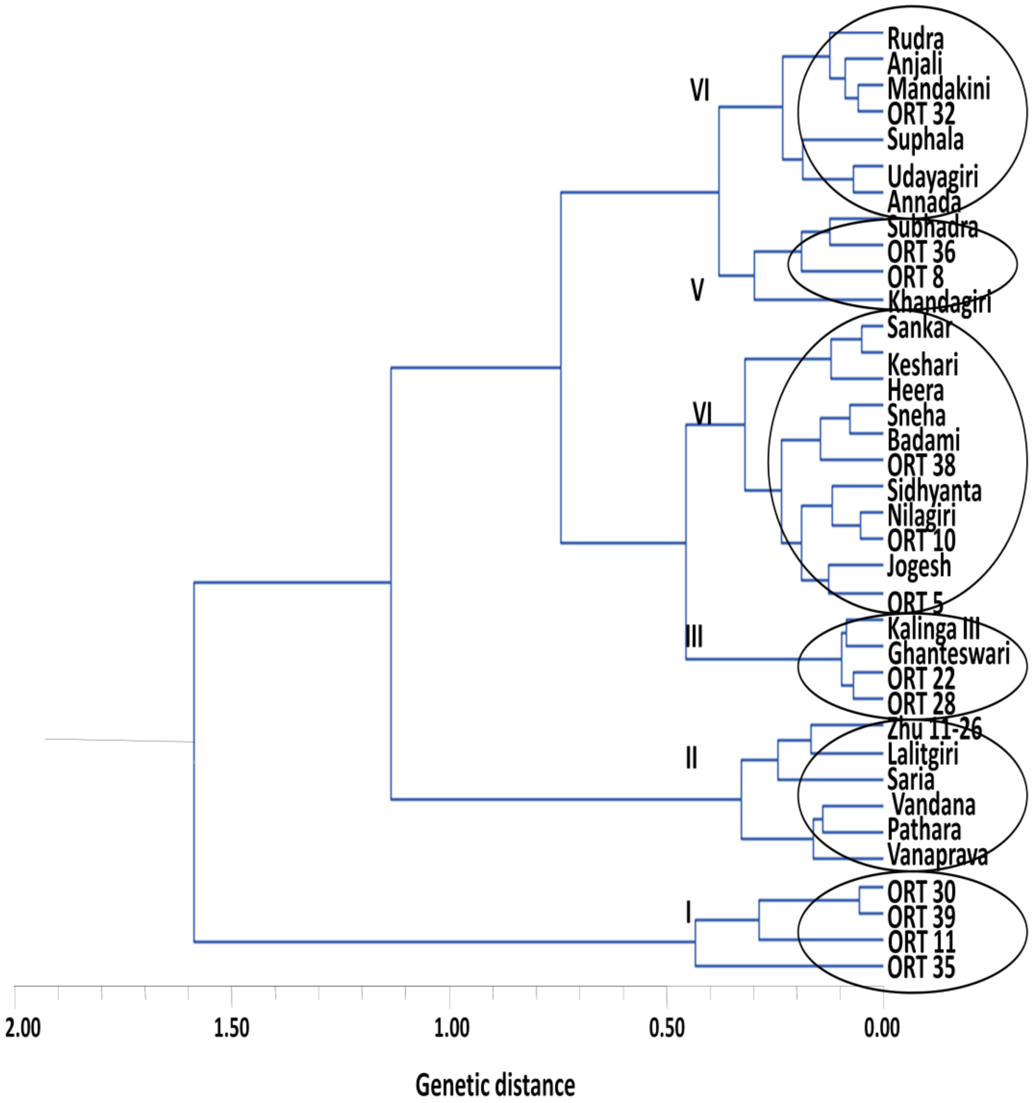

Fig. 1. Dendrogram showing genetic diversity of short duration upland rice genotypes based on morpho-economic traits.

Table 4. Cluster composition and Comparative performance of Upland rice genotypes for morpho-economic traits.

