

SELECTION CRITERIA, YIELD RELATIONSHIP WITH COMPONENT TRAITS AND GROUPING OF TROPICAL JAPONICA, INDICA LINES AND DERIVED HYBRIDS OF RICE (*Oryza sativa* L.)

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ABSTRACT

Forty-five rice lines comprising of thirty derived hybrid lines obtained from ten tropical *Japonica*, three *Indica* and two national checks viz. Pusa Basmati 1121 and Sarjoo-52 were evaluated for selection parameters, yield contributing components and genetic divergence. Fifteen quantitative and three qualitative traits were studied from experimentation with randomized block design during *Kharif* 2011. The phenotypic coefficient of variability was higher than genotypic coefficient of variability for all of the traits. The highest estimates of broad sense heritability coupled with genetic advance in per cent of mean was recorded for spikelets per panicle, plant height followed by L:B ratio, spikelets per panicle, grains per panicle, biological yield per plant, flag leaf area, days to 50% flowering, plant height which might be due to the additive nature of gene action. Such results indicated that these traits will be reliable for the effective selection. Highly positive and significant correlation was observed at both phenotypic and genotypic level between grain yield per plant and biological yield per plant, followed by panicle bearing tillers per plant, spikelet fertility, panicle length, 1000-grain weight, grains per panicle, panicle weight, flag leaf length, spikelet per panicle, flag leaf area, kernel length, flag leaf width, days to 50% flowering, and harvest index. This relationship reflected that grain yield and aforesaid economic traits can be increased simultaneously in breeding programme to develop high yielding *Indica* as well as Tropical *Japonica* rice varieties. Whole genotypes grouped in 8 non-overlapping clusters exhibited maximum genetic diversity between clusters III i.e., TJ-

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64897 × NDR-359, TJ-64897 × CSR36, TJ-64897 × PB-1 and VIII i.e., TJ-11010 × NDR359, TJ-11010 × PB-1, TJ-16081 × NDR-359, TJ-16081 × PB-1. These clusters also stand for early days to flowering, short slender, second highest harvest index and panicle bearing tillers per plant, spikelets per panicle, grains per panicle, spikelet fertility, 1000-grain weight, long bold slender, biological yield per plant, and grain yield per plant. These genotypes showing higher mean performance for aforesaid traits can be exploited for enhancing hybrid vigour of desired New Plant Type with higher number of panicle bearing tillers per plant, spikelet per panicle and grains per spike in *Indica* as well as Tropical *Japonica* rice varieties for achieving higher yield.

Keywords: Clustering pattern, Correlations, Genetic diversity, *Indica*, *Japonica*, New Plant Type, Path analysis and Selection parameters.

INTRODUCTION

Rice as lifeline for a large segment of the world's population, more than 91% of world's rice is produced in Asia and provides 20% of the per capita energy and 13% of the per capita protein worldwide. However, in Asia rice contributes about 35% of the energy and 28% of the protein. In India it plays an integral role for 65 per cent population, food security, income generation, employments and foreign currencies gains for the nation. India has the largest area, about 4.5×10^7 ha, under rice in the world and produced 9.5×10^9 tone in year 2010-11. In accordance with current population growth, rice requirement by 2025 is estimated to be around 1.3×10^{10} tone (Anonymous 2010). Hence it is very crucial to develop high yielding varieties. It is cultivated on foot hills of the Himalaya in the North Western parts of Indian sub-continent comprising the states of Haryana, Punjab, Uttaranchal, Uttar Pradesh, Himachal Pradesh and Delhi. Current *Indica* rice varieties have higher yield potential of 100 t ha^{-1} with harvest index of 0.4-0.5 under tropical conditions.

The hybrid vigour between *Indica* and *Japonica* inter-subspecies can be used to improve the yield of *Indica* and *Japonica* hybrids by introducing parts of the *Indica* genomic segments into the *Japonica* background or vice versa, after several generations of backcrossing. For developing New Plant Type with increased vigour, *Indica* and *Japonica* materials are an effective source of breeding for the many pleasing and desirable traits such as less and productive tillers, canopy structure, increased biomass production, reduced carbon assimilation, increased harvest index, increased sink-source and spikelet fertility.

Crop improvements depend upon the magnitude of genetic variability present in the base population. The expected improvement in yield components primarily depends on the nature and magnitude of heritable total variation. Selection based on a single character may not always be effective while it is impractical for a researcher to consider a large number of component characters simultaneously in a particular selection procedure. Correlation analysis between yield and its components provides

useful information for right choice of characters in the selection programme. Path coefficient analysis provides an effective tool for partitioning the correlation coefficient in to direct and indirect effects of yield attributes on yield, with their cause and effect relationship.

The varieties originated from widely distinct localities or geographical areas were usually presumed to be diverse and were utilized in hybridization programmes because earlier workers regarded this geographical isolation as reasonable index of genetic diversity. However, several workers have found the lack of parallelism between geographical distribution and genetic diversity in different crop species and have also reported that genetic drift and selection in different environments could cause greater diversity than geographic distances. (Murty and Arunachalam, 1966; Bhanumathi et al., 2010; Manikya and Reddy, 2011). For improving genetic diversity of best suited germplasm across the location, it is very important to know the extent of existing genetic diversity. Genetic diversity is the heritable difference among germplasm, is crucial at an optimum level within a population to facilitate and sustain an effective, continuous breeding programme. Exotic introduced materials have specific genetic background and also may play a greater role to enhance heterosis.

