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Genetic Variability, Character Association and Path Analysis in Boro Rice (*Oryza sativa* L.) Germplasm from Bangladesh

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ABSTRACT

The success of varietal development programmme largely depends on the nature and magnitude of genetic variability, heritability and characters association of the crop. The objective of the present study was to estimate the extent of genetic variability and relation between yield and related characters of rice. Forty Boro rice germplasm were evaluated in a randomised complete block design with three replications. Analysis of variance indicated significant differences among the genotypes for 14 quantitative characters. The presence of slightly higher phenotypic coefficient of variation than genotypic coefficient of variation indicated the negligible influence of environment on the expression of yield and its component traits. Leaf length, days to flowering, days to maturity and 1000 grain weight showed highly positive significant correlation present with yield hill^{-1}. High heritability had been observed for yield contributing traits during the study, suggested that these traits would respond to selection owing to their high genetic variability and transmissibility. Therefore, a thorough understanding of the inheritance of traits, their heritability and relationship with other important characteristics is important for the choice of breeding and selection methods for crop improvement.

Key words: Variability, heritability, correlation coefficients, path analysis, rice (*Oryza sativa* L.)

INTRODUCTION

There are thousands of rice varieties, genotypes and landraces which differ from each other with respect to plant types of various nature and grain characteristics such as, grain size, texture, glutinous or non glutinous, aromatic or non aromatic and quality (Islam *et al*., 2016). Asian and African farmers selected different types of rice to suit local condition and needs (Singh *et al*., 2000). It continues to be the major source of livelihood, especially in the rural areas and the main staple food for more than half of the world's population.

Rice plays a vital role in Bangladesh's economy and agriculture, accounting for nearly 18% of the gross domestic product (BBS, 2017). About 76% of the total cropped land is covered by rice and more than 66% of the total agriculture labour force is employed in rice production, processing, marketing and distribution. It provides about 62% of the calorie and 46% of the protein in the average daily diet for the people of the country (HIES, 2010). Bangladesh is the fourth largest producer and consumer of rice in the world with an annual production of 34.71 million metric tons (BBS, 2017). In Bangladesh, three major rice seasons namely Aus, T. Aman and Boro constitute 100% of total rice production and grow in three overlapping seasons. Among three growing seasons, Boro rice (irrigated rice) occupied the second highest, which is about 41.94% of total rice land and contributes 54.57% of the total rice production (Anonymous, 2017). Although

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Bangladesh is now on the verge of attaining self sufficiency in cereal production, there is still a gap between the production and demand. Again, population in the country is increasing rapidly and land under rice cultivation is decreasing day by day due to rapid urbanization and development of infrastructures. