Genetic diversity of New Plant Type rice selections in relation to *indica, tropical japonicas, temperate japonicas* and irrigated cultures

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ABSTRACT

New Plant Type (NPT) breeding is one of the potential approaches for raising yield ceiling in irrigated rice. Fourty two promising NPT selections along with 6 indica, 4 tropical japonica, 3 temperate japonica and 3 irrigated cultures were studied for the possibility of further exploitation of these lines for breaking yield ceiling. The analysis of variance revealed sufficient variation among the genotypes for all the ten quantitative characters, whereas significant G x E were observed for all the characters except panicle length, flag leaf length and width. High phenotypic (PCV), genotypic (GCV) coefficient of variation and high heritability along with high expected genetic advance were recorded for panicle length, flag leaf length, fertile grains panicle^{-1}, total no. of spikelet, 100 grain wt. and grain yield. Grain yield had positive association for most of the characters except test weight. Higher and positive direct effect on grain yield was exerted by panicle length, no. of fertile grains/panicle and no. of tillers/hill. The D^2 analysis revealed that genotypes exhibited considerable diversity and were grouped in to eight clusters. The clustering pattern indicated that the NPT selections had clustered differently in comparison to the tropical japonicas and temperate japonicas. Canonical analysis with PCA further clarified that most of the NPT selections had sufficient diversity with respect to tropical japonicas, temperate japonicas, derivatives of indica/ temperate japonicas and even specific popular indica varieties. Therefore, NPTs could be potentially exploited for recombination breeding with these genotypes.

Key words: Rice, new plant type, variability, genetic diversity, tropical japonica, temperate japonica

Rice is the most widely consumed staple food for a major part of the world's population, especially in Asia. Around 11% of the arable land is occupied by rice with a total production of 600 million ton representing 21% of the entire calorie supply (Guimaraes, 2009).The UN/FAO forecasts that global food production will need to increase by over 40% by 2030 and 70% by 2050 (FAO, 2009). India occupies the world's largest area under rice with 42.5 million ha and is the second highest producer with106.65 million tonnes (2013-14) followed by China, contributing 21 % of global rice production. It has a vital role in the food and livelihood security of the country. However, productivity of rice is only 2.54 tonnes ha^{-1} as against the global average productivity of 3.28 tonnes ha^{-1} (Anonymous, 2015). Considering the current growth rate in population, the supply projection falls short of expected demand of 121.6 m.

tons by the year 2030, and 137.3 m. tons by the year 2050. This is far below the current growth rate of production (0.36%) in comparison to population growth rate of 1.63% (Anonymous, 2013). In order to achieve this target, the productivity of rice has to be brought to the level of 3.3 tons ha^{-1}, from the present scenario. The irrigated rice has a share of 70% of total rice production in Indian sub-continent, although it has a share of about 50% of total rice area (Singh, 2009). In this context, increasing its genetic potential for higher yield of the cultures would be the key for meeting world rice requirements.

Going through the productivity pattern, a ceiling of grain yield potentiality is mostly reported in semi-dwarf inbred *indicas* since release of IR 8, a variety supposedly initiated green revolution (Peng *et.*

al., 2008). In this context, physiologists hypothesized that this stagnation might be the result of the plant type having high tillering and small panicles. Several unproductive tillers along with lodging susceptibility supposed to limit sink size thereby limiting yield enhancement. Furthermore, these have excessive leaf area that may cause mutual shading and a reduction in canopy photosynthesis and sink size, especially when grown under direct seeded conditions (Dingkuhn *et al*., 1991).