MATERIALS AND METHODS

The reported experiment included forty-five rice lines comprising of ten Tropical *Japonica* as lines and three *Indica as* testers and their thirty crosses along with two checks viz. Pusa Basmati 1121 and Sarjoo-52. The genotypes were evaluated in Randomized Block Design with three replications during *kharif* 2011. The crosses were made during *kharif* 2010 at Crop Research Farm, Nawabganj of C.S. Azad University of agriculture and Technology, Kanpur, situated between 27.24° N latitude, 77.5° E longitudes and at an altitude of 178 meters above the msl. in the gangetic plain of central Uttar Pradesh. The climate of district Kanpur is semi-arid with hot summer and cold winter. Nearly 80 percent of total rainfall occurs during the monsoon (only up to September) with a few showers in the winter. The site of experiment was salt affected clay loam (natrustalf) soil having pH = 10.5, EC =2.03 and low in organic carbon, nitrogen and phosphorus.

Observations were recorded on ten competitive plants randomly selected in each replications for fifteen quantitative and three qualitative traits viz., days to 50% flowering, plant height (cm), panicle bearing tillers per plant, flag leaf length (cm), flag leaf width (cm), flag leaf area (cm²), panicle length (cm), panicle weight (g), spikelets per panicle, grains per panicle, spikelet fertility (%), 1000-grains weight (g), kernel length (mm), kernel breadth (mm), L:B ratio, biological yield per plant (g), harvest index (%) and grain yield plant (g). Each genotype was accommodated in three-row of 5 m length following row to row and plant to plant spacing of 20 × 15 cm, respectively. The recommended dose of fertilizers N: P: K @ 120:60:60 kg ha⁻¹, cultural packages and practices were followed to raise a good healthy crop.

Standard statistical techniques such as analysis of variance (Panse and Sukhatme, 1967), genotypic and phenotypic coefficients of variation (Burton and de Vane, 1953), estimate of broad sense heritability (h^2_b) (Hanson et al., 1956), genetic advance as percent of the mean (Johnson et al., 1955), phenotypic and genotypic correlation coefficient (Searle 1961), path analysis (Dewey and Lu, 1959) and standard statistical techniques such as Non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973) were applied for assessing variability and genetic divergence present in the germplasm (using MASTA-C software). Grouping and arrangement of genotypes were done by Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

Genetic variability parameters

The analysis of variance revealed presence of highly significant differences among all the genotypes for eighteen characters and indicated considerable amount of variability in the genotypes. Significant variability due to treatment for all the characters (Table 1) was also confirmed by Jayasudha and Sharma (2010). Phenotypic coefficient of variability (PCV) was higher than genotypic coefficient of variability (GCV) (Table 2). A perusal of coefficient of variability indicates that PCV and GCV were quite high for flag leaf area (47.79 & 47.06), panicle bearing tillers per plant (46.94 & 44.65), grains per panicle (45.92 & 45.14), grain yield per plant (44.32 & 43.07), biological yield per plant (40.73 & 39.22), spikelets per panicle (38.88 & 38.33), panicle weight (38.71 & 38.22), flag leaf width (28.86 & 28.36), and flag leaf length (25.16 & 24.26). Moderate PCV and GCV were recorded in panicle length (19.1 & 18.35), L:B ratio (17.18 & 16.56), 1000-grain weight (16.05 & 15.89), kernel breadth (14.82 & 14.21), days to 50% flowering (14.82 & 14.14), spikelet fertility (12.09 & 8.94), plant height (11.68 & 11.29) and kernel length (10.95 & 10.69) by Seyoum et al., 2012, Yadav et al., 2011, Manikaya and Reddy, 2011 and Barber et al., 2009. The highest estimates of broad sense heritability coupled with genetic advance in per cent of mean was recorded for spikelets per panicle (96.60 & 149.86), plant height (98.9% & 65.13%) followed by L:B ratio (99.99 & 39.30), spikelets per panicle (97.20 & 32.39), grains per panicle (96.60 & 141.11), biological yield per plant (92.70 & 42.47), flag leaf area (97.00 & 40.47), days to 50% flowering (91.10 & 26.75), and plant height (93.40 & 25.04). Due to the additive nature of gene action these traits will be reliable for the effective selection. High heritability coupled with moderate genetic advance for grain yield per plant (94.40 & 15.22) and flag leaf length (93.00 & 13.62) indicated preponderance of non-additive gene action, hence selection cannot be rewarded which was also agreed with by Seyoum et al., 2012; Yadav et al., 2011 and Suman et al., 2005. The most preferable genotypes having high variability, heritability and genetic advance for characters other than grain yield per plant can also be used as donor parents in hybridization programme to improve desirable characters for which they showed high value of heritability and genetic advance.

