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Study of Correlation, Magnitude of Genetic Diversity and Selection Indices in Popular Rice (*Oryza sativa* L.) Landraces of Bangladesh

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ABSTRACT: The study was attempted with an objective to evaluate the relationship among yield and yield contributing characters, genetic diversity and selection indices of 76 rice genotypes. Number of tillers plant^{-1}, number of effective tillers plant^{-1} and number of filled grain panicle^{-1} were positively and significantly correlated with yield plant^{-1} suggesting that genotypes with high partitioning efficiency gave increase in yield plant^{-1}. Path analysis suggested that number of effective tiller plant $^{-1}$, number of filled grains panicle^{-1} and 1000- seed weight were related to the yield plant^{-1} mostly through their direct effects. The genotypes were grouped into seven clusters based on Euclidean distance following Ward's method and the highest intra-cluster distance was found in cluster VI and inter-cluster distance between the cluster I and VI. Study of selection indices through discriminate functions observed that Bhute shalot possessed the highest selection score index (301.41) and rank as the best followed by Hati bajore, Jamai naru, Bazra muri and Enghi which suggests that the highest scoring genotypes might be recommended for farmer's cultivation for better yield. Among this landraces the superior genotypes may be used in future plant breeding program.

KEYWORDS: Cultivars, Association, Additive genetic model, Environmental fluctuation, D^2-value, Dendrogram, Genetic distance, Genetic gain

1 INTRODUCTION

Rice occupies the unique position in many nations because for its importance in traditional diets and the main source of income of many peoples in the whole world. For many Bangladeshis, it signifies both life and culture. It is deeply ingrained in Bangladesh culture and even the words 'food' and 'rice' are synonymous in Bengali. The wide environmental diversity in Bangladesh, attributed mainly to the considerable variation in topographic and seasonal components, is reflected in the range of rice groups cultivated, *viz.,* transplanted (t.) aus, broadcast (b.) aus, transplanted (t.) aman, broadcast (b.) aman, and boro. Land under cultivation for T. aman, Boro and Aus season is 5.64 million hectares, 4.77 million hectares and 1.11 million hectares, respectively. In rice production ranking Bangladesh stands fourth although in here average production of rice is only 4.32 tons per hectares [1]. A large number of the Bangladeshi farmers are adopted with local landraces and a few landraces have been incorporated into modern breeding programs; the vast majority of traditional Bangladeshi landraces remains uncharacterized and underutilized. Grain yield in rice is correlated with different yield contributing traits. These traits are also correlated between themselves. Therefore, the relationship between grain yield and different contributing traits establishes a complex chain. The complex chain of such relationship is further analyzed in more simple way through path co-efficient. The path co-efficient breaks the correlation co-efficient of the yield with its contributing traits into direct and indirect effects. Such analysis reflects light on the real causes of relationship. As the yield is influenced by its components characters, therefore direct selection for yield is often misleading. The technique of discriminate function developed by Fisher [2] and adopted for selection by Smith [3] is useful in improvement of yield by combination characters. For improving yield, selection index is superior on the basis of yield alone. Therefore, discriminate function based on important characters for selection has proved to be very useful in plant to discriminate undesirable genotypes on the basis of their performance. Genetic diversity represents the heritable variation within and between populations of organisms [4]. Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains. When uniformity becomes the cause of genetic vulnerability, genetic diversity is the only insurance against it [5]. Therefore, the aim of the present study was to provide genetic variation and relatedness of some rice genotypes through phenotypically and conservation of their diverse gene pool.