Several approaches were there for raising yield ceiling in irrigated ecosystem, and ideotype breeding is one of the potential approach among them (Dash *et.al*., 2013). New Plant Type (NPT) rice was designed to maximize solar radiation interception, minimize lodging and high response to inputs with a view to improve biomass and harvest index that paves the way for high grain yield. It was conceptualized to break the yield ceiling through modifications of the existing high-yielding *indica* plant type which may result into increment of 30-50% higher yield potential in the late 1980s and early 1990s (Khush, 1995). Earlier approach of recombining characters from different strains of *indica*s or from *japonica*s was not immensely successful in getting a good ideotype raising yield ceiling. Therefore, *Tropical japonica*s specifically *bulu* type germplasm with heavy panicle were thought of becoming a prospective donor for supplementing necessary genes for higher panicle weight, higher culm strength and lower tiller character for proposed ideotype to develop a NPT. IRRI scientists finally developed second generation NPT recombining some suitable features of popular *indica* rice with *tropical japonica*s. However, those 2nd generation NPTs do not perform as per expectation in India. It necessitates the indigenous development of NPTs. In this context, the second generation NPTs were collected in the segregating stage and further selection were exercised to develop fixed lines *i.e*., NPT selections (NPTsl).These NPTsl performed exceptionally well and even some of those showed productivity of more than 10.0 t ha^{-1} during dry season 2011 (Anonymous, 2011-12). Here a study was undertaken to assess the diversity of those NPTsl among themselves as well as from *indica*s, *tropical japonica*s (*Javanica*s) and *temperate japonica*s. This study was necessary because of two reasons. First of all, 2nd

generation NPTs were supposed to be highly potential broad based breeding materials as those have descended from *indica* and *tropical japonica*s. Secondly, the plant type has been modified with inclusion of superior yield traits with subsequent selections. Therefore, the prospect of credible heterosis/ transgressive segregaton was more if NPTsl were chosen as parents in hybridization programme.

Study of diversity is prerequisite to any breeding programme. More heterotic F1s and broad spectrum variability along with transgressive segregants could be obtained by crossing diverse genotypes. In the process of choosing diverse parents, for complementing NPTs, the selection of other parent is really a deciding factor for getting proper recombinants. In this context*, indica*, *tropical japonica*s and *temperate japonica*s along with some promising irrigated cultures were studied for assessing necessary diversity from NPTsl.

MATERIALS AND METHODS

Fifty nine genotypes, including 42 second generation new plant type selections (NPTsl) along with 17 checks/ varieties were evaluated for 10 quantitative traits (Table 1). The checks included seven highly popular *indica varieties* (Annada, Swarna, Naveen, IR64, Lalat, Samba Mashuri and MTU 1010), three *temperate japonica* cultures (Niponnbare, AC105A51 and AC41009), four *tropical japonica* (Azucena, Curinga, EC491229 and EC491403) and three selections from high yielding irrigated genotypes *viz*., IR82489-7-2-2-2-1, CR3855-2-1 and IR77700-84-2-2-2-1. The experiment was carried out for two seasons in the experimental field of the National Rice Research Institute (NRRI), Cuttack during dry and wet seasons of 2011, in randomized complete block design (RCBD) with two replications. Standard cultural practices were adopted. Fertilizer was applied in splits. Full Phosphorus (50 kg ha^{-1} P$_2$O$_5$) and 50% of potassium (25 kg ha^{-1} K$_2$O) were applied as recommended at planting as basal, in transplanted conditions. Rest 50% potassium was applied at panicle initiation stage. Urea was used as source of N in three split doses. The first application was made as basal, with 30 kg N ha^{-1}(25% of total) followed by 60 kg N (50% of total) at active tillering stage and the rest 30 Kg (25% of total) at panicle initiation stage.