Relationship analysis

The genotypic correlation coefficient was higher in magnitude than the corresponding phenotypic correlation coefficient in general for most of the characters (Table 3). This is possibly due to the linkage or modifying effect of the gene and environment in genetic association between characters (Swain and Reddy 2006). There were strong positive and significant correlation at both phenotypic and genotypic level, between grain yield per plant and biological yield per plant (0.931 & 0.884) followed by panicle bearing tillers per plant (0.823 & 0.593), spikelet fertility (0.823 & 0.593), panicle length (0.809 & 0.752), 1000-grain weight (0.738 & 0.710), grains per panicle (0.699 & 0.666), panicle weight (0.683 & 0.660), flag leaf length (0.678 & 0.625), spikelet per panicle (0.633 & 0.604), flag leaf area (0.628 & 0.599), kernel length (0.579 & 0.549), flag leaf width (0.516 & 0.499), days to 50% flowering (0.385 & 0.351), and harvest index (0.368 & 0.366). This relationship reflected that grain yield and aforesaid traits can be improved simultaneously (Jaisudha and Sharma, 2010; Manikaya and Reddy, 2011 and Seyoum et al., 2012). Besides, biological yield was positively and highly significantly correlated with panicle bearing tillers per plant (0.881 & 0.821), grains per panicle (0.794 & 0.756), spikelet fertility (0.863 & 0.620) and panicle length (0.828 & 0.771) and 1000-grain weight (0.764 & 0.730). This indicates that vigorous plant population may enhance economic yield. 1000-grain weight was significantly and positively associated with spikelet fertility and panicle length and other yield contributing traits. A highly significant and positive correlation was noted between grains per panicle and panicle length (0.679 & 0.639), panicle bearing tillers per plant (0.597 & 0.570) and panicle weight (0.843 & 0.816). Panicle weight showed highly significant and positive association with panicle per plant (0.528 & 0.501) and panicle length (0.772 & 0.736). Such type of results were reported by Petchiammal and Khan, 2007. This association reflected that above character can be considered as new plant type for enhancing the economic yield.

Path coefficient analysis

The highest direct effect of grains per panicle (1.208 & 0.235) was noted over grain yield per plant, followed by flag leaf width (1.197 & 0.477), biological yield per plant (1.132 & -0.340), harvest index (0.854 & 0.725), kernel breadth (0.825 & -0.330), flag leaf length (0.818 & 0.373) on grain yield via panicle weight (1.018 & 0.192), spikelets per panicle (1.195 & 0.230), spikelet fertility (1.013 & 0.162), biological yield per plant (0.959 & 0.178), 1000-grain weight (0.852 & 0.160), panicle length (0.820 & 0.150), flag leaf area (0.787 & 0.150), flag leaf length (0.724 & 0.135), flag leaf width (0.723 & 0.137) and panicle bearing tillers per plant (0.721 & 0.134) (Table 4). Almost similar relationships were also reported by Borbora et al., 2005; Veni and Rani, 2007; and Kisore et al., 2007. Therefore, these traits can be used for selection criteria in breeding programme to develop high yielding new plant type rice varieties.

Clustering pattern and genetic divergence analysis

Non-hierarchical Euclidean cluster analysis grouped the forty-five aforesaid genotypes, into 8 non-overlapping clusters (Table 5 and 6). Cluster II had the maximum 13 genotypes, followed by cluster VIII, I, and cluster III, IV, V, VI which had same number of 4 genotypes. Cluster VII comprised of 3 genotypes which reflected narrow genetic diversity (Dushyantha and Kantti 2010).

Maximum inter-cluster diversity was observed between III & VIII, followed by cluster III & IV, III & VII, II & VIII, III & VI, II & IV, IV & V, I & VIII and I & IV. Similar inter-cluster distances were reported by Vaithiyalingan et al., 2007. The genotypes grouped in cluster I consisted of eleven genotypes, only three genotypes i.e. TJ-25966 × NDR-359, TJ-25966 × CSR36, TJ-25966 × PB-1 showed short bold grain and harvest index. It is big information that genotype TJ-64897 × NDR-359, TJ-64897 × CSR36, TJ-64897 × PB-1 from cluster III and genotype TJ-11010 × NDR359, TJ-11010 × PB-1, TJ-16081 × NDR-359, TJ-16081 × PB-1 from cluster VIII expressed maximum genetic diversity and also stands for early days to flowering, short slender, second highest harvest index and panicle bearing tillers per plant, spikelets per panicle, grains per panicle, spikelet fertility, 1000-grain weight, biological yield per plant, grain yield per plant. Chandra et al., 2007 also observed similar results in their study. Therefore, it is suggested that any superior genotype of cluster III may be crossed with any superior genotypes of cluster VII to produce desirable recombinants with more suitable traits for higher yield.

Maximum genetic divergence within the cluster was estimated for cluster V (3.058) followed by cluster II (2.205), VII (1.995), I (1.892), VII (1.378) and VI (1.288) while cluster IV (1.140) showed minimum intra cluster distance. Almost similar inter-cluster distance was estimated by Suman et al., 2005 in rice. The maximum intra cluster value indicated maximum divergence among various genotypes within the cluster whereas; minimum value reflected minimum diversity among the genotypes within the respective cluster.