2 MATERIALS AND METHODS

The experiment was conducted at the experimental farm of Bangladesh Institute of Nuclear Agriculture, Mymensingh, during July 2011 to January 2012. Geographically the experimental area is located at $24^{0}75$ N latitude and $90^{0}5$ E longitudes at the elevation of 18 m above the sea level. Fifty four rice landraces (i.e. Dudh kalam, Hati bajore, Malagoti, Kuchra, Enghi, Kajol shail, Hogla, Jamai naru, Hari, Dakh shail, Moina moti, Marish shail, Patnai, Bhute shallot, Kute patnai, Mohini shallot, Moghai balam, Sada gotal, Khak shail, Mohime, Holde gotal, Jota balam, Tilek kuchi, Rani Shalot, Kathi goccha, Bashful balam, Bazra muri, Durga bhog, Kumra ghor, Khainol, Ghunshi, Chinikani, Dhar shail, Khejur chori, Shaheb kachi, Raja shail, Hamai, Mura bajal, Lal gotal, Kalmilata, Volanath, Rupessor, Sylhet balam, Karengal, Kalo mota, Mota aman, Ghochi, Chap shail, Mondeshor, Nona kochi, Ghocca, Tal mugur, Ghigoj and Tor balam) were collected from the farmer's field of southern Bangladesh. Rest of the rice genotypes (21 landraces i.e. Fulkainja, Piarjat, Koicha binni, Lal biroi, Lalanamia, Golapi, Asam binni, Kakua binni, Nona bokhra, Jongli boro, Kashrail, Ledra binni, Nunnia, Rotisail, Genggeng binni, Chinisail, Jolkumri, Ponkhiraj, Mowbinni, Bogi, Kali boro and Binadhan-8) was collected from Plant Breeding Division, Bangladesh Institute of Nuclear Agriculture, Mymensingh. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. The experimental field was divided into three blocks each representing one replication. Each block was then sub-divided in to seventy six plots. The seventy six rice genotypes were placed in each plot. The size of the unit plot was one square meter in size. Row to row and plant to plant distances were 20 cm and 20 cm, respectively in each plot. The genotypic and phenotypic correlations were estimation by the formula suggested by Miller *et al.* [6]. Direct and indirect path co-efficient were calculated as described by Lynch and Walsh [7]. The genotypes were arranged in different clusters followed by the method suggested by Ward's Method based on Euclidean distance and hierarchical cluster analysis. Average intra and inter-cluster distances were calculated as suggested by Singh and Chaudhary [8]. Selection indices were constructed using the methods developed by Smith [3] based on discriminative function of Fisher [2].

3 RESULTS AND DISCUSSION

3.1 ESTIMATION OF CORRELATION CO-EFFICIENTS

Relationship between physiological and yield contributing characters was studied through analysis of correlation between them. Phenotypic and genotypic correlation co-efficient among different yield components of 76 rice genotypes are presented in Table 1. Correlation analysis among yield and its contributing character revealed that the genotypic correlation co-efficient of 19 associations were higher than their phenotypic correlation co-efficient indicating the association is largely due to genetic reason. The phenotypic correlation co-efficient of 20 associations were higher than genotypic correlation indicating suppressing effect of the environment which modified the expression of the characters at phenotypic level. In the present study out of 45 associations 18 associations were significant both at genotypic and phenotypic level. Among the 18 associations, 11 associations were positively significant and the rest 7 were negatively significant. The significant and positive association between the characters suggested additive genetic model thereby less affected by the environmental fluctuation. Besides, 8 relationship were positive and non significant. The positive and non-significant association referred information of inherent relation among the pairs of combination. On the other hand 19 relationship were found negative and non significant. The negative and non significant association referred a complex linked of relation among the pair of combinations. It appears from Table 16 that plant height was positively and significantly correlated with days to 50% flowering and days to maturity. It was negatively and significantly correlated with number of tillers plant^{-1}. Panicle length, effective tillers plant^{-1}, filled grain panicle^{-1}, unfilled grain panicle^{-1} and yield plant^{-1} was negatively correlated with plant height and statistically was non-significant. Finally, Plant height was positively and non-significantly correlated with 1000 seed weight (g). Panicle length was positively correlated with filled grain panicle indicating that long panicle produced more grains. It also showed positive correlation with number of tillers plant^{-1}, effective tillers plant^{-1}, unfilled grain panicle^{-1} and yield plant^{-1}; among this only unfilled grain panicle^{-1} was significantly correlated with panicle length. Days to 50% flowering was positively and significantly correlated with days to maturity, number of filled grain panicle^{-1}, number of unfilled grain panicle^{-1} and 1000 seed weight. It was also negatively and non-significantly correlated with number of tillers plant^{-1}, number of effective tillers plant^{-1} and yield plant^{-1}. Days to maturity was negatively correlated with number of tillers plant^{-1}, number of effective tillers plant^{-1}, number of filled grains panicle^{-1}, number of unfilled grains panicle^{-1} and yield plant^{-1} but positively correlated with 1000-seed weight. Number of tillers plant^{-1} showed significant positive correlation with number of effective tillers plant^{-1} and yield plant^{-1} but negative correlation with number of unfilled grains panicle^{-1}and 1000-seed weight. Present experiment indicated that number of filled grains panicle^{-1} and 1000- seed weight were most important characters which exhibited positive correlation with yield plant^{-1}. The result was supported by Osman *et al.* [9] and Selvaraj *et al.* [10]. Kiani and Nematzadeh [11] also observed that filled grains panicle^{-1} correlated significantly with grain yield.