Sl. No.	Clusters	No. of genotypes	Genotypes	Maturity duration (dyays)	Plant height (cm.)	No. of tillers $/m^2$	Panicle length (cm.)	No. of seeds /panicle	Grain Fertility (%)	100-seed wt.(g)	Seed yield (kg/ha)
1.	CLUSTER - I	4	ORT 35	98	84.0	558	23.0**	92**	95.35**	2.35	3260**
			ORT 11	105	72.0	685**	22.0**	92**	88.18	2.34	3420**
			ORT 39	118	82.0	582**	24.2**	112**	92.5**	2.75**	3600**
			ORT 30	125	77.0	580**	23.0**	105**	91.23**	2.65	3560**
	Cluster mean			111.5	78.75	601.25	23.0	100.25	91.815	2.52	3460
2.	CLUSTER - II	6	Vanaprava	105	68.0	505	18.0	68	88.31	2.34	1780
			Pathara	82**	79.0	504	17.0	59	72.83	2.30	1885
			Vandana	102	96.0	420	20.0	73	84.88	2.20	1850
			Saria	88**	78.0	356	22.0**	67	58.05	2.05	2030
			Lalitgiri	95	74.5	515	20.0	86	90.52**	2.12	2080
			Zhu 11-26	80**	62.5**	502	17.5	42	65.62	2.41	1980
	Cluster mean			92.0	76.83	467.0	19.08	65.83	76.70	2.23	1934
3.	CLUSTER - III	4	ORT 28	105	73.0	558	17.5	96**	77.41	2.52	2265
			ORT 22	108	67.0	582**	19.0	86	84.84	2.23	2223
			Ghanteswari	102	56.0**	543	20.5	44	89.87**	2.36	2230
			Kalinga III	70**	92.0	548	21.0	68	81.92	2.25	2205
	Cluster mean			96.25	72.0	557.75	19.5	73.5	83.51	2.34	2230.75
4.	CLUSTER-IV	11	ORT 5	95	76.0	480	19.5	78	81.05	2.26	2410
			Jogesh	103	83.0	423	16.5	76	83.33	2.52	2400
			ORT 10	95	78.0	456	21.0	59	70.23	2.25	5.11
			Nilagiri	106	78.0	455	22.0**	75	82.22	2.38	2540
			Sidhyanta	98	79.0	509	16.5	83	86.45	1.92	2475
			ORT 38	106	74.0	560	18.5	103**	85.21	1.86	2400
			Badami	103	79.0	635**	18.0	90**	84.90	1.96	2480
			Sneha	95	63.0**	585**	17.5	76	75.24	2.42	2480
			Heera	68**	59.0**	608	17.0	57	77.02	2.16	2675
			Keshari	103	66.0	603**	17.0	71	86.42	1.98	2585
			Sankar	88**	74.0	603**	18.5	57	87.69	2.36	2615
	Cluster mean			96.36	73.54	537.90	18.36	75.0	81.79	2.18	2278.6
5.	CLUSTER -V	4	Khandagiri	108	72.0	484	18.0	69	89.61**	2.02	3020
			ORT 8	101	73.0	556	25.0**	82	73.8	2.35	2950
			ORT 36	97	83.0	624**	25.0**	115**	88.46	2.53	3034
			Subhadra	102	66.0	680**	19.0	58	78.37	2.05	3010
	Cluster mean			102.0	73.5	586.0	21.75	81.0	82.56	2.23	3003.5
6.	CLUSTER-VI	7	Annada	100	66.0	595**	18.0	75	84.26	2.52	2820
			Udayagiri	102	67.0	579**	20.0	60	85.71	2.20	2775

	Suphala	92**	63.0**	506	16.0	109**	72.18	1.75	2715
	ORT 32	95	75.0	450	18.0	69	78.40	2.48	2830
	Mandakini	105	70.0	410	19.5	78	83.87	2.15	2830
	Anjali	97	82.0	435	18.0	79	65.28	2.13	2775
	Rudra	90**	68.0	452	18.5	61	89.70**	2.26	2885
Cluster mean		97.29	70.14	489.6	18.29	75.86	79.91	2.21	2804.3
Grand Mean		97.8	74.03	529.9	19.49	76.94	81.97	2.26	2599.5
C.D.1%		5.7	10.3	35.6	2.08	10.8	6.60	0.40	220.0

N.B.: ** - indicates significantly above grand mean value at 1% significance level over the best standard check (Khandagiri)