Based on cluster mean performance (Table-7), cluster VII showed the highest cluster mean for productive tillers per plant (17.73), flag leaf length (35.91), panicle length (31.23), grains per panicle (245.04), 1000-grain weight (32.54), biological yield per plant (85.02), grain yield per plant (28.24). Gahalain et al., 2006 reported similar type of cluster mean in rice.. From this cluster, the genotypes TJ-11010 × NDR359, TJ-11010 × PB-1, TJ-16081 × NDR-359, TJ-16081 × PB-1 expressed superiority over the checks for aforesaid respective characters. Cluster IV showed maximum mean performance for genotypes TJ-10365 × NDR-359 and TJ-10365 × PB-1 for flag leaf width (2.87), flag leaf area (71.97) and spikelet per panicle (284.33). Cluster VII showed third highest mean performance for days to 50% flowering (87.78), panicle bearing tillers per plant (15.11), panicle length (30.10), spikelet per panicle (275.22), grains per panicle (238.00) and 1000-grain weight (31.00). The highest mean performance for panicle weight (4.16), kernel breadth

(3.25) were recorded in the two most superior genotypes TJ-25892 × NDR359 and TJ-25892 × PB-1 of cluster VII. Earliness (87.78 days) and desirable medium plant height (116.00) of the above mentioned genotypes can be taken under consideration in crossing program. On the basis of eight genetically diverse clusters, superior genotypes listed in table 8 from the different clusters were selected. Interacting from different clusters and diverse genotypes would lead greater opportunity for crossing over which release latent genetic variability by breaking linkage drag and progenies derived from cross are expected to show broad spectrum of genetic variability providing a greater scope for screening transgressive segregants as new plant type for sustaining yield of existing varieties.

CONCLUSIONS

The study of fifteen quantitative and three qualitative traits ranging for trait to trait among the genotype, indicated that selection can be practiced for background selection to sort-out superior parent with higher spikelets per panicle, grains per panicle, and panicle bearing tillers per plant due to the additive nature of gene action. The direct yield contributing characters showing strong positive association with grain yield reflected that these characters can be enhanced simultaneously. Similarly genotypes falling under cluster III and VIII having high mean performance for respective character can be used for getting better combinations with desirable character in *Indica* as well as in *Japonica* rice varieties for foreground selection to achieve higher yield with desirable new plant type.

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Table 1: Estimates of variance for 18 characters in *Indica* and Tropical *Japonica* rice lines and their hybrids

Sl. No.	Characters	Sources of variation				
		Replication (2)	Treatment (44)	Error (88)	CV%	CD
1.	Days to 50% flowering	1.50	573.36**	18.10	4.42	6.89
2.	Plant height (cm)	42.93	485.82**	11.22	3.00	5.42
3.	Panicle bearing tillers/plant	2.61	73.62**	2.49	14.48	2.56
4.	Flag leaf length	2.16	144.59**	3.56	6.67	3.06
5.	Flag leaf Breadth	0.03	0.89**	0.01	5.36	0.16
6.	Flag leaf area	3.41	1206.68**	12.45	8.32	5.72
7.	Panicle length (cm)	1.04	70.18**	1.88	5.28	2.23
8.	Panicle weight (g)	0.02	3.10**	0.02	6.15	0.26
9.	Spikelets/panicle	413.75	16496.41**	158.16	6.53	20.38
10.	Grains/spike	178.37	14739.39**	169.98	8.44	21.15
11.	Spikelet fertility (%)	17.59	187.43**	40.54	8.13	10.31
12.	1000- grain weight (g)	1.96	56.87**	0.39	2.29	1.01
13.	Kernel length	0.01	1.42**	0.02	2.34	0.24
14.	Kernel breadth	0.03	0.35**	0.01	4.22	0.16
15.	L:B ratio	0.02	0.62**	0.01	4.57	0.19
16.	Biological yield/plant (g)	138.51	1410.99**	35.88	10.97	9.72
17.	Harvest index	124.69	106.30**	21.90	14.37	7.59
18.	Grain yield/plant (g)	2.71	176.87**	3.41	10.46	2.98

*, ** Significant at 5% and 1% probability levels, respectively

Table 2: Estimates of general mean, variability parameters for 18 characters in *Indica* and Tropical *Japonica* rice lines and their hybrids

Characters	Range		G. mean ±SE(m)	Coefficient of variation (%)			h ² b (%)	G a (%)
	Minimum	Maximum		PCV	GCV	ECV		
Days to 50% flowering	66.25	114.00	96.19 ± 3.47	14.82	14.14	0.68	91.10	26.75
Plant height (cm)	94.00	143.33	111.41 ± 2.73	11.68	11.29	0.39	93.40	25.04
Panicle bearing tillers/plant	4.65	22.67	10.90 ± 1.29	46.94	44.65	2.29	90.50	9.54
Flag leaf length	17.15	41.70	28.26 ± 1.54	25.16	24.26	0.9	93.00	13.62
Flag leaf Breadth	0.84	2.92	1.91 ± 0.08	28.86	28.36	0.5	96.00	1.10
Flag leaf area	11.06	86.56	42.39 ± 2.88	47.79	47.06	0.73	97.00	40.47
Panicle length (cm)	18.57	34.23	25.99 ± 0.11	19.10	18.35	0.75	92.30	9.44
Panicle weight (g)	1.35	4.37	2.64 ± 0.13	38.71	38.22	0.49	97.50	2.06
Spikelets/panicle	90.67	328.67	192.55 ± 10.26	38.88	38.33	0.55	97.20	149.86
Grains/spike	65.11	292.67	154.38 ± 10.64	45.92	45.14	0.78	96.60	141.11
Spikelet fertility (%)	64.97	89.09	78.25 ± 5.19	12.09	8.94	3.15	54.70	10.66
1000- grain weight (g)	18.29	34.38	27.30 ± 0.51	16.05	15.89	0.16	98.0	8.85
Kernel length	4.77	7.44	6.39 ± 0.12	10.95	10.69	0.26	95.40	1.38
Kernel breadth	1.71	3.56	2.38 ± 0.08	14.82	14.21	0.61	91.90	0.67
L:B ratio	1.93	3.97	2.73 ± 0.10	17.18	16.56	0.62	92.90	0.90
Biological yield/plant (g)	18.27	110.73	54.59 ± 4.89	40.73	39.22	1.51	92.70	42.47
Harvest index	20.86	50.28	32.56 ± 3.82	21.72	16.29	5.43	56.20	8.19
Grain yield/plant (g)	5.59	34.98	17.65 ± 1.50	44.32	43.07	1.25	94.40	15.22