Table 1. Phenotypic (above) and genotypic (below) correlation co-efficient among different yield components of 76 rice genotypes

Items		Panicle length (cm)	Days to 50% flowering	Days to maturity	Number of tiller plant^{-1}	Number of effective tiller plant^{-1}	Number of filled grains panicle^{-1}	Number of unfilled grains panicle^{-1}	1000 seed weight (g)	Grain yield plant^{-1} (g)
Plant height (cm)	P	-0.138	0.256*	0.255*	-0.254*	-0.204	-0.128	-0.089	0.127	-0.145
	G	-0.145	0.252*	0.237*	-0.264*	-0.206	-0.133	-0.093	0.124	-0.151
Panicle length (cm)	P		-0.090	-0.114	0.165	0.169	0.197	0.313**	-0.078	0.190
	G		-0.104	-0.112	0.163	0.176	0.202	0.317**	-0.079	0.190
Days to 50% flowering	P			0.970**	-0.126	-0.100	-0.421**	-0.245*	0.339**	-0.204
	G			0.986**	-0.126	-0.104	-0.424**	-0.246*	0.342**	-0.207
Days to maturity	P				-0.167	-0.145	-0.483**	-0.247*	0.360**	-0.268*
	G				-0.184	-0.149	-0.492**	-0.252*	0.359**	-0.272*
Number of tiller plant^{-1}	P					0.977**	0.205	-0.048	-0.202	0.384**
	G					0.985**	0.205	-0.050	-0.203	0.382**
Number of effective Tiller plant^{-1}	P						0.237*	-0.079	-0.219	0.417**
	G						0.237*	-0.079	-0.220	0.419**
Number of filled grains panicle^{-1}	P							0.125	-0.431**	0.685**
	G							0.124	-0.436**	0.685**
Number of unfilled grains panicle^{-1}	P								-0.197	-0.042
	G								-0.198	-0.043
1000 seed weight (g)	P									0.127
	G									0.125

** and ** indicates significant at 0.05 and 0.01 probability, respectively*

3.2 ESTIMATION OF PATH CO-EFFICIENT

The relations between grain yield and yield contributing characters were studied in detail by path co-efficient analysis. Yield plant^{-1} being the complex outcome of different characters, was considered as the resultant variable and other characters as causal variable. Estimates of direct and indirect effects of ten yield contributing characters both at phenotypic and genotypic level are shown in Table 2 and Table 3, respectively. Path co-efficient at phenotypic level revealed that number of filled grains panicle^{-1} (0.8218), 1000- seed weight (0.5703), number of effective tiller plnat^{-1} (0.5623), days to 50% flowering (0.1503), panicle length (0.00824) had direct positive effect on grain yield plant^{-1}, indicating these are the main contributors to yield. However, plant height, days to maturity, number of tillers plant^{-1} and number of unfilled grains panicle^{-1} had direct negative effect on grain yield plant^{-1}. Path co-efficient at genotypic level revealed that number of effective tiller plant $^{-1}$ (3.01), days to 50% flowering (2.490), 1000- seed weight (0.585), number of filled grains panicle^{-1}(0.500) and number of unfilled grains panicle^{-1} (0.0246) had direct positive effect on grain yield plant^{-1}, indicating these are the main contributors to yield. However, plant height, panicle length, days to maturity and number of tillers plant^{-1} had direct negative effect on grain yield plant^{-1}. The residual effect at phenotypic level was 0.1989 indicating that the ten characters contributed 80.11% of variability in yield plant^{-1} studied in path analysis. The residual effect at genotypic level was 0.1456 indicating that the ten characters contributed 85.44% of variability in yield plant^{-1} studied in path analysis. The residual effects towards yield plant^{-1} in this study may be due to several reasons such as casual factors (characters) not included in the analysis and sampling errors. Though days to 50% flowering showed direct effects on yield plant^{-1} but its genotypic and phenotypic correlation is negative. It indicates that days to 50% flowering would not be reliable criteria for improving yield plant^{-1}. On the other hand number of effective tiller plant $^{-1}$, number of filled grains panicle^{-1} and 1000- seed weight showed direct effects on yield plant^{-1} and their genotypic and phenotypic correlation is also positive. The above information revealed that number of effective tiller plant $^{-1}$, number of filled grains panicle^{-1} and 1000- seed weight were related to the yield plant^{-1} mostly through their direct effects and this information and the present findings suggest that these characters should be used as selection index for selecting higher yield plant^{-1}. The recent research also emphasized the importance of these characters. Similar results had also been reported by Osman *et al.* [9], Kiani and Nematzadeh [11] and Akhtar *et al.* [12].

