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RESEARCH ARTICLE

Maximizing rice yield gains through component trait analyses in eastern Indo-Gangetic plains of India

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Abstract

An investigation was carried out to evaluate the yield performance of a set of 145 indigenous collections of rice along with ten popular varieties as checks in eastern Indo-Gangetic plains of India. The study revealed considerable phenotypic diversity among the accessions for seed yield and its components, besides genotype × environment interactions. Statistical analyses including pooled analysis, biplot analysis and cluster analysis demonstrated significant genetic variability among the accessions for most of the traits studied. The accessions were also screened for major biotic stresses like leaf blast and yellow stem borer and found that 99 accessions were resistant and moderately resistant for leaf blast and 56 accessions showed moderate resistance against yellow stem borer. The study was successful in identifying some highly promising accessions on the basis of their performance for various seed yield component and biotic stress resistance. Among these, IC463183, IC462334, IC577390, IC466655 and IC579017 are particularly worth noting due to their excellence performance for various yield attributes across the years and resistance to both leaf blast and yellow stem borer. Such accessions could be potentially utilized breeding for superior rice cultivars suitable to the eastern Indo-gangetic plains of India.

Keywords: Biotic stresses, Biplot analysis, Diversity, G × E interaction, Indo-Gangetic plains.

Introduction

Rice is the most important food crop that feeds more than half of the world's population (Khush and Jena 2009). Rice is grown in 158million hectares around the world with a production of 700 mt (Ricepedia, IRRI). A larger share of production statistics i.e 89% area as well as 90% of world paddy production is contributed by Asia. In India rice is grown in an area of44 mha with a production of 104.3 mt. Rice also provides 20 per cent of the World's dietary energy supply compared to wheat and maize which provides 19 and 5 per cent, respectively (FAO, 2013). Much of India's food grains supply comes from Indo-Gangetic Plain (IGP), contributed significantly towards India's food security. Eastern plain zone under upper Indo-gangetic plains is one of the important rice growing areas of Uttar Pradesh. On the other hand, the area is facing severe problems of soil degradation and environmental calamities. In recent yearsthe rice yields of Indo-Gangetic plains decreased from 4.84 t/ha to 3.25 t/ha indicating 33 % decline. In addition to that, the agro-climatic zone based study of Uttar Pradesh by Bhatt et al. (2019) noticed large number ofextreme rainfall events.They warned that the spatio-temporally uncertain rainfall is likely to inflict a significant impact on the productivity of rice crop in this region. These problems have reduced the agricultural productivity resulting in low economic returns, and poor quality of life for farmers of this region.

The frequency, timing, intensity and duration of each of these stresses, as well as their specific combinations, vary from year to year (Patel et al. 1987). One of the most effective ways of combating these problems is to breed varieties more adaptable to specified areas and thereby increase the crop productivity and inturn economic returns to the farmers. Similarly, Ceccarelli (1994) concluded that selection under low input conditions is essential if significant yield gains for such conditions are to be achieved. Therefore, response to

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selection is maximized when selection is conducted in the environment where the future varieties will be grown.

During the green evolution era,the rapid development of high yielding, semi-dwarf, input responsive rice varieties resistant to pests and diseases led to the replacement of local low yielding landraces leading to erosion of genetic diversity. Rice diversity was further reduced due to continuous breeding activities involving crossing of genetically related parents. Hence, it necessitated the screening of available rice germplasm in that particular area and selection of best performing lines for breeding high yielding and highly adaptable varieties to targeted region. Hence, a location based study over the yearspertinent to the magnitude and direction of genetic variability on diverse sources of germpalsm for traits of economic importance is a prerequisite for continued genetic improvement and to cater to the needs ofthis region. Keeping this in view, the present study was undertaken to evaluate the agronomic performances of Indian germplasm accessions in the target area, to classify the accessions based on their agronomic performance and resistance to biotic stresses, and to identify promising accessions for potential use in breeding of varieties suitable to eastern Indo-Gangetic plains.

Materials and methods

The present investigation was carried out at ICAR- Indian Institute of Seed Science, Kushmaur, Mau, Uttar Pradesh, India, situated at 25°.57 N latitude, 83°.36 E longitude and altitude of 63.70 m above mean sea level. The soil of the experimental field was clayloam in texture, slightly alkaline in reaction (pH 8.0 to 8.4), low in organic carbon (0.30%) and available N (121 kg/ha), medium in available P (12.50 kg/ha) and available K (142.0 kg/ha). The major meteorological parameters recorded during the experimental seasons (2018 and 2019) are presented as Fig. 1. The plant materials consisted of 145 rice germplasm lines (Supplementary Table S1) representing diverse genetic material, comprising land races with short, medium, long duration groups, irrigated and rainfed ecotypes, basmati and non-basmati grain types obtained from ICAR- Indian Institute of Rice Research, Hyderabad (Singh et al. 2017). In addition to that, ten rice varieties were used as checkscomprising popular varieties of Indo-Gangetic plains (Sarjoo-52, HUR 105, PR-113, PS-3 and PS-5), popular local land race (Kala namak), varieties adopted to saline soil (NDR-359) and poor quality of ground water used for irrigation (PR-118) and varieties of national importance with better grain quality characters (BPT-5204, MTU-7029). The experimental material was planted in a randomized complete block design (RCBD) with two replications for two seasons during *kharif* 2018 and 2019. Twenty-five days old seedlings were transplanted 20cm apart between rows and 15cm within the row in one m^2 area. All the recommended package of practices were followed. Five representative plants for each germplasm from each replication were randomly selected to record observations on twelve quantitative characters under study *viz.,*plant height (PH), uppermost internodes (UI), number of tillers/plant (NTP), flag leaf length (FLL), flag leaf width (FLL), days to 50% flowering (DFF), days to maturity (DM), number of panicles/plant (NPP),panicle length (PL), number of primary branches/panicle (PBPP), test weight (TW) and grain yield per m^2 plot (GY).