Table 1. Details of the genotypes taken up in the experiment

Sl. No	Designation	Category		Sl. No	Designation	Category	
1.	01	IR71700-247-5-3-2-1-2-2-1	NPTsl	31	IR73930-31-3-2-2-20-2	NPTsl	
2.	02	IR71700-5-3-2-1-3	NPTsl	32	IR73930-31-3-2-2-2-2	NPTsl	
3.	03	IR72158-154-3-2-1-1-2-1	NPTsl	33	IR73933-8-2-2-3-5-10	NPTsl	
4.	04	IR72158-68-6-3-3-1	NPTsl	34	IR73933-8-2-2-3-5	NPTsl	
5.	05	IR71701-28-1-4-1	NPTsl	35	IR73930-313-2-2-2-2	NPTsl	
6.	06	IR72158-26-3-2-3-1-1	NPTsl	36	IR73930-313-2-2-1	NPTsl	
7.	07	IR72158-26-3-2-3-3	NPTsl	37	IR73930-41-5-3-1-3-1	NPTsl	
8.	08	IR73933-8-2-2-3-4	NPTsl	38	IR72058-26-3-2-3-6-6-1	NPTsl	
9.	09	IR73995-13-1-3-2-4-1	NPTsl	39	IR71700-247-5-3-2-1-12-1	NPTsl	
10.	10	IR73930-31-3-2-2-2	NPTsl	40	IR71700-5-3-2-2-1	NPTsl	
11.	11	IR73930-31-3-2-2-2-2	NPTsl	41	IR73931-40-1-2-3-2-2-1	NPTsl	
12.	12	IR73896-51-2-1-3-1-1	NPTsl	42	IR73931-40-1-2-3-2-2	NPTsl	
13.	13	IR73896-51-2-1-3-4	NPTsl	43	IR82489-7-2-2-2-1	Selection from Irrigated culture	
14.	14	IR75163-45-2-5-3-5-1-1	NPTsl	44	CR3855-2-1	Selection from Irrigated culture	
15.	15	IR73930-41-5-3-1-3	NPTsl	45	IR77700-84-2-2-2-1	Selection from Irrigated culture	
16.	16	IR72158-154-3-2-1-1-1-3-1	NPTsl	46	Annada	*Indica*	
17.	17	IR74714-141-3-3-2-4-3	NPTsl	47	Swarna	*Indica*	
18.	18	IR72158-148-4-2-6-2-5-5-1	NPTsl	48	Naveen	*Indica*	
19.	19	IR71700-247-5-3-2-1-3-1	NPTsl	49	IR-64	*Indica*	
20.	20	IR71700-247-5-3-2-1-3-1	NPTsl	50	Lalat	*Indica*	
21.	21	IR72158-154-3-2-1-1-1-2-2	NPTsl	51	Samba Mashuri	*Indica*	
22.	22	IR72158-68-6-3-1-1	NPTsl	52	MTU 1010	*Indica*	
23.	23	IR71701-28-1-4-1-1	NPTsl	53	Niponnbare	*Temperate japonicas*	
24.	24	IR72158-68-3-3	NPTsl	54	C 105A51	*Temperate japonicas*	
25.	25	IR73933-106-2-1-2-1-1	NPTsl	55	AC41009	*Temperate japonicas*	
26.	26	IR72158-26-3-2-3-3-2	NPTsl	56	Azucena	*Tropical japonicas*	
27.	27	IR73931-40-1-2-3-2-4-1	NPTsl	57	Curinga	*Tropical japonicas*	
28.	28	IR71700-247-5-3-2-1-5	NPTsl	58	EC491229	*Tropical japonicas*	
29.	29	IR71700-247-5-3-2-1-11-1-3	NPTsl	59	EC491403	*Tropical japonicas*	
30.	30	IR71701-28-1-4-11-1-1	NPTsl				

All plant protection measures were taken as and when required. Weeds were controlled by hand weeding. Observations were recorded for the traits *viz.*, days to 50 % flowering (DFF), plant height (PH), tiller hill^{-1} (T/H), panicle length (PL), flag leave length (FLL), flag leave width (FLW), no. of fertile grains panicle^{-1} (FGP), total no. of spikelets (TNS) , 1000 grain wt. (TGW) and grain yield (GY). The data were analyzed with appropriate statistical analysis (Gomez and Gomez, 1984) using CropStat 7.2 (IRRI, 2009). The genetic parameters including the genotypic and phenotypic coefficients of variation, heritability and genetic advance and correlation coefficients between different characters were computed following Singh and Chaudhury (1985). Multivariate analysis of genetic divergence among varieties was done using Mahalanobis D^2 statistics (1936) and grouping of varieties into clusters by Tochers method (Rao, 1970) followed by the principal component analysis (PCA) using the software Windowstat 9.1 (Indostat Services, Hyderabad, India, 2014)