Table 2. Partitioning of phenotypic correlations into direct and indirect effects of ten important characters of 76 rice genotypes by path analysis

Characters	Plant height (cm)	Panicle length (cm)	Days to 50% flowering	Days to maturity	Number of tiller plant^{-1}	Number of effective tiller plant^{-1}	Number of filled grains panicle^{-1}	Number of unfilled grains panicle^{-1}	1000 seed weight (g)	Grain yield plant^{-1} (g)
Plant height (cm)	**-0.0546**	-0.00113	0.0384	-0.0432	0.0619	-0.1147	-0.1051	0.00107	0.0724	-0.145
Panicle length (cm)	0.00754	**0.00824**	-0.0135	0.0193	-0.0402	0.0950	0.1619	-0.00379	-0.0444	0.190
Days to 50% flowering	-0.01399	-0.00074	**0.1503**	-0.1644	0.0307	-0.0562	-0.346	0.0029	0.1933	-0.204
Days to maturity	-0.01394	-0.00094	0.1458	**-0.1695**	0.0407	-0.0815	-0.3969	0.0030	0.2053	-0.268*
Number of tiller plant^{-1}	0.0138	0.00136	-0.0189	0.0283	**-0.2438**	0.5494	0.1685	0.00058	-0.1152	0.384**
Number of effective tiller plant^{-1}	0.0112	0.0014	0.0150	0.0246	-0.2382	**0.5623**	0.1948	0.00096	-0.1249	0.417**
Number of filled grains panicle^{-1}	0.0069	0.0016	-0.0633	0.0818	-0.0499	0.1333	**0.8218**	-0.00152	-0.2458	0.685**
Number of unfilled grains panicle^{-1}	0.00049	0.00258	-0.0368	0.0418	0.0117	-0.0444	0.1027	**-0.0121**	-0.1123	-0.042
1000 seed weight (g)	-0.00694	-0.00064	0.0509	-0.0610	0.0492	-0.1231	-0.3542	0.00239	**0.5703**	0.127

Bold figures indicate the direct effect
Residual effect = 0.1989

Table 3. Partitioning of genotypic correlations into direct and indirect effects of ten important characters of 76 rice genotypes by path analysis

Characters	Plant height (cm)	Panicle length (cm)	Days to 50% flowering	Days to maturity	Number of tiller plant^{-1}	Number of effective tiller plant^{-1}	Number of filled grains panicle^{-1}	Number of unfilled grains panicle^{-1}	1000 seed weight (g)	Grain yield plant^{-1} (g)
Plant height (cm)	**-0.271**	0.0037	0.629	-0.641	0.742	-0.619	-0.0665	-0.0023	0.0726	-0.151
Panicle Length (cm)	0.0393	**-0.0254**	-0.259	0.303	-0.458	0.529	0.101	0.0078	-0.0462	0.190
Days to 50% Flowering	-0.0682	0.0027	**2.490**	-2.66	0.354	-0.312	-0.212	-0.0061	0.2002	-0.207
Days to Maturity	-0.064	0.0028	2.46	**-2.70**	0.517	-0.448	-0.246	-0.0062	0.210	-0.272*
Number of Tiller plant^{-1}	0.0714	-0.0042	-0.315	0.497	**-2.81**	2.96	0.103	-0.0012	-0.118	0.382**
Number of effective tiller plant^{-1}	0.0557	-0.0045	-0.259	0.403	-2.77	**3.01**	0.118	-0.0019	-0.128	0.419**
Number of filled grains panicle^{-1}	0.036	-0.0052	-1.05	1.33	-0.576	0.713	**0.500**	0.0031	-0.255	0.685**
Number of unfilled grains panicle^{-1}	0.0252	-0.0081	-0.615	0.681	0.141	-0.238	0.062	**0.0246**	-0.116	-0.043
1000 seed weight (g)	-0.034	0.0020	0.854	-0.970	0.571	-0.662	-0.218	-0.0048	**0.585**	0.125

Bold figures indicate the direct effect
Residual effect = 0.145

3.3 NATURE AND MAGNITUDE OF GENETIC DIVERSITY

Using Euclidean distance following Ward's method, the genotypes were grouped into distinct clusters. Based on D2-value, the genotypes were grouped into seven clusters (Table 4). Cluster VI and VII had same no. of genotypes i.e. eight. The cluster II contained 24 genotypes which is the largest one and the cluster IV contained only six genotypes which is the smallest one. The average intra and inter cluster distances are presented in Table 5. It was observed that inter cluster distance were always higher than those of intra cluster distance. The intra cluster distance of cluster VI had 947.44 which was the highest value and cluster I had the second highest (678.13) intra cluster distance. The mutual relationships among the seven clusters are presented in the diagram (Fig. 1). The averages inter and intra cluster distance (Table 5) have been used to denote cluster distance. The maximum inter cluster distance was observed between genotypes of cluster I and VI (2046.48) followed by clusters II and VI (1751.03). Thus, hybridization among genotypes drawn from these widely divergent clusters with high yield potential would likely to produce heterotic combinations and wide variability in segregating generations.