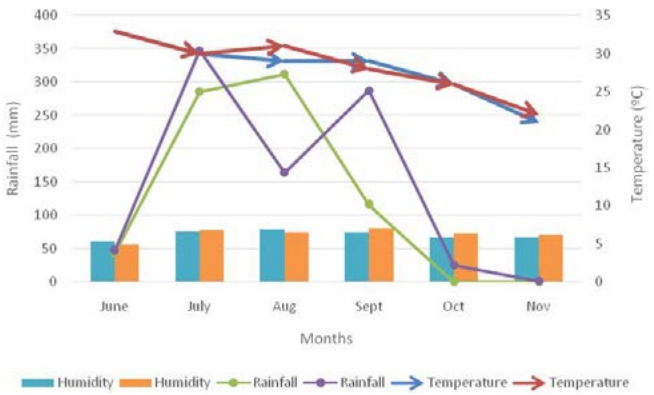

Fig. 1. Monthly average weather conditions in eastern Uttar Pradesh during the rice growth period in 2018 and 2019

Screening for biotic stresses

All the accessions along with two susceptible genotypes (HR-12 and Pusa Basmati 1121) were used to screen for leaf blast resistance under natural condition in the Uniform Blast Nursery (UBN) at the experimental farm of ICAR–IISS, Mau. Each line was planted in 50 cm long rows in raised nursery beds at row spacing of 10 cm apart. In addition, the susceptible checks were sown in borderlines as spreader rows as well as after every 10 test entries for the uniform spread of the disease. The UBN was exposed to an inoculum of *Magnoporthegrisea* from heavily sporulated lesions in leaves of susceptible checks. Disease reaction was recorded when the spreader row/ susceptible genotypes showed 85% of the disease symptom. Disease evaluation was performed according to the Standard Evaluation System (SES) of IRRI, (2002) for screening of leaf blast, with scores ranging from 0 to 9. Blast lesion type and the leaf area covered with infection were recorded. The test entries with 0-3 scores were graded as highly resistant (HR), 4-5 as moderately resistant (MR), and 6-9 as susceptible (S). The natural incidence of stem borer was estimated in field as per cent white earheads at reproductive stage (IRRI 2002). Observations on the incidence of stem borer in terms of white ears were recorded at reproductive stage. For each entry ten hills were selected randomly in each replication and per cent white ear damage was calculated, such as proportion ofnumber of white ears to thenumber of productive tillers expressed in percentage.

Statistical analysis

Analysis of variance (ANOVA) of all the traits was performed for both individual season and pooled data using the online

software available at http://stat.iasri.res.in/sscnarsportal and error variance was tested for homogeneity. The descriptive statistics, correlation, cluster analysis and principle component analysis was performed using R v3.6.2 (R Core Team 2019) and Microsoft excel. Descriptive statistics suchasrange and coefficient of variation were estimated (Snedecor and Cochran 1994) to quantify variability and compare across the traits. The broad sense heritability (H^{2}b) was worked out across the environment using the following formula.

$$H^2b=s^2g/ [s^2g + (s^2ge) / e) + (s^2error / re)]$$

Where s^{2}g is the genotype variance, s^{2}ge is the genotype × environment interaction variance, and s^{2}error is the residual variance, r is the number of replication and e is the number of environments. The Genetic Advance as percentage of Mean (GAM) was calculated by using the formula given by Robinson et al. (1949). Correlation analysis was computed as per Karl Pearson (1932). Hierarchical clustering of genotypes was performed by Euclidean distance using Wards method of clustering (Ward 1963). The principal component analysis (PCA) was computed on standardized data by correlation matrix (Pearson 1 1901).

Results and discussion

Variance and other genetic parameters

Identification of genetic variation is the key to future crop improvement. Domestication and modern breeding has reduced genetic diversity of crop plants by concentrating only on productivity of the crop (Tanksley and McCouch 1997). However new varieties are continuously bred to meet the existing consumer demand and also for protection of crops against unpredictable outbreak of biotic and abiotic stresses. Therefore, understanding the extent of genetic variability in crop genetic resources available in seed bank collections is important for effective future collection, development of conservation strategies and efficient use of theses genetic resources.Analysis of the phenotypic performance of the 155 lines for various yield attributes in the present study revealed the significant genetic variability among the accessions. Analysis of variance (ANOVA) of individual seasons as well as in pooled analysis over seasons revealed highly significant effects of years (environments), genotypes as well as genotype × environment (G × E) interaction for different yield components (Table 1). Seed yield per plant showed significant year effect, genotypic effect as well as G × E interaction. The mean squares attributable to environments were also significant for majority of the traits except for test weight ($P \geq 0.01$), plant height and flag leaf width (P d" 0.05). This indicated that two environments that we used to evaluate the genotypes were diverse and sufficient to differentiate the genotypes. Although the mean squares of G × E interaction were significant for UI, FLL, DFF, PBPP, DM and GY, their magnitude remained low compared to the mean squares of genotypes. Hence, contribution of G × E was low to moderate (0.42%-35.15%) relative to the genotypic contribution towards the total variability for all the traits.