Table 3: Genotypic and Phenotypic correlation coefficients for 18 characters in *Indica* and Tropical *Japonica* rice lines and their hybrids

Traits	Level	PH	PBT/P	FLL	FLW	FLA	PL	PW	S/P	G/S	SF	TW	KL	KB	L:B	BY/P	HI	GY/P
DF	rg	0.515**	0.309*	0.647**	0.661**	0.697**	0.518**	0.358**	0.398**	0.430**	0.457**	0.414**	0.618**	-0.049	0.387**	0.571**	-0.462	0.385**
	rp	0.468**	0.298*	0.598**	0.621**	0.658**	0.476**	0.341*	0.370**	0.398**	0.316*	0.394**	0.587**	-0.042	0.363**	0.525**	-0.332	0.351**
PH	rg	1.000	0.101	0.412**	0.654**	0.608**	0.586**	0.708**	0.555**	0.568**	0.445**	0.676**	0.393**	0.236	0.000	0.461**	-0.128	0.349*
	rp	1.000	0.086	0.382**	0.624**	0.579**	0.532**	0.672**	0.524**	0.536**	0.322*	0.642**	0.377**	0.215	0.008	0.426**	-0.108	0.325*
PBT/P	rg		1.000	0.550**	0.239**	0.412**	0.697**	0.528**	0.534**	0.597**	0.741**	0.579**	0.639**	0.250	0.210	0.881**	0.204	0.880**
	rp		1.000	0.515**	0.220**	0.390**	0.638**	0.501**	0.506**	0.570**	0.543**	0.547**	0.595**	0.225	0.189	0.821**	0.138	0.817**
FLL	rg			1.000	0.711**	0.906**	0.708**	0.481**	0.589**	0.599**	0.607**	0.505**	0.642**	-0.004	0.370**	0.759**	-0.087	0.678**
	rp			1.000	0.665	0.892**	0.655**	0.455**	0.563**	0.573**	0.443**	0.486**	0.616**	0.009	0.340	0.711**	-0.105	0.625**
FLW	rg				1.000	0.924**	0.650**	0.665**	0.578**	0.599**	0.555**	0.577**	0.325*	0.226	-0.044	0.628**	-0.194	0.516**
	rp				1.000	0.911	0.608**	0.641**	0.561**	0.581**	0.410**	0.556**	0.302*	0.216	-0.048	0.596**	-0.123	0.499**
FLA	rg					1.000	0.728**	0.620**	0.632**	0.651**	0.622**	0.621**	0.521**	0.076	0.211	0.732**	-0.129	0.628**
	rp					1.000	0.686**	0.599**	0.616**	0.635**	0.462**	0.605**	0.501**	0.080	0.194	0.698**	-0.103	0.599**
PL	rg						1.000	0.772**	0.599**	0.679**	0.855**	0.691**	0.689**	0.238	0.249	0.828**	0.182	0.809**
	rp						1.000	0.736**	0.569**	0.639**	0.606**	0.663**	0.640**	0.210	0.237	0.771**	0.114	0.752**
PW	rg							1.000	0.806**	0.843**	0.759**	0.801**	0.402**	0.528**	-0.181	0.760**	0.034	0.683**
	rp							1.000	0.783**	0.816**	0.558**	0.781**	0.388**	0.490**	-0.164	0.724**	0.028	0.660**
S/P	rg								1.000	0.989**	0.760**	0.641**	0.489**	0.333*	0.014	0.733**	-0.088	0.633**
	rp								1.000	0.977**	0.534**	0.622**	0.471**	0.310*	0.015	0.700**	-0.086	0.604**
G/S	rg									1.000	0.839**	0.705**	0.545**	0.350*	0.038	0.794**	-0.059	0.699**
	rp									1.000	0.686**	0.682**	0.522**	0.326*	0.036	0.756**	-0.055	0.666**
SF	rg										1.000	0.701**	0.651**	0.272*	0.198	0.863**	0.073	0.823**
	rp										1.000	0.511**	0.463**	0.191	0.136	0.620**	0.079	0.593**
TW	rg											1.000	0.520**	0.412**	-0.069	0.764**	0.121	0.738**
	rp											1.000	0.504**	0.391**	-0.066	0.730**	0.092	0.710**
KL	rg												1.000	0.137	0.537**	0.701**	-0.216	0.579**
	rp												1.000	0.126	0.535**	0.656**	-0.159	0.549**
KB	rg													1.000	-0.745	0.308**	-0.276	0.197
	rp													1.000	-0.751	0.284*	-0.188	0.188
L:B	rg														1.000	0.164	0.109	0.178
	rp														1.000	0.152	0.065	0.160
BY/P	rg															1.000	0.021	0.931**
	rp															1.000	-0.068	0.884**
HI	rg																1.000	0.368**
	rp																1.000	0.366**
GY/P	rg																	1.000
	rp																	1.000