Table 4. Clustering pattern of 76 rice genotypes based on Euclidean distance following Ward's method and the member present in each respective cluster

Cluster number	Number of genotypes	Percent	Name of genotypes
I	11	14.47	Dudh kalam, Khak shail, Khainol, Hamai, Ghocca, Tal mugur, Tor balam, Fulkainja, Koicha binni, Kashrail, Binadhan-8
II	24	31.58	Hati bajore, Kajol shail, Hogla, Mohini shalot, Sada gotal, Mohime, Holde gotal, Bashful balam, Bazra muri, Kumra ghor, Ghunshi, Shaheb kachi, Raja shail, Mura bajal, Lal gotal, Kalmilata, Volanath, Rupessor, Karengal, Kalo mota, Mota aman, Chap Shail, Mondeshor, Nona kochi
III	9	11.84	Malagoti, Durga bhog, Chinikani, Dhar shail, Ghochi, Jongli boro, Chinisail, Ponkhiraj, Kali boro
IV	6	7.89	Kuchra, Jamai naru, Marish shail, Bhute shalot, Rani shalot, Khejur chori
V	10	13.16	Enghi, Hari, Dakh shail, Moghai balam, Tilek kuchi, Sylhet balam, Piarjat, Lalanamia, Rotisail, Genggeng binni
VI	8	10.53	Moina moti, Jota balam, Lal biroi, Golapi, Kakua binni, Ledra binni, Nunnia, Bogi
VII	8	10.53	Patnai, Kute patnai, Kathi goccha, Ghigoj, Asam binni, Nona bokhra, Jolkumri, Mowbinni

Table 5. Average intra and inter cluster D2 and D values of seven clusters

Cluster	I	II	III	IV	V	VI	VII
I	**678.13** (26.04)	891.95 (29.87)	1044.22 (32.31)	1005.34 (31.71)	1287.58 (35.88)	2046.48 (45.24)	1264.41 (35.56)
II		**455.26** (21.34)	799.49 (28.28)	374.74 (19.36)	1179.38 (34.34)	1751.03 (41.85)	866.85 (29.44)
III			**527.15** (22.96)	772.60 (27.80)	806.73 (28.40)	1307.28 (36.16)	726.14 (26.95)
IV				**189.89** (13.78)	929.17 (30.48)	1264.72 (35.56)	620.99 (24.92)
V					**394.24** (19.86)	852.00 (29.19)	456.75 (21.37)
VI						**947.44** (30.78)	828.93 (28.79)
VII							**331.96** (18.22)