The wide range of variability was found for all the traits studied corroborating results obtained in individual and pooled analysis of variances. Except for UI, PL and NPBP which showed moderate values, all the other traits recorded higher estimates of PCV and GCV (>20%) (Supplementary Table S2). The character SY recorded highest estimates of PCV (84.45%) and GCV (83.02%) followed by DFF. Similar trend was observed for heritability in broad sense. Heritability worked out from the pooled analysis was highest for PH (99.4%) followed by DFF (99.16%). In the present study, high heritability followed by the high genetic advance was recorded for seven traits (SY, DFF, TW, NPP, FLW, DM and NTP) indicated the predominance of additive type of gene action in the inheritance of these characters as proposed by Abebe et al. (2017), while similar findings were reiterated from Akinwale et al. (2011) and Sadeghi (2011). The lower G × E interactions and high heritability coupled with high GAM for the above mentioned traits suggested the possibility of a good response toselection. Similar high heritability and low G × E interaction for these traits have been reported in rice by Kumar et al. (2016); Osundare et al. (2017) and Oladosu et al. (2018). The summary statistics over the years depicts that the improved (check) varieties outperformed the land races in both the years, but there were notable exceptions; some of the landrace accessions recorded promising performance for specific yield components.

Disease reaction of germplasm against biotic stresses

Rice leaf blast caused by *Magnoporthegrisea* and yellow stem borer (*Scirpophagaincertulas)* remains the most destructive disease and pest of rice (Vasudevan et al. 2014). Deployment of resistance genes have been suggested as the most effective and eco-friendly way of managing them. However, the existence of geographically diverse strains of these pathogens are challenging for the rice breeders. Hence, it is important to build a repertoire of resistant accessions/donors that could be readily incorporated in breeding programs according to the needs of the local climatic conditions. A large majority of the rice genotypes exhibited complete resistance when compared to the susceptible control lines. We found 68 accessions (43.87 %) to be blast resistant with scores between 0 and 3. 28 of these accessions exhibited highly resistant reaction with score 0 including the cultivated varieties HUR 105, NDR-359, PS-5, Kalanamak and PR-118. 16 accessions including the cultivated variety Sarjoo-52 and PR-113 showed score of 1; and 23 accessions with score of 2 and 3 including the cultivated variety PS-3. A relatively smaller set of 31 accessions (20.65%) exhibited moderate resistance with scores 4 and 5, which consisted of

Table 1. Mean squares of pooled analysis of variance for 12 traits evaluated in two different environments

Trait df	Environment (1)		Replication (1)	Genotype (154)	G × E (154)	Error (308)	Mean	SE	CD	CV (%)
PH	2018	41.77*	4.06	1831.00**	9.84	4.06	154.79	1.42	3.95	1.30
	2019		0.15	1707.00**		4.21	154.27	1.45	4.02	1.33
	Pooled		2.11	3528.00**		4.13	154.53	1.57	4.35	1.44
UI	2018	58277**	0.34	64.22**	91.77**	2.63	37.90	1.15	3.18	4.28
	2019		0.76	196.84**		7.99	57.29	2.00	5.54	4.93
	Pooled		0.55	169.29**		5.31	47.59	4.79	13.20	14.2
NTP	2018	54.13**	0.34	7.64**	1.45	0.75	10.233	0.61	1.70	8.47
	2019		0.85	4.34**		0.45	10.824	0.47	1.31	6.18
	Pooled		0.60	10.54**		0.60	10.528	0.60	1.67	8.08
FLL	2018	306.4**	63.80**	112.67**	66.89**	5.94	38.88	1.72	4.78	6.27
	2019		1.14	90.54**		3.43	37.47	1.31	3.63	4.94
	Pooled		32.50*	136.32**		4.69	38.17	4.09	11.30	15.1
FLW	2018	0.03*	0.00	0.16**	0.01	0.0034	1.532	0.041	0.11	3.81
	2019		0.01	0.13**		0.0031	1.518	0.040	0.11	3.68
	Pooled		0.00	0.28**		0.0033	1.525	0.045	0.12	4.13
DFF	2018	900.1**	9.7-*	1250.00**	10.11**	2.17	106.05	1.04	2.89	1.39
	2019		19.6-**	1150.00**		2.24	108.46	1.06	2.93	1.38
	Pooled		14.60*	2390.00**		2.20	107.25	1.59	4.41	2.10
NPP	2018	26.19**	0.31	7.93**	0.76	0.75	9.123	0.61	1.70	9.52
	2019		0.17	4.67**		0.42	9.535	0.46	1.27	6.80
	Pooled		0.24	11.84**		0.59	9.329	0.44	1.21	6.60
PL	2018	71.55**	0.21	13.07**	1.25	0.77	27.31	0.62	1.72	3.21
	2019		0.05	11.90**		0.71	26.63	0.59	1.65	3.16
	Pooled		0.13	23.73**		0.74	26.97	0.56	1.55	2.93
NPBP	2018	132.6**	0.58	4.21**	2.21**	0.42	12.31	0.46	1.28	5.29
	2019		0.15	2.52**		0.07	11.38	0.19	0.52	2.35
	Pooled		0.37	4.53**		0.25	11.85	0.74	2.06	8.86
DM	2018	17757**	694.00**	1584.00**	157**	6.32	131.43	1.78	4.93	1.91
	2019		33.50**	990.00**		2.74	142.13	1.17	3.24	1.16
	Pooled		364.00**	2417.00**		4.53	136.78	6.28	17.40	6.49
TW	2018	6.41	2.91	36.51**	0.56	0.41	21.59	0.45	1.26	2.97
	2019		0.77	34.98**		0.23	21.39	0.34	0.93	2.22
	Pooled		1.84	70.94**		0.32	21.49	0.37	1.04	2.46
GYP	2018	639753**	143.00	148881.00**	28121**	2122.00	447.50	32.60	90.30	10.30
	2019		18969.00**	205678.00**		1149.00	511.70	24.00	66.50	6.60
	Pooled		9556.69	326438.00**		1636.00	479.60	83.80	232.40	24.70