RESULTS AND DISCUSSION

The three subspecies includes *indica*, *japonica* and *javanica* constitute a huge reservoir of rice germplasm containing varieties of local landraces and cultivars (Londo *et al.*, 2006; Second, 1982). Genetic diversity mostly plays a vital role in developing a promising recombinant or transgreesive segregant. During the process of domestication and cultivation of crop plants, profuse genetic diversity has been utilized and retained to a significant extent. It is estimated that not even 15

percent of the potential diversity has been utilized (FAO, 2002). Numerous valuable allelic variations of traits of economic importance remain unutilized in the available germplasm (Pachauri *et al*., 2013). In this context, genetic diversity plays very important role in rice improvement. Success of a good programme depends on the magnitude of genetic variability and the extent to which the desirable characters are heritable (Ravi *et al*., 2003).

The experiment started with some of the promising NPT selections performed exceedingly well during dry season, 2011. The grain yield along with other quantitative parameters has been depicted in Table 2. Here the study focused upon the traits which were pivotal for realizing such a high grain yield. This would help for trait specific intervention for further improvement towards breaking yield ceiling.

Variability studies indicated that there was sufficient variation among the fifty-nine NPTsl of rice for ten quantitative characters. The analysis revealed

that variance due to treatments was highly significant (Table 3) for all the characters suggesting that there is an inherent genetic difference among all the genotypes.

Significant differences among the genotypes w.r.t. to different seasons were observed for the characters viz., DFF, PH, TH, NFG, TNS, TGW and GY as revealed in the analysis of variance of pooled data (Table 3). But significant differences between the environments were observed only for three characters *viz*., DFF, NFG and TNS. High values of PCV closely followed by GCV recorded in traits *viz*., FLL, FLW, NFG, TNS and GY indicated greater opportunities for desired gain through phenotypic selection and rest of the characters showed moderate to low PCV and GCV values (Table 4). Small differences between estimates of PCV and GCV for most of the traits indicated that lesser influence of environment towards expression of these traits. Similar findings were reported by Mall et al. (2013) and Ubarhande *et al*. (2009). In the present study, genetic advance as % of mean (GA) showed a

Table 2. Performances of best genotypes during dry season, 2011

Genotypes	GY	DFF	PH	TH	PL	FLL	FLW	NFG	TNS	TGW
IR-71700-247-5-3-2-1-3-1	10.91	104.0	108.3	12.2	30.5	33.3	1.50	124.2	155.5	2.00
IR-71700-247-5-3-2-1-3-1	10.82	104.5	116.8	12.6	32.5	42.7	1.42	130.8	152.3	1.77
IR 73930-31-3-2-2-20-2	10.33	94.0	102.05	9.7	29	32.5	1.45	126.9	149.9	2.34
IR-72158-154-3-2-1-1-1-2-2	10.09	106.5	106.1	10.2	28.8	37.3	1.50	122.7	140.4	2.31
IR-72158-68-6-3-1-1	9.69	100.3	104.1	9.9	28.9	34.9	1.48	124.8	145.2	2.32
IR 64	5.48	112.5	89.2	9.1	27.4	28.5	1.57	101.2	116.3	1.93

DFF: Days to 50 % flowering, PH: Plant height (cm), TH: Tiller hill[-1], PL: Panicle length (cm), FLL: Flag leaf length (cm), FLW: Flag leaf width (cm), NFG: No. of fertile grains panicle[-1,] TNS: Total no. of spikelet, TGW: 100 grain wt. (g) and GY: Grain yield (T ha^{-1} extrapolated from g m^{-2} data).

Table 3. Pooled analysis of variance for quantitative traits in 59 rice genotypes

Characters	Replications (1)	Environments (1)	Genotypes (58)	Genotype x Environment (58)
DFF	6.78	40.69**	169.11**	82.12**
PH	22.15	2.97	566.22**	120.31**
TH	5.07	0.01	4.64**	1.68*
PL	19.31	0.28	30.45**	3.97
FLL	39.36	1.48	93.08**	15.87
FLW	0.16	0.03	0.14**	0.045
NFG	68.56	3.94**	988.03**	293.27**
TNS	145.21	70.60**	1188.49**	373.16**
TGW	0.04	0.01	0.24**	0.092**
GY	28680.44	1023.82	137869.05**	22530.1**

DFF: Days to 50 % flowering, PH: Plant height (cm), TH: Tiller hill[-1], PL: Panicle length (cm), FLL: Flag leaf length (cm), FLW: Flag leaf width (cm), NFG: No. of fertile grains panicle[-1,] TNS: Total no. of spikelet, TGW: 100 grain wt. (g) and GY: Grain yield (gm[-2]).