*, ** Significant at 5% and 1% probability levels, respectively. Legents: DF=GY/P

Table 4: Genotypic and Phenotypic path of 18 traits on grain yield in *Indica* and Tropical *Japonica* rice lines and their hybrids

Traits	Level	DF	PH	PBT/P	FLL	FLW	FLA	PL	PW	S/P	G/P	SF	TW	KL	KB	BY/P	HI	GY/P	Corrl. of GY/P
DF	Pg	-0.141	0.063	0.042	0.529	0.791	-1.235	0.097	-0.272	-0.281	0.519	-0.155	0.194	-0.548	-0.041	-0.438	0.488	-0.105	0.385
	Pp	-0.040	-0.028	0.020	0.223	0.294	-0.473	0.003	0.001	-0.065	0.094	-0.021	0.033	0.176	0.014	-0.123	0.381	-0.137	0.351
PH	Pg	-0.073	0.123	0.014	0.337	0.783	-0.078	0.110	-0.537	-0.391	0.686	-0.151	0.316	-0.349	0.195	0.000	0.394	-0.029	0.349
	Pp	-0.019	-0.059	0.006	0.143	0.295	-0.416	0.003	0.002	-0.092	0.126	-0.021	0.054	0.113	-0.071	-0.003	0.309	-0.045	0.325
PBT/P	Pg	-0.044	0.012	0.135	0.449	0.287	-0.731	0.131	-0.401	-0.377	0.721	-0.251	0.271	-0.566	0.206	0.238	0.752	0.046	0.880
	Pp	-0.012	-0.005	0.066	0.192	0.104	-0.281	0.003	0.002	-0.089	0.134	-0.035	0.046	0.178	-0.074	-0.064	0.595	0.057	0.817
FLL	Pg	-0.091	0.050	0.074	0.818	0.850	-1.606	0.133	-0.365	-0.416	0.724	-0.206	0.236	-0.569	-0.003	0.419	0.648	-0.020	0.678
	Pp	-0.024	-0.023	0.034	0.373	0.315	-0.641	0.004	0.002	-0.099	0.135	-0.029	0.041	0.184	-0.003	-0.116	0.515	-0.043	0.625
FLW	Pg	-0.093	0.080	0.032	0.581	1.197	-1.638	0.122	-0.504	-0.408	0.723	-0.188	0.270	-0.288	0.186	-0.050	0.536	-0.044	0.516
	Pp	-0.025	-0.037	0.015	0.248	0.474	-0.655	0.003	0.002	-0.099	0.137	-0.027	0.047	0.090	-0.071	0.016	0.432	-0.051	0.499
FLA	Pg	-0.098	0.075	0.056	0.741	1.106	-1.773	0.137	-0.470	-0.446	0.787	-0.211	0.291	-0.462	0.062	0.239	0.625	-0.029	0.628
	Pp	-0.026	-0.034	0.026	0.333	0.432	-0.719	0.004	0.002	-0.109	0.150	-0.030	0.051	0.150	-0.027	-0.066	0.506	-0.042	0.599
PL	Pg	-0.073	0.072	0.094	0.579	0.778	-1.290	0.188	-0.586	-0.422	0.820	-0.289	0.323	-0.611	0.197	0.282	0.707	0.041	0.809
	Pp	-0.019	-0.031	0.042	0.244	0.288	-0.493	0.005	0.003	-0.100	0.150	-0.039	0.056	0.192	-0.069	-0.081	0.559	0.047	0.752
PW	Pg	-0.050	0.087	0.071	0.393	0.795	-1.099	0.145	-0.759	-0.569	1.018	-0.257	0.375	-0.357	0.436	-0.205	0.649	0.008	0.683
	Pp	-0.014	-0.040	0.033	0.170	0.304	-0.431	0.004	0.004	-0.138	0.192	-0.036	0.065	0.116	-0.162	0.056	0.525	0.011	0.660