Values in the parenthesis are degrees of freedom (df) for individual environment. **Significant at the 0.05, 0.01 probability levels, respectively. PH = plant height, UI = Uppermost internodes, NTP = Number of tillers/plant, FLL = Flag leaf length, FLW = Flag leaf width, DFF = Days to 50% flowering, DM = Days to maturity, NPP = Number of panicles/plant, PL = Panicle length, NBPP = Number of primary branches/panicle (PBPP), TW = Test weight and GY = Seed yield per m^2 plot, SE = Standard error, CD = Critical difference and CV = Coefficient of variation

MTU-7029. Along with the variety BPT-5204, 56 genotypes (36.13%) showed susceptible reaction to the blast pathogen *Magnorporthegrisea* with a score of 6-9.The damage intensity by yellow stem borer, *Scirpophagaincertulas* was measured on the basis of percentage of white ears. No germplasm accessions or varieties were found to have complete resistance against stem borer infestation. Only 58 (37.41%) accessions showed moderate resistance reaction with white ear percentage of 5-10 %. Among the cultivated varieties; HUR-105, Sarjoo-52, PS-5, PR-113, PR-118 and NDR-359

exhibited moderate resistance reaction against stem borer. White ear infestation of more than 10% was recorded in 97 (62.58%) of accessions exhibiting susceptibility. Besides complete resistance to leaf blast pathogen by some of the accessions, several lines conferring moderate resistance against leaf blast and yellow stem borer were identified in the present study. Considering the chances of breakdown of major gene conferred resistance in future, lines with moderate resistance could serve as potential donors for characterizing weaker yet more durable sources of resistance (Dean et al. 2005). Further, a set of 35 accessions showed complete to moderate resistance reaction against both leaf blast and yellow stem borer. Literature suggests that, there are evidences for genes conferring resistance against multiple pathogens. For example, the highly studied wheat leaf rust resistance gene *Lr34* confers broad spectrum and durable resistanceto leaf rust, stripe rust and powdery mildew (Kou and Wang 2010). Therefore, it would be highly interesting to test the lines showing resistance to both leaf blast and yellow stem borer for their response to other economically important rice pathogens.

Character association and cluster analysis

As per Falconer selection for a targeted trait will result in correlated response of associated traits. Based on the two season pooled data, the correlationanalysis was conducted to determine the direction and magnitude of relationships among the 12 agronomic traits (Supplementary Table S3). The traits such as PH, UI, FLL, FLW, PL and PBPP possessed significant positive correlation with each other and also significant negative correlation to NTP, DFF and DM with few exceptions.The trait GY showed significant positive correlation with TW, UI and FLL (P de 0.05), and highly significant negative correlation with DFF and DM (Sabri et al. 2020). It was also observed that TW has significant positive correlation with PL, PBPP, FLL and FLW. Hence, for enhancing the SY; due attention must be paid for the selection of a line with higher inter-correlated traits *viz.*, TW, PL, PBPP, UI, FLL and FLW. A total of 155 genotypes were grouped into seven different clusters considering 12 quantitative traits based on Ward's method of clustering. As evident from Fig. 2 and Table 2, Cluster I was the biggest (34 accessions)

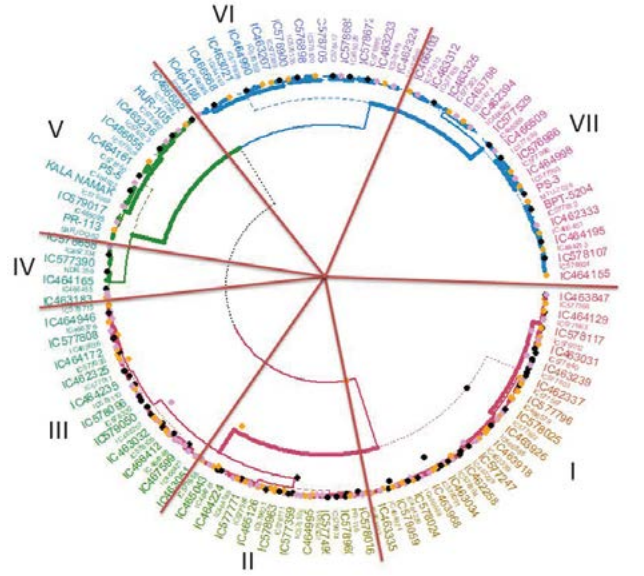

Fig. 2. **Cluster diversity of 155 rice germplasm accessions based on 12 quantitative characters**

Table 2. Estimates of traits means of the rice germplasm accessions belonging to different clusters