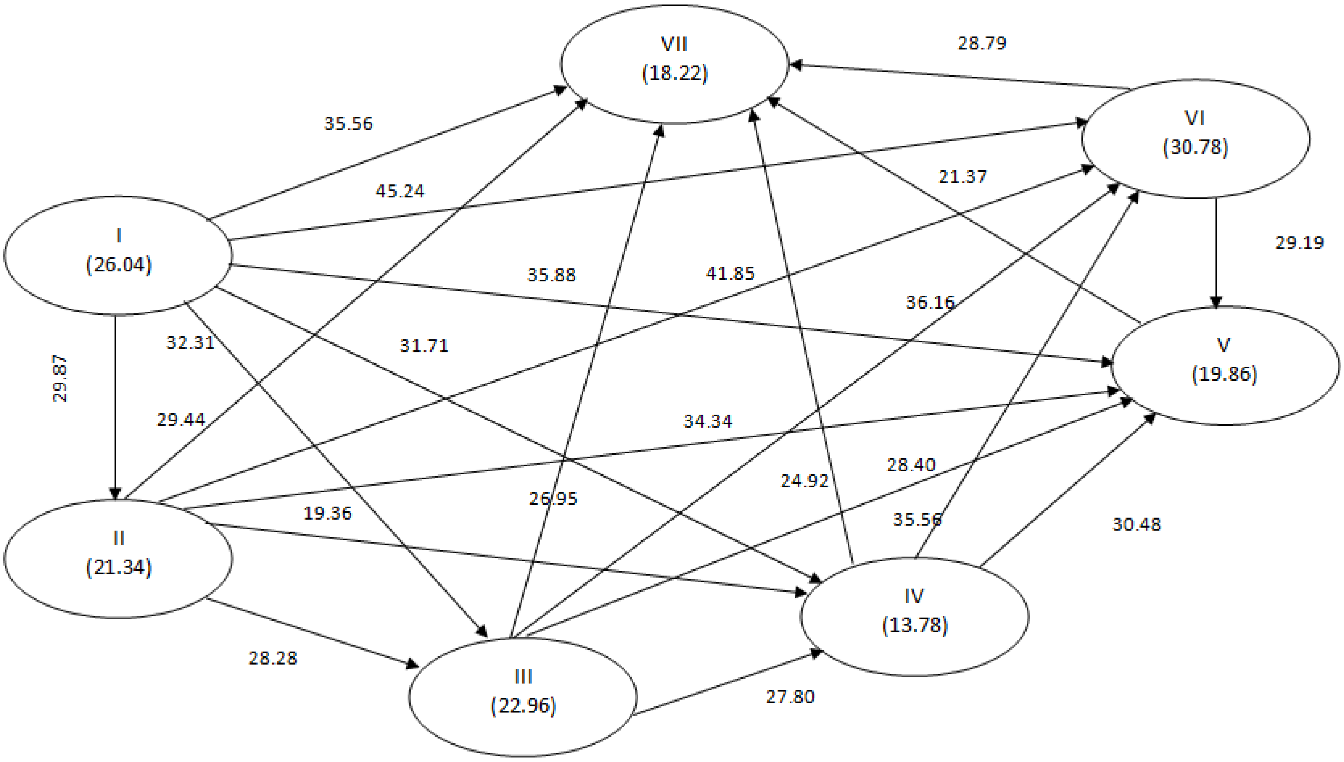

Fig. 1. Cluster diagram showing the average intra and inter cluster distances (D = $\sqrt{D^2}$ values) of 76 rice genotypes. The values along the lines inter cluster distances and the values within the circle indicate intra cluster distance

3.4 NATURE AND MAGNITUDE OF GENETIC DIVERSITY

Dendrogram based on Ward's method indicated grouping of 76 genotypes of rice into seven clusters (Fig. 2). Genetic distance of cluster I, cluster II, cluster III, cluster IV, cluster V, cluster VI and cluster VII was 26.04, 21.34, 22.96, 13.78, 19.86, 30.78 and 18.22, respectively. Highest genetic distance (30.78) was present in cluster VI and the lowest (13.78) was in Cluster IV. The mean values of each cluster for eleven characters are presented in Table 6. There was wide range of variation in the cluster mean values for all the characters. The mean values of all characters for the respective character were categorized into low (L), intermediate (I) and high (H) classes. With regards to plant height, cluster V showed low value (129.10 cm). Cluster I, II, III, VI and VII showed intermediate values (138.82 cm, 143.63 cm, 145.51 cm, 135.37 cm and 146.05 cm respectively) and cluster IV showed high value (146.83 cm). In panicle length, cluster VII showed low value (23.92 cm) and cluster V showed high value (27.67 cm). Cluster I required minimum (100.18) days for 50% flowering, cluster IV required maximum (134.83) days for 50% flowering and cluster II, III, V, VI and VII showed intermediate values (101.77-126.0). With regards to days to maturity, cluster I required minimum days (140.18) for maturity and cluster IV required maximum days (172.16). In number of tiller plant^{-1}, cluster VII showed low value (11.92) and cluster VI showed high value (19.60). In number of effective tiller plant^{-1}, cluster VII showed low value (11.52) and cluster VI showed high value (18.95). With regards to number of filled grains panicle $^{-1}$, cluster II showed low value (92.27) and cluster VI showed high value (167.42). For number of unfilled grains panicle $^{-1}$, cluster I showed high value (44.15) and cluster VII showed low value (20.5). With regards to 1000 seed weight, cluster IV showed high value (27.25 g) and cluster III showed low value (18.27 g). With regards to yield plant^{-1}, cluster VI showed high value (48.71 g) and cluster III showed low value (21.45 g).

Table 6 . Cluster mean for 10 yield and yield related characters in 76 rice genotypes

Characters	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**
Plant height (cm)	138.82 (I)	143.63 (I)	145.51 (I)	146.83 (H)	129.10 (L)	135.37 (I)	146.05 (I)
Panicle length (cm)	27.18 (I)	24.73 (I)	24.22 (I)	26.74 (I)	27.67 (H)	25.72 (I)	23.92 (L)
Days to 50% flowering	100.18 (L)	126.0 (I)	101.77 (I)	134.83 (H)	111.50 (I)	107.50 (I)	108.87 (I)
Days to maturity	140.18 (L)	165.87 (I)	142.11 (I)	172.16 (H)	151.30 (I)	145.87 (I)	146.62 (I)
Number of tiller plant^{-1}	13.74 (I)	12.39 (I)	13.39 (I)	16.10 (I)	12.84 (I)	19.60 (H)	11.92 (L)
Number of effective tiller plant^{-1}	12.60 (I)	11.68 (I)	12.49 (I)	15.30 (I)	12.44 (I)	18.95 (H)	11.52 (L)
Number of filled grains panicle^{-1}	109.67 (I)	92.27 (L)	130.59 (I)	102.96 (I)	166.86 (I)	167.42 (H)	149.48 (I)
Number of unfilled grains panicle^{-1}	44.15 (H)	23.84 (I)	24.46 (I)	20.67 (I)	27.66 (I)	22.29 (I)	20.5 (L)
1000 seed weight (g)	25.46 (I)	26.69 (I)	18.27 (L)	27.25 (H)	22.20 (I)	20.41 (I)	25.92 (I)
Grain yield plant $^{-1}$ (g)	28.62 (I)	24.47 (I)	21.45 (L)	32.91 (I)	40.42 (I)	48.71 (H)	40.80 (I)