S/P	Pg	-0.056	0.068	0.072	0.482	0.692	-1.120	0.112	-0.612	-0.706	1.195	-0.257	0.300	-0.434	0.275	0.016	0.626	-0.020	0.633
	Pp	-0.015	-0.031	0.033	0.210	0.266	-0.443	0.003	0.003	-0.177	0.230	-0.035	0.052	0.141	-0.102	-0.005	0.508	-0.035	0.604
G/S	Pg	-0.061	0.070	0.081	0.490	0.717	-1.155	0.127	-0.639	-0.698	1.208	-0.284	0.330	-0.483	0.289	0.043	0.678	-0.013	0.699
	Pp	-0.016	-0.032	0.038	0.214	0.275	-0.457	0.003	0.003	-0.173	0.235	-0.045	0.057	0.156	-0.108	-0.012	0.548	-0.023	0.666
SF	Pg	-0.064	0.055	0.100	0.497	0.664	-1.104	0.160	-0.576	-0.536	1.013	-0.339	0.328	-0.578	0.225	0.224	0.728	0.017	0.823
	Pp	-0.013	-0.019	0.036	0.165	0.194	-0.332	0.003	0.002	-0.094	0.162	-0.065	0.043	0.139	-0.063	-0.046	0.450	0.033	0.593
TW	Pg	-0.058	0.083	0.078	0.413	0.691	-1.102	0.130	-0.608	-0.453	0.852	-0.237	0.468	-0.461	0.340	-0.078	0.653	0.027	0.738
	Pp	-0.016	-0.038	0.036	0.181	0.263	-0.435	0.004	0.003	-0.110	0.160	-0.033	0.084	0.151	-0.129	0.022	0.529	0.038	0.710
KL	Pg	-0.087	0.048	0.086	0.525	0.389	-0.924	0.129	-0.305	-0.345	0.658	-0.220	0.243	-0.887	0.113	0.608	0.598	-0.049	0.579
	Pp	-0.024	-0.022	0.039	0.230	0.143	-0.360	0.003	0.001	-0.083	0.123	-0.030	0.042	0.300	-0.042	-0.182	0.476	-0.065	0.549
KB	Pg	0.007	0.029	0.034	-0.003	0.270	-0.134	0.045	-0.401	-0.235	0.423	-0.092	0.193	-0.121	0.825	-0.843	0.263	-0.063	0.197
	Pp	0.002	-0.013	0.015	0.003	0.102	-0.058	0.001	0.002	-0.055	0.077	-0.012	0.033	0.038	-0.330	0.255	0.206	-0.077	0.188
L:B	Pg	-0.055	0.002	0.028	0.303	-0.053	-0.374	0.047	0.137	-0.010	0.046	-0.067	-0.032	-0.476	-0.615	1.132	0.140	0.025	0.178
	Pp	-0.015	0.001	0.013	0.127	-0.023	-0.139	0.001	-0.001	-0.003	0.008	-0.009	-0.006	0.160	0.248	-0.340	0.110	0.027	0.160
BY/P	Pg	-0.081	0.057	0.119	0.621	0.752	-1.299	0.155	-0.577	-0.518	0.959	-0.292	0.358	-0.621	0.254	0.185	0.854	0.005	0.931
	Pp	-0.021	-0.025	0.054	0.265	0.282	-0.502	0.004	0.003	-0.124	0.178	-0.040	0.061	0.196	-0.094	-0.052	0.725	-0.028	0.884
HI	Pg	0.065	-0.016	0.028	-0.071	-0.232	0.229	0.034	-0.026	0.062	-0.072	-0.025	0.056	0.192	-0.228	0.124	0.018	0.227	0.368
	Pp	0.013	0.006	0.009	-0.039	-0.058	0.074	0.001	0.000	0.015	-0.013	-0.005	0.008	-0.048	0.062	-0.022	-0.049	0.411	0.366