Particulars	Clusters and their means						
	I	II	III	IV	V	VI	VII
Traits							
PH	159.61	156.39	151.83	159.48	148.28	154.12	152.07
UI	44.62	47.90	49.39	49.59	48.66	48.14	48.00
NTP	10.27	10.83	10.24	10.36	10.59	10.79	10.58
FLL	35.71	38.99	40.09	41.42	37.87	38.83	37.96
FLW	1.43	1.60	1.47	1.57	1.48	1.62	1.55
DFF	122.96	109.53	99.81	95.50	110.69	99.47	99.65
NPP	9.04	10.03	8.90	8.87	9.31	9.52	9.38
PL	27.12	27.09	26.53	28.33	26.86	26.77	26.93
NBPP	11.96	11.84	11.93	12.24	11.92	11.74	11.61
DM	154.25	138.65	131.29	127.79	137.17	128.10	128.07
TW	20.23	22.34	21.06	22.90	22.78	21.95	21.06
GY	98.48	288.59	417.08	1072.29	865.38	699.73	542.27
Proportion (%)	**21.94**	**12.90**	**14.19**	**4.52**	**11.61**	**16.13**	**18.71**

PH = Plant height, UI = Uppermost internodes, NTP = Number of tillers/plant, FLL = Flag leaf length, FLW = Flag leaf width, DFF = Daysto50% flowering, DM = Days to maturity, NPP = Number of panicles/plant, PL = Panicle length, NBPP = Number of primary branches/panicle (PBPP), TW = Test weight and GY = Seed yield per m^2 plot.

and cluster IV was the smallest (7 accessions). Clusters II, III, V, VI and VII consisted of 20, 22, 18, 25 and 29 accessions, respectively.The cluster I recorded lowest mean values for the characters UI, FLL, FLW, TW, SY and as such took longer duration for flowering and maturity. On the other hand, cluster IV had the highest mean for eight traits under study *viz*., SY, TW, PL, PBPP, UI, FLL, early to flower and maturity followed by cluster V. The accessions under cluster IV and cluster V together possessed 25 accession out of which 6 are popular varieties (Checks) along with5 accessions with performanceon par with the checks, whereas remaining 14 accessions showed promising performance over the years for seed yield and related traitswhile being superior to the checks tested. The cluster I is highly diverse when compare to the clusters IV and V. Hence, the accessions of cluster IVand V in cross combination with cluster I might be useful in multiple crossing programme to recover transgressive segregants with high genetic yield potential and early to medium maturity.

Promising accessions were identified based on seed yield per plot, maturity and associated characters along with their resistance to biotic stresses (Leaf blast and Yellow stem borer). Fourteen accessions showed far superior performance compared to the check varieties with respect to yield and associated characters (Table 3). These are: IC463183, IC462334, IC466455, IC463236, IC464922, IC577390, IC464161, IC464165, IC466655, IC465095, IC577809, IC578089, IC578658 and IC579017. Comparison of the days to flowering and maturity in the 14 promising accessions showed that the lines, IC466455, IC463236 and IC466655 are early; IC462334, IC464922,IC577390, IC465095, IC577809 and IC579017 are medium; IC463183 and IC578658 are late; and IC464161, IC464165 and IC578089 were very late to flower and mature. Among the 14 best performing accessions, five showed resistance to moderate resistance against both leaf blast and yellow stem borer.

Principle Component Analysis (PCA)

PCA is a useful technique for analysing a wide data set consisting of number of variables for a sample (Mohammadi and Prasanna 2003). The PCA carried out for twelve quantitative characters on 155 genotypes,where in four principal components (PC) together explained 70.68% of cumulative variation (Table 4). The principal components with standard deviation greater than 1 are often the most important in reflecting the variation patterns among accessionsand the traits associated with these are more useful in differentiating them. Bifurcation of cumulative variance revealed highest contribution of 27.42% from PC1, followed by PC2 (21.5%). Component 3 and 4 contributed 13.73% and 8% towards cumulative variance, respectively. Partitioning of eigen values of the PCs (factor loadings) indicated correlation among traits FLL, FLW and UI within the PC1. Component 2 (PC 2) comprised PH, DFF PBPP and DM. Similarly, PC3 was associated with NTP and NPP, whereas PC4 indicated association with TW and GY. Madhubabu et al. (2020) through principle component analysis of 281 rice accessions opined that days to 50% flowering, total number of tillers, effective tiller number, panicle length and thousand grain weight were important traits useful for classification. Gour et al. (2017) and Chakravarthy et al. (2013) have also reported analogues results when working with 83 and 51 rice genotypes, respectively.

Table 3. Promising accessions for grain yield and associated characters, resistance to leaf blast and yellow stem borer in 145 germplasm accessions along with checks