H= High value
I= Intermediate value
L= Low value

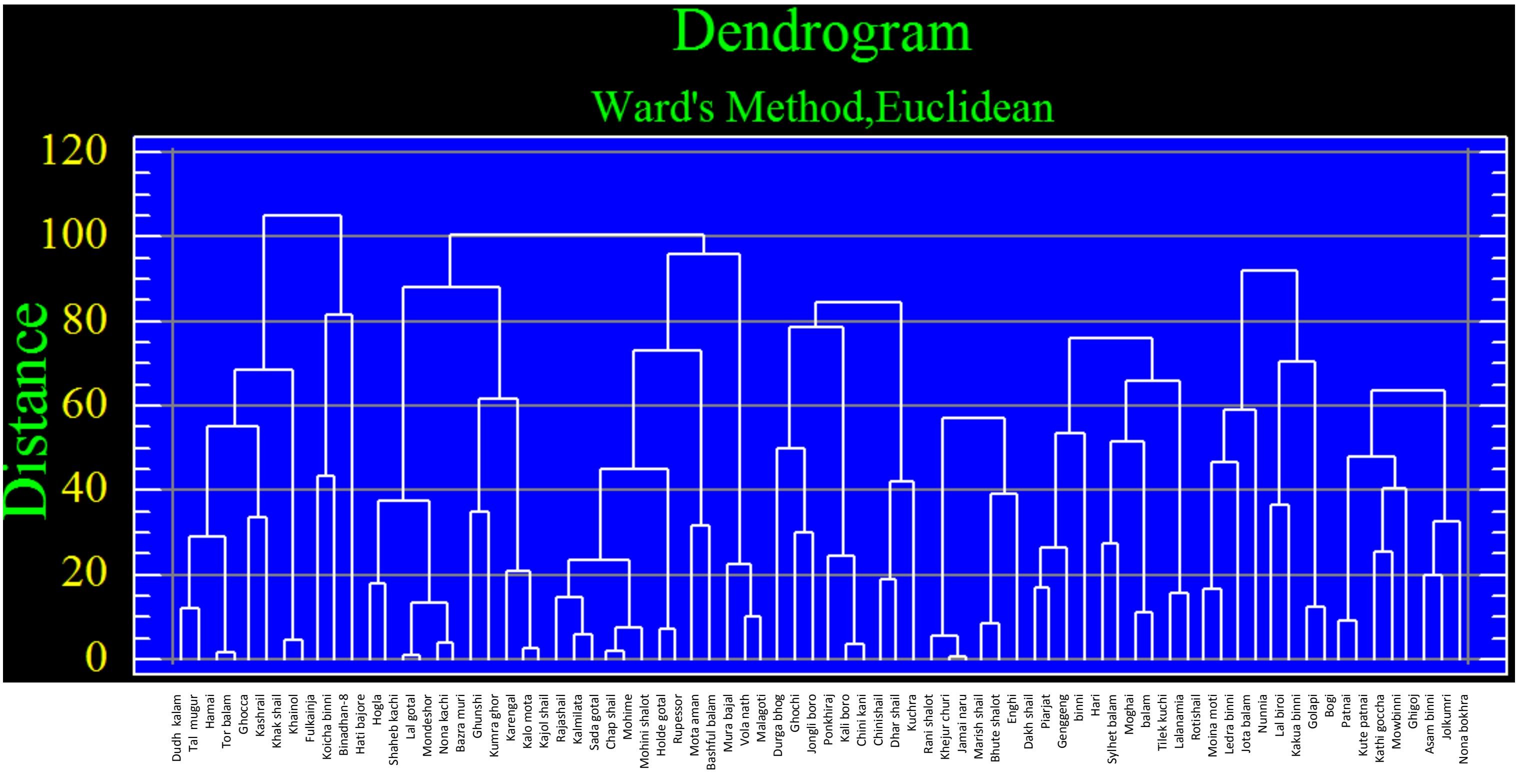

Fig. 2. Dendrogram based on summarized data on differentiation among 76 genotypes of rice according to Ward's method

3.5 SELECTION INDEX

Selection index was constructed to identify suitable genotypes among 76 genotypes of rice in order to recommendation for farmers' cultivars, following simultaneous selection model, considering 10 characters (Table 7). Among the genotypes studied Bhute shalot possessed the highest selection score index (301.41) and rank as the best followed by Hati bajore, Jamai naru, Bazra muri and Enghi with selection score 300.08, 299.73, 299.56 and 293.30, respectively. The genotype Binadhan-8 was the worst having the lowest selection score of 207.29 followed by Rupessor (233.82) and Ghigoj (235.45). The expected genetic gain (ΔG) was 37.32 at 5% selection intensity i.e. 3-4 highest scoring genotypes from these 76 rice genotypes might be recommended for farmers' cultivation for better yield.