Table 4. Pooled estimates of mean, range, coefficient of variation, heritability and genetic advance for quantitative characters of 59 genotypes evaluated for two seasons

Characters	Mean± SE m	Range		Coefficient of Variation		Heritability (h^2b)	Genetic advance (GA) as per cent of mean (5%)
		Min.	Max.	GCV	PCV		
DFF	101.36±1.17	77.5	128.5	7.29	7.45	95.7	6.64
PH	104.62±4.84	60.35	147.92	12.31	13.94	78.0	22.39
TH	8.63±0.62	5.37	11.65	10.06	13.65	54.3	15.27
PL	27.98±0.95	19.7	32.98	10.18	11.26	81.7	13.23
FLL	34.97±1.96	17.58	42.93	14.18	16.26	89.1	25.48
FLW	1.35±0.09	0.68	1.83	13.97	16.92	68.2	23.78
NFG	102.84±4.37	67.75	150.72	6.59	17.64	88.4	32.12
TNS	125.94±4.85	82.12	174.05	14.74	15.17	87.9	35.85
TGW	2.31± 0.091	1.45	2.99	11.67	12.92	81.6	21.72
GY	622.67±43.89	189.50	998.00	27.22	28.99	88.2	52.66

DFF: Days to 50 % flowering, PH: Plant height (cm), TH: Tiller hill[-1], PL: Panicle length (cm), FLL: Flag leaf length (cm), FLW: Flag leaf width (cm), NFG: No. of fertile grains panicle[-1,] TNS: Total no. of spikelet, TGW: 100 grain wt. (g) and GY: Grain yield (gm-[2]).

wide range in its magnitude. High heritability (h^2b) estimate were associated with the high GA for the traits viz., PL, FLL, NFG, TNS, TW and GY (Table 4). The grain yield demonstrated high estimates of GA coupled with high h^2b values while, rest of the characters recorded values in medium to high range. Similar result reported by Kole *et al*.(2008) supports the present findings. The GA is a potential indicator of the promotion expected due to selection on the relevant population. Heritability associated with genetic advance would give a more dependable indicator of selection value (Johnson *et al*., 1955). This indicated that these yield attributing traits could be selected in effective manner towards very high grain yield in NPT selections/ high yielding

cultures. Other traits obtained with high heritability along with moderate or low genetic advance could be improved by intermating superior genotypes of segregating population developed from combination breeding (Samadia, 2005). But Flag leaf width expressed high estimate of GA with low heritability may be under the control of non additive type of gene action and G x E interaction plays a significant role in the expression of the traits (Iftekharuddaula *et al*., 2001).

Association study at phenotypic level found that all the characters under study except TGW had positive and significant correlation with grain yield (Table 5). However, maximum positive association was recorded by PL followed by TNS, NFG, FLW, FLL,

Table 5. Estimates of phenotypic correlation coefficients between different characters in rice for 59 genotypes considering pooled data across two seasons.

Traits	DFF	PH	TH	PL	FLL	FLW	NFG	TNS	TGW	GY
DFF	1	0.233*	0.188*	0.330**	0.235*	0.293**	0.454**	0.397**	-0.327	0.328**
PH		1	0.182*	0.655*	0.655**	0.386**	0.368**	0.332**	0.126	0.478**
TH			1	0.356**	0.151	0.271**	0.285**	0.312**	-0.085	0.501**
PL				1	0.717**	0.521**	0.539**	0.551**	0.149	0.743**
FLL					1	0.346**	0.380**	0.333**	0.330**	0.513**
FLW						1	0.421**	0.473**	0.213	0.543**
NFG							1	0.923**	-0.076	0.678**
TNS								1	-0.037	0.690**
TGW									1	0.099
GY										1

*Significant at P = 0.05 and ** Significant at P = 0.01

DFF: Days to 50 % flowering, PH: Plant height (cm), TH: Tiller hill[-1], PL: Panicle length (cm), FLL: Flag leaf length (cm), FLW: Flag leaf width (cm), NFG: No. of fertile grains panicle[-1,] TNS: Total no. of spikelet, TGW: 1000 grain wt. (g) and GY: Grain yield (g m-[2]).