Residual factors: Genotypic= 0.0072 and phenotypic= 0.0234, Bold figures Indicate direct effects. Legends: DF= PH=GY/P

Table 7: Clusters means, standard deviation and coefficient of variation for 18 traits in *Indica* and *Tropical Japonica* rice lines and hybrids

Character Clusters	DF	PH	PBT/P	FLL	FLW	FLA	PL	PW	S/P	G/P	SF	TW	KL	KB	L:B	BY/P	HI	GY/P	
	Mean	82.80	106.40	8.73	23.75	2.08	37.31	24.51	3.02	158.87	118.13	73.86	25.42	5.23	2.65	1.97	42.66	36.46	15.48
Cluster I	SD	8.25	2.77	2.24	1.86	0.30	7.38	2.04	0.31	51.01	43.88	8.73	1.37	0.38	0.13	0.05	1.85	3.80	1.57
	CV	9.96	2.60	25.66	7.83	14.42	19.78	8.32	10.26	32.11	37.15	11.82	5.39	7.27	4.91	2.54	4.34	10.42	10.14
	Mean	95.79	105.21	6.98	24.68	1.67	31.04	20.92	1.64	156.40	113.50	72.61	23.57	6.17	2.36	2.62	37.73	27.90	10.46
Cluster II	SD	8.74	8.08	1.56	5.09	0.17	7.18	2.24	0.23	58.66	42.70	5.15	2.10	0.44	0.18	0.24	6.91	4.33	2.48
	CV	9.12	7.68	22.35	20.62	10.18	23.13	10.71	14.02	37.51	37.62	7.09	8.91	7.13	7.63	9.16	18.31	15.52	23.71
	Mean	73.08	103.17	7.18	17.99	0.90	12.10	20.32	1.63	117.50	81.50	69.38	24.78	5.65	1.89	3.02	25.13	39.51	9.77
Cluster III	SD	3.98	5.71	0.19	0.72	0.05	0.84	1.01	0.12	9.48	9.37	3.14	0.92	0.08	0.21	0.32	0.97	3.0	0.47
	CV	5.45	5.53	2.65	4.00	5.56	6.94	4.97	7.36	8.07	11.50	4.53	3.71	1.42	11.11	10.60	3.86	7.59	4.81
	Mean	109.08	140.67	7.30	33.44	2.87	71.97	30.66	4.13	284.33	240.00	84.36	32.16	6.67	2.30	2.90	65.11	32.80	21.22
Cluster IV	SD	5.35	3.03	1.87	1.94	0.08	0.78	1.43	0.25	5.98	13.93	3.60	1.53	0.32	0.15	0.13	5.85	1.73	1.59
	CV	4.90	2.15	25.62	5.80	2.79	1.08	4.66	6.05	2.10	5.80	4.27	4.76	4.80	6.52	4.48	8.98	5.27	7.49
	Mean	92.31	95.26	15.50	30.23	1.49	33.74	28.79	2.02	143.56	118.59	82.63	23.81	6.92	2.05	3.44	61.54	39.64	24.54
Cluster V	SD	17.89	0.83	4.79	4.49	0.20	7.84	1.78	0.20	11.97	12.41	2.29	5.58	0.37	0.27	0.61	14.28	9.75	9.11
	CV	19.38	0.87	30.90	14.85	13.42	23.24	6.18	9.90	8.34	10.46	2.77	23.44	5.35	13.17	17.73	23.20	24.60	37.12
	Mean	110.58	122.25	12.32	34.85	2.15	56.24	29.04	2.71	142.58	111.58	77.62	29.79	6.70	2.31	2.90	65.80	29.17	19.05
Cluster VI	SD	1.20	1.19	1.45	3.24	0.12	7.01	1.32	0.30	21.95	25.85	7.88	0.87	0.07	0.02	0.03	6.85	2.51	2.34
	CV	0.11	0.10	1.18	0.93	0.56	1.25	0.45	1.11	1.54	2.32	1.02	0.29	0.10	0.09	0.10	1.04	0.86	1.23
	Mean	87.78	116.00	15.11	26.32	1.65	32.48	30.10	4.16	275.22	238.00	86.46	31.00	6.96	3.25	2.15	67.44	28.34	18.95
Cluster VII	SD	1.17	3.53	0.69	3.63	0.03	3.91	3.66	0.15	5.72	7.37	1.39	0.97	0.59	0.29	0.07	8.82	0.34	2.42
	CV	1.33	3.04	4.57	13.79	1.82	12.04	12.16	3.61	2.08	3.10	1.61	3.13	8.48	8.92	3.26	13.08	1.20	12.77
	Mean	108.25	115.08	17.73	35.91	2.40	65.52	31.23	3.54	282.46	245.04	86.64	32.54	7.09	2.43	2.92	85.02	33.88	28.24
Cluster VIII	SD	4.72	4.60	3.66	5.32	0.24	15.95	0.56	0.60	24.73	27.05	2.17	1.43	0.21	0.09	0.15	17.63	3.17	4.28
	CV	4.36	4.00	20.64	14.81	10.00	24.34	1.79	16.95	8.76	11.04	2.50	4.39	2.96	3.70	5.14	20.74	9.36	15.16

Table 8: Important superior genotypes and hybrids identified on the basis of their important traits, and cluster means in *Indica* and *Tropical Japonica* rice lines and hybrids

Genotypes/hybrids	Cluster	Important traits
TJ-25966 × NDR-359	I	Short bold grain, harvest index
TJ-25966 × CSR36	I	Short bold grain, harvest index
TJ-25966 × PB-1	I	Short bold grain, harvest index
TJ-64897 × NDR-359	III	Fourth early days to flowering, short slender, second highest harvest index
TJ-64897 × CSR36	III	Fifth early days to flowering, short slender, fifth highest harvest index
TJ-64897 × PB-1	III	Third early days to flowering, short slender
TJ-10365 × NDR-359	IV	Third highest flag leaf width, fourth highest flag leaf area, second highest flag leaf length, first highest panicle weight, third highest spikelet grains/panicle
TJ-10365 × PB-1	IV	Fourth highest flag leaf area, fifth highest panicle weight, fourth highest spikelet grains/panicle
NDR-359	V	Medium days to flowering, first harvest index, fourth highest grain yield/plant
Pusa Basmati-1	V	Second dwarf plant height, long slender
Pusa Basmati 1121	V	Fifth dwarf plant height, long slender
Sarjoo 52	V	Third dwarf plant height, first highest tillers/plant, third highest second highest grain yield/plant
TJ-25892 × NDR359	VII	First highest panicle length, third highest panicle weight, spikelet/panicle, long bold slender
TJ-25892 × PB-1	VII	Fifth highest panicle weight, long bold slender
TJ-11010 × NDR359	VIII	Second highest panicle bearing tillers/plant, second panicle weight, spikelets/panicle, first highest grains/panicle, first highest spikelet fertility, second highest biological yield/plant, third highest grain yield/plant
TJ-11010 × PB-1	VIII	Third highest panicle bearing tillers/ plant, second highest spikelets/panicle, highest grains/panicle, second highest spikelet fertility, first highest test weight, long bold highest biological yield/plant, first highest grain yield/plant
TJ-16081 × NDR-359	VIII	Fourth panicle bearing tillers/plant, first flag leaf length, fourth flag leaf area, fifth highest grains/ panicle, third highest test weight, long slender, second highest biological yield/plant, highest grain yield/plant
TJ-16081 × PB-1	VIII	Fifth highest panicle bearing tillers/plant, second flag leaf length, first flag leaf area, fourth highest panicle length, fifth highest test weight, long slender, fifth biological yield/plant