Table 7. Selection score, rank and expected genetic gain of 76 genotypes of rice considering ten characters

Genotype Sl. No.	Genotypes	Score	Rank order	Expected genetic advance
14	Bhute shalot	301.41	1	37.32
2	Hati bajore	300.08	2	
8	Jamai naru	299.73	3	
27	Bazra muri	299.56	4	
5	Enghi	293.30	5	
26	Bashful balam	288.92	6	
10	Dakh shail	287.41	7	
7	Hogla	286.87	8	
52	Tal mugur	286.39	9	
69	Genggeng binni	283.47	10	
3	Malagoti	283.34	11	
50	Nona kochi	282.98	12	
24	Rani shalot	282.13	13	
4	Kuchra	281.96	14	
30	Khainol	281.50	15	
62	Kakua binni	279.28	16	
54	Tor balam	277.98	17	
34	Khejur chori	277.97	18	
61	Asam binni	277.48	19	
57	Koicha binni	276.94	20	
15	Kute patnai	276.50	21	
49	Mondeshor	276.22	22	
56	Piarjat	275.75	23	
35	Shaheb kachi	273.81	24	
12	Marish shail	273.70	25	
48	Chap shail	273.52	26	
31	Ghunshi	273.28	27	
22	Jota balam	271.47	28	
51	Ghocca	270.60	29	
13	Patnai	269.09	30	
18	Sada gotal	268.25	31	
40	Kalmilata	268.24	32	
39	Lal gotal	267.83	33	
37	Hamai	267.66	34	
55	Fulkainja	267.35	35	
19	Khak shail	266.06	36	
38	Mura bajal	264.12	37	

Table 7. Continued

Genotype Sl. No.	Genotypes	Score	Rank order	Expected genetic advance
45	Kalo mota	263.76	38	37.32
20	Mohime	263.74	39	
23	Tilek kuchi	261.91	40	
71	Jolkumri	261.58	41	
16	Mohini shalot	260.58	42	
66	Ledra binni	260.41	43	
17	Moghai balam	260.19	44	
9	Hari	258.90	45	
58	Lal biroi	258.55	46	
41	Volanath	258.14	47	
74	Bogi	257.00	48	
1	Dudh kalam	256.59	49	
11	Moina moti	256.55	50	
33	Dhar shail	256.40	51	
25	Kathi goccha	255.95	52	
75	Kali boro	255.23	53	
32	Chinikani	255.22	54	
72	Ponkhiraj	254.92	55	
36	Raja shail	254.14	56	
6	Kajol shail	254.03	57	
65	Kashrail	252.74	58	
47	Ghochi	252.70	59	
59	Lalanamia	252.24	60	
60	Golapi	251.79	61	
29	Kumra ghor	251.35	62	
44	Karengal	250.65	63	
70	Chinisail	250.60	64	
21	Holde gotal	248.72	65	
43	Sylhet balam	247.12	66	
63	Nona bokhra	246.32	67	
64	Jongli boro	246.28	68	
28	Durga bhog	244.57	69	
67	Nunnia	244.56	70	
73	Mowbinni	244.48	71	
68	Rotisail	241.42	72	
46	Mota aman	236.97	73	
53	Ghigoj	235.45	74	
42	Rupessor	233.82	75	
76	Binadhan-8	207.29	76	

4 CONCLUSION

The results clearly revealed that the number of tillers plant^{-1}, number of effective tillers plant^{-1} and number of filled grain panicle^{-1} were positively and significantly correlated with yield plant^{-1} suggesting that genotypes with high partitioning efficiency gave increase in yield plant^{-1}. The maximum inter cluster distance was observed between genotypes of cluster I and VI followed by clusters II and VI. Thus, hybridization among genotypes drawn from these widely divergent clusters with high yield potential would likely to produce heterotic combinations and wide variability in segregating generations. Among 76 genotypes of rice Bhute shalot possessed the highest selection score index (301.41) and rank as the best followed by Hati bajore, Jamai naru, Bazra muri and Enghi with selection score 300.08, 299.73, 299.56 and 293.30, respectively. The expected genetic gain (ΔG) was 37.32 at 5% selection intensity i.e. 3-4 highest scoring genotypes from these 76 rice genotypes might be recommended for farmers' cultivation for better yield or may be used for further varietal improvement program.

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