TH, PH and DFF. This indicates that phenotypic selection based on these characters could result in an appreciable improvement of GY similar findings were reported by Kole *et al.*(2008).

IIt was always a challenge to have higher grain yield through conventional breeding. In order to have more productivity to break the yield ceiling, one has to concentrate upon few traits, that could be supplemented further through trait specific selection (phenotypic or marker assisted). Therefore, it needs further dissection of the phenotypic association of grain yield into directly or indirect components, for which path analysis were carried out (Fig 1). The trait, PL had the highest positive direct effect towards grain yield, followed by NFG and TH. Coming to the estimation of indirect contribution, it was found that TNS was having highest sum of indirect contributions followed by FLL and PH. This indicated that there should me more emphasis for traits viz., PL, NFG and TH along with FLL, PH and TNS while selection efforts should be made for very high grain yield in NPTsl. However, for plant height one should be cautious because of risk of lodging after a
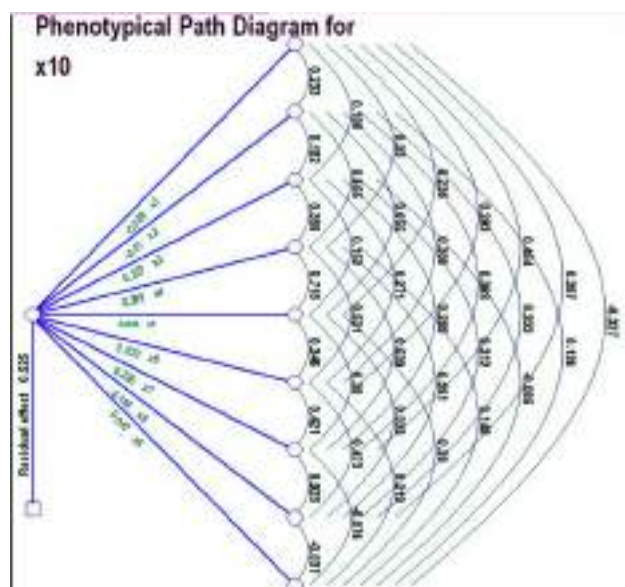

Fig 1. Phenotypic path diagram for grain yield (X10) in relation to other traits viz., Days to 50 % flowering (x1), Plant height (cm)(x2), Tiller hill^{-1}(x3), Panicle length (cm) (x4), Flag leave length (cm) (x5), Flag leave width (cm) (x6), No. of fertile grains panicle^{-1}(x7), Total no. of spikelet (x8), 1000 grain wt. (Grams) (x9).

certain limit. Similar findings w.r.t. panicles m^{-2} (Li *et al.*, 2014), filled grains/panicles (Saikumar *et al.*,2014) corroborates the present findings.

The fifty nine genotypes in the present study could be divided in to eight distinct clusters (Fig. 2). Cluster I consisted of maximum number of genotypes (45) followed by cluster II with 8 genotypes and cluster IV with two genotypes. Other clusters viz., III, V, VI, VII and VIII were represented by single genotype each. It was impressive to note that, the genotypes that originated in one region had been distributed into different clusters. The non appearance of association between genetic diversity and geographic diversity implies that factors other than geographic origin, such as exchange of breeding material, genetic drift, variation, selection are responsible for diversity, as reported earlier (Murthy and Arunachalam, 1966 ; Bose and Pradhan, 2007 and Mall *et al.*, 2013). The *tropical japonicas* and *temperate japonicas* have clustered differently in comparison to NPTsl. The irrigated cultures however, did not place them separately and found within the first group. Further, it was interesting to note that two mega varieties viz., Swarna and Sambhamashuri (derived from common parent, Mashuri) have been found within the same cluster. Similarly, two *tropical japonicas* (EC491229 and EC491403) and one *temperate japonica* (Nipponbare) have placed themselves differently indicating that most of the NPT selections derived from second generation NPTs were more nearer to *indica* genotypes and distinctly different from *tropical and temperate japonica* genotypes. This indicates that there is further scope of introgressing genes from both of these relatives for improving *indica* parents for development of super rice towards breaking yield ceiling.