S.No.	Genotypes	Traits of economic importance							LB	YSB
		NTP	NPP	PL	PBPP	DM	TW	GY		
1	IC463183	12.08	9.93	27.91	13.18	141.50	24.72	1020.00	MR	MR
2	IC462334	9.75	8.18	27.29	11.80	121.67	23.42	1099.00	R	MR
3	IC466455	9.05	8.10	29.25	13.30	110.75	17.79	1033.75	S	MR
4	IC463236	9.88	9.20	29.44	11.40	110.75	18.85	975.25	S	S
5	IC464922	11.45	9.40	28.31	11.65	124.50	23.03	1012.00	S	MR
6	IC577390	9.85	7.80	27.96	12.10	126.50	22.35	1078.75	MR	MR
7	IC466655	9.28	8.45	27.77	11.10	106.00	17.93	986.00	R	MR
8	IC465095	9.30	8.45	28.00	11.60	124.00	25.72	1009.21	S	S
9	IC464161	8.55	6.95	27.59	12.80	167.50	33.43	983.00	R	S
10	IC464165	10.55	8.63	33.18	13.25	170.50	23.91	1092.25	R	S
11	IC577809	9.85	9.05	28.85	12.30	124.00	21.89	986.00	MR	S
12	IC578089	11.28	9.65	28.96	11.20	170.00	21.68	991.50	S	S
13	IC578658	12.63	11.75	25.92	10.95	140.50	24.25	1101.25	S	S
14	IC579017	10.38	8.83	25.76	12.00	123.25	23.83	1027.00	R	MR
15	NDR-359(C)	8.60	7.73	26.82	11.13	118.25	23.89	1007.00	R	MR
16	PS-5(C)	9.60	7.48	26.40	10.45	123.50	25.50	962.00	R	MR
17	Kala namak(C)	11.85	10.55	25.26	13.25	163.50	14.12	923.25	R	MR
18	PR-113(C)	12.08	10.95	24.55	12.20	131.50	26.91	894.25	R	MR
19	Sarjoo-52(C)	9.55	8.15	28.42	12.75	129.25	21.85	876.50	R	MR

LB = Leaf blast, YSB = Yellow stem borer, C = Checks, R = Resistant, MR = Moderately resistant, S = Susceptible, NTP = Number of tillers/plant, DM = Days to maturity, NPP = Number of panicles/plant, PL = Panicle length, NBPP = Number of primary branches/panicle, TW = Test weight and SY = Seed yield per m^2 plot

Table 4. Principle components (PCs) extracted for 12 quantitative traits based on correlation matrix and factor variable correlations (Factor loadings)

Parameters	Principal components			
	PC1	PC2	PC3	PC4
Standard Deviation	1.81	1.59	1.28	1.00
Proportion of variance	0.274	0.211	0.137	0.083
Cumulative Variance (%)	27.4	48.6	62.3	70.6
Eigen Value	3.29	2.54	1.65	1.01
Traits	Factor loadings			
PH	-0.244	-0.364	-0.287	-0.060
UI	-0.366	0.052	-0.261	0.387
NTP	0.302	0.249	-0.529	-0.170
FLL	-0.397	0.012	-0.348	-0.008
FLW	-0.320	0.132	0.016	-0.155
DFF	0.279	-0.496	-0.083	0.112
NPP	0.308	0.248	-0.527	-0.205
PL	-0.313	-0.190	-0.254	-0.331
NBPP	-0.153	-0.389	-0.200	0.122
DM	0.292	-0.497	-0.073	0.077
TW	-0.228	-0.085	0.224	-0.572
SY	-0.153	0.191	-0.060	0.531

PH= plant height, UI = Uppermost internodes, NTP = Number of tillers/ plant, FLL = Flag leaf length, FLW = Flag leaf width, DFF = Days to 50% flowering, DM = Days to maturity, NPP = Number of panicles/plant, PL = Panicle length, NBPP = Number of primary branches/panicle (PBPP), TW = Test weightand SY = Seed yield per m^2 plot

PCA scatter diagram was drawn from the PC scores of the individual genotypefor each trait, depicting the genotype by trait (GT) biplot of PC1 and PC2 (Fig. 3). GT biplot is an excellent tool for visualizing genotype by trait data. First, it depicts the contribution of individual traits to the total variability and reveals the interrelationships among the traits studied. Second, it provides a tool for visual comparison among the genotypes on the basis of multiple traits. Third, it can be used for selection of trait specific genotypes and comparing selection strategies for improvement. Largest variations explained by the biplotcame from DFF, DM, NTP and NPP because these are the traits contributing more towards PC1 and PC2. Acute angle between the traits TW, PL, FLL, UI, FLW and PL with GY indicated a positive association, whereas DFF and DM had negative association (obtuse angle) with SYcorroborating the result obtained in cluster analysis and correlation studies. Bhatti et al. (2005) have reported positive correlation between 1000-grainweight and grain yield. Mohamed et al. (2012) and Fiyaz et al. (2013) have reported thatpanicle length and 1000-grain weight had significant positive correlation with grain yield; this indicates that genotypes with bold seed size have long panicle length, increased number of spikelet and finally resulting in higher yield, hence proposed it as selection criteria of genotypes for improving yield in rice.Among the 14 accessions which out-performed check varieties with respect to seed yield and related characters, 11 accessions such as IC463183 (24),