Further, the genetic distance could be more clearly visualized from 3D plot considering principal components (PCA I and PCA II) through canonical root analysis (Fig.3). The positioning of genotypes were mostly in line with dendogram, however, *temperate japonicas* as well as derivates of *temperate Japonica* (Swarna and Sambamashuri) have been distinctly different and away from NPTs indicating their genetic distance. Similarly*, tropical japonicas* were distinctly away apart from NPTsl, in which Azucaena was an exception. This shows that NPTsl still maintains sufficient genetic diversity from temperate as well as
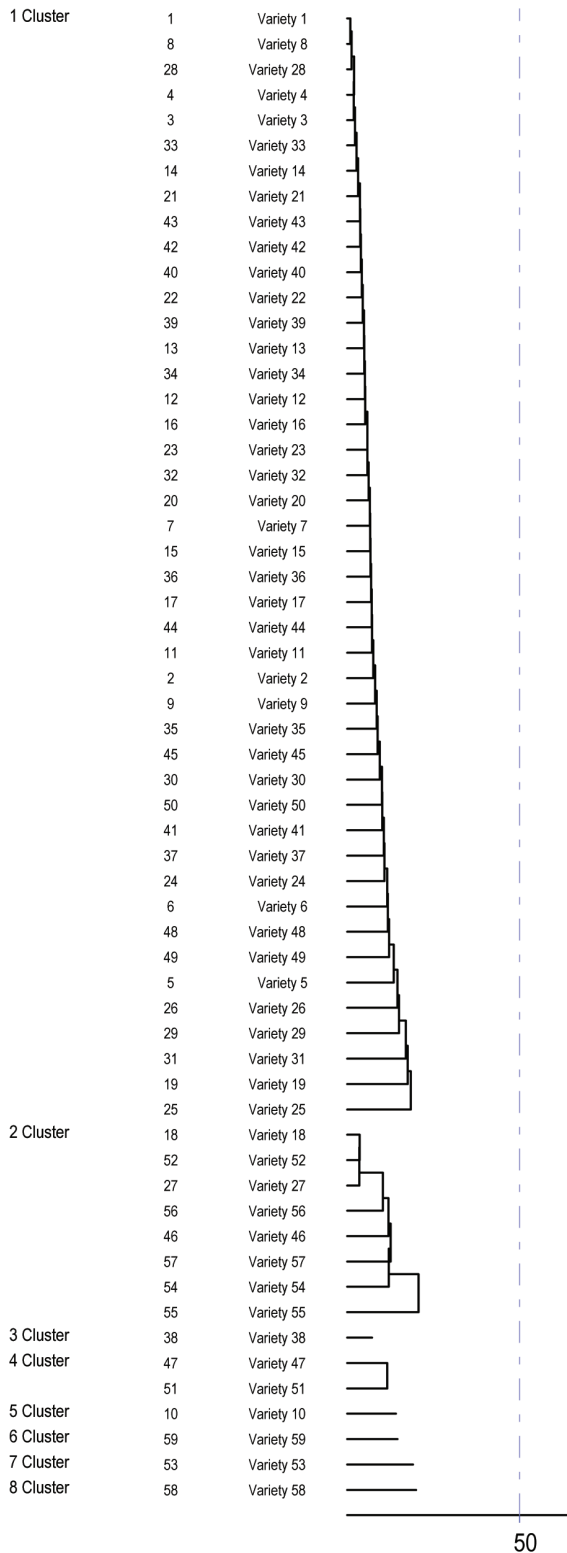
Fig 2. Composition of 59 genotypes into eight different clusters (Ref: Variety names in Table 1)
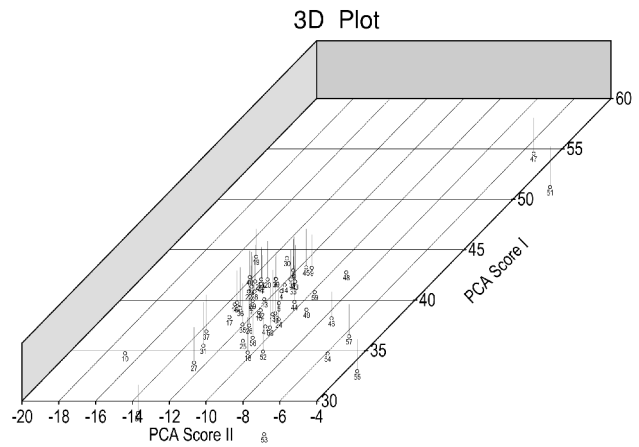