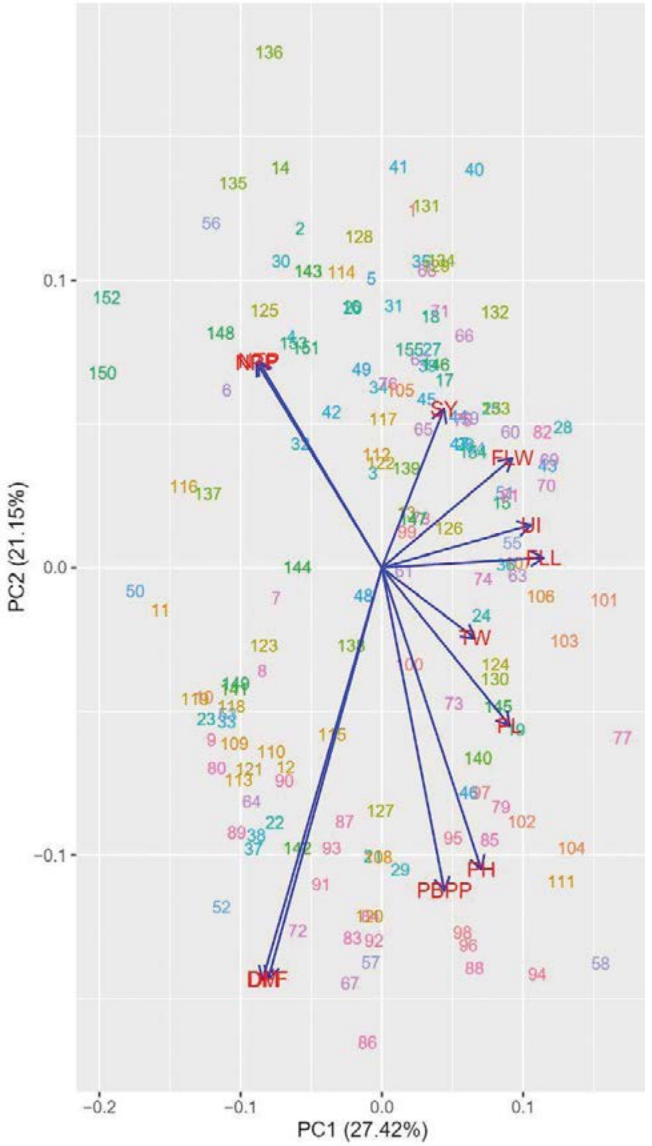

Fig. 3. PCA scatter diagram depicting the contribution of individual genotypes towards major principal component (PCs) for 12 quantitative characters

IC462334 (25), IC466455 (28), IC463236 (34), IC464922 (47), IC577390 (63), IC466655 (75), IC465095 (81), IC577809 (106), IC578658 (131) and IC579017 (139) within the cluster IV and V had narrow angle with SY vector, indicating their importance for future targeted breeding efforts in rice. Yan and Rajcan (2002) analysed seed yield component of soybean for six years and used GT biplot for selection of superior lines for seed yield.

The study led to the identification of some highly promising accessions with location-specific performance. It is significant to note that at least 14 accessions recorded far superior performance across the years compared to the standard checks. Among these five accessions (IC463183, IC462334, IC577390, IC466655 and IC579017) were worth noting, as these have recorded excellent performance for different yield related traits as well as resistance to both the biotic stresses, leaf blast and yellow stem borer. Such accessions could be potentially utilized in developing broad-based gene pools for improving diverse agronomic important traits and also biotic and abiotic stress tolerance in lieu with future climatic anomalies. From the breeding viewpoint, the rice accessions identified could also be potentially used to design a strategy for development of high yielding, stable and climate resilient varieties more suitable for eastern Indo-Gangetic plains of India.

Suplementary materials

Three Supplementary tables are supplied.

Authors' contribution

Conceptualization of research (BKN, CS); Designing of theexperiments (BKN, UBK); Contribution of experimental materials(CS, SK); Execution of field/lab experiments and data collection (BKN, CS, SKV); Analysis of data and interpretation (BKN, RP); Preparationof the manuscript (BKN, RP).

Declaration

The authors declare no conflict of interest.

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Supplementary Table S1. List of germplasm lines and its IC numbers

Sl. No.	IC No.	Sl. No.	IC No.	Sl. No.	IC No.	Sl. No.	IC No.
1	IC576895	40	IC466509	79	IC465043	118	IC578102
2	IC576898	41	IC577011	80	IC577640	119	IC578104
3	IC576900	42	IC577012	81	IC465095	120	IC578106
4	IC576902	43	IC463312	82	IC464140	121	IC578107
5	IC576923	44	IC577035	83	IC464129	122	IC578110
6	IC576924	45	IC577098	84	IC464126	123	IC578111
7	IC463032	46	IC463636	85	IC577655	124	IC578117
8	IC462258	47	IC464922	86	IC577663	125	IC578120
9	IC463034	48	IC464946	87	IC464172	126	IC578135
10	IC462257	49	IC466582	88	IC464161	127	IC578150
11	IC463021	50	IC464990	89	IC466669	128	IC578320
12	IC463031	51	IC466579	90	IC464155	129	IC578417
13	IC463051	52	IC466585	91	IC464148	130	IC578419
14	IC576935	53	IC464974	92	IC464165	131	IC578658
15	IC466376	54	IC464995	93	IC464189	132	IC578672
16	IC466360	55	IC464998	94	IC464195	133	IC578685
17	IC576976	56	IC463798	95	IC577768	134	IC578705
18	IC466403	57	IC577247	96	IC466682	135	IC578715
19	IC466421	58	IC463847	97	IC577771	136	IC578960
20	IC462325	59	IC577322	98	IC464186	137	IC578963
21	IC462333	60	IC577359	99	IC577796	138	IC579012
22	IC462339	61	IC577364	100	IC577803	139	IC579017
23	IC466412	62	IC577389	101	IC577805	140	IC579021
24	IC463183	63	IC577390	102	IC467599	141	IC579050
25	IC462334	64	IC463918	103	IC465126	142	IC579059
26	IC576986	65	IC465028	104	IC577808	143	IC579074
27	IC463207	66	IC577472	105	IC464235	144	IC579838
28	IC466455	67	IC463926	106	IC577809	145	IC464781
29	IC466451	68	IC577495	107	IC577812	146	NDR-359
30	IC462337	69	IC463960	108	IC464224	147	Sarjoo-52
31	IC463233	70	IC466668	109	IC464220	148	HUR105
32	IC463239	71	IC577529	110	IC464213	149	Kala namak
33	IC463229	72	IC463968	111	IC577922	150	MTU-7029
34	IC463236	73	IC577584	112	IC578016	151	PR-118
35	IC462324	74	IC577587	113	IC578024	152	BPT-5204
36	IC462394	75	IC466655	114	IC578025	153	PR-113
37	IC463335	76	IC577593	115	IC578089	154	PS-3
38	IC463332	77	IC464046	116	IC578091	155	PS-5
39	IC463325	78	IC577599	117	IC578096	-	-

IC. No.: Indigenous collection number

Supplementary Table S2. Genetic variance parameters of the rice accession for 12 traits evaluated from pooled data of two different environments

Traits	Mean	Range		Coefficient of Variation		H^2(bs) (%)	GA	GAM
		Minimum	Maximum	PCV (%)	GCV (%)			
PH	154.53	91.95	218.42	27.20	27.17	99.44	86.09	55.71
UI	47.59	23.99	74.33	19.63	19.03	29.70	5.72	12.01
NTP	10.53	5.95	16.50	22.42	21.17	75.85	3.69	35.03
FLL	38.17	21.29	60.40	22.00	21.25	34.17	5.91	15.48
FLW	1.53	0.88	2.33	24.83	24.54	94.55	0.74	48.36
DFF	107.25	60.00	158.50	32.25	31.22	99.16	70.65	65.87
NPP	9.33	4.90	15.60	26.72	25.43	87.96	4.52	48.42
PL	26.97	18.88	34.10	12.97	12.57	90.02	6.49	24.05
PBPP	11.85	8.20	15.60	13.04	12.35	34.48	1.10	9.26
DM	136.78	82.00	185.50	25.44	25.39	87.76	62.91	46.00
TW	21.49	9.49	33.52	27.78	27.65	98.43	12.10	56.33
SY	479.62	40.50	1258.00	84.45	83.02	84.14	701.98	146.36

PCV = Phenotypic Coefficient of Variation, GCV = Genotypic Coefficient of Variation, H^2(bs) = Heritability in broad sense, GA = Genetic advance, GAM = Genetic Advance as Percent of Mean, PH = Plant height, UI = Uppermost internodes, NTP = Number of tillers/plant, FLL = Flag leaf length, FLW = Flag leaf width, DFF = Days to 50% flowering, DM = Days to maturity, NPP = Number of panicles/plant, PL = Panicle length, PBPP = Number of primary branches/panicle (PBPP), TW = Test weight and SY = Seed yield per m^2 plot.

Supplementary Table S3. Genotypic and phenotypic correlation coefficient among 12 quantitative traits evaluated

Trait		UI	NTP	FLL	FLW	DFF	NPP	PL	PBPP	DM	TW	SY
PH	G	0.463**	-0.243**	0.597**	0.106	0.230**	-0.228**	0.466**	0.528**	0.230**	0.148	-0.056
	P	0.253**	-0.216**	0.369**	0.107	0.228**	-0.218**	0.446**	0.319**	0.214**	0.148	-0.053
UI	G		-0.225**	0.923**	0.367**	-0.458**	-0.230**	0.511**	0.265**	-0.479**	0.056	0.286**
	P		-0.145	0.431**	0.228**	-0.241**	-0.151	0.272**	0.113	-0.294**	0.026	0.174*
NTP	G			-0.206*	-0.213**	0.038	0.966**	-0.229**	-0.261**	0.061	-0.323**	0.041
	P			-0.084	-0.173*	0.033	0.938**	-0.167*	-0.140	0.032	-0.284**	0.041
FLL	G				0.494**	-0.438**	-0.156	0.563**	0.426**	-0.405**	0.206*	0.232**
	P				0.314**	-0.258**	-0.086	0.371**	0.183*	-0.292**	0.122	0.131
FLW	G					-0.383**	-0.214**	0.145	0.143	-0.409**	0.172*	0.134
	P					-0.374**	-0.193*	0.150	0.105	-0.390**	0.168*	0.112
DFF	G						0.045	-0.062	0.451**	0.994**	-0.107	-0.253**
	P						0.044	-0.058	0.259**	0.941**	-0.107	-0.233**
NPP	G							-0.222**	-0.309**	0.056	-0.314**	-0.008
	P							-0.174*	-0.176*	0.044	-0.296**	-0.005
PL	G								0.438*	-0.075	0.231**	0.020
	P								0.276**	-0.088	0.222**	0.015
PBPP	G									0.465**	0.173*	-0.002
	P									0.251**	0.096	0.017
DM	G										-0.110	-0.289**
	P										-0.101	-0.269**
TW	G											0.174*
	P											0.165*

G, P = Genotypic and Phenotypic correlation coefficients, respectively, *,**Significant at the 0.05, 0.01 probability levels, respectively. PH = Plant height, UI = Uppermost internodes, NTP = Number of tillers/plant, FLL = Flag leaf length, FLW = Flag leaf width, DFF = Days to 50% flowering, DM = Days to maturity, NPP = Number of panicles/plant, PL = Panicle length, PBPP = Number of primary branches/panicle (PBPP), TW = Test weight and SY = Seed yield per m^2 plot