Fig 3. 3D plot basing upon first two vectors of Principal Component Analysis for the genotypes under study (Ref: Variety names in Table 1)

tropical *japonicas* which could be further exploited. Even, some of the highly popular *indica* varieties are still genetically distant (viz., Swarna, Samba Mashuri, Annada and Naveen), which could be well exploited for hybridization programme. However, high yielding irrigated cultures were very much within the first group consisting of NPTsl indicating their proximity with them.

The intra and inter cluster distances are presented in Table 6. The highest inter cluster distance (725.72) was found between cluster IV and VIII followed by cluster IV and VII (682.10), cluster IV and V (550.63) and cluster II and IV (379.75). The members of these clusters are to be given importance in hybridization programme basing on trait specific complementation. Further, looking into the contribution of characters towards divergence (Table 7), PH contributed maximum followed by NFG, TNS, TGW and GY. The cluster means of genotypes revealed considerable genetic differences between the groups. The cluster IV registered the highest mean value for NFG, whereas the highest mean value for PH, TH, PL, FLL were recorded by cluster V and highest mean for GY by cluster I. Accordingly selection of parents should be prioritized basing upon cluster distance and *per se performance* for specific traits or grain yield or for trait specific improvement or for overall improvement.

Table 6. Intra and inter-cluster D^2 among eight clusters

	I	II	III	IV	V	VI	VII	VIII
I	27.76	79.78	57.61	255.36	95.67	74.39	237.68	186.32
II		41.89	122.79	379.75	109.22	80.46	105.19	103.77
III			0.00	256.91	154.07	135.36	251.61	241.72
IV				30.94	550.63	284.29	682.10	725.72
V					0.00	124.11	212.95	68.00
VI						0.00	246.82	178.77
VII							0.00	115.10
VII								0.00

Table 7. Cluster mean for ten quantitative characters evaluated

TraitsClusters	DFF	PH	TH	PL	FLL	FLW	NFG	TNS	TGW	GY
I	102.6	107.5	8.8	29.2	36.5	1.4	107.8	131.6	2.3	697.1
II	93.7	88.7	7.9	23.9	28.2	1.2	81.4	99.9	2.3	375.8
III	107.0	107.6	7.5	28.3	37.8	1.8	117.4	160.8	2.6	592.5
IV	125.9	97.3	9.5	24.1	26.7	1.3	121.3	139.9	1.6	474.6
V	93.0	147.9	10.1	31.3	41.2	1.21	88.5	110.6	2.6	641.4
VI	103.8	101.6	5.4	24.6	38.2	0.69	70.9	82.13	2.5	297.8
VII	77.50	71.1	7.3	20.1	20.5	0.7	75.8	114.3	1.9	222.8
VII	82.8	116.8	8.2	22.9	38.7	1.23	80.3	91.6	2.9	357.1
No. of times ranked 1st	474	74	32	71	38	94	314	215	207	192
Contribution (%)	27.7	4.3	1.9	4.2	2.2	5.5	18.4	12.6	12.1	11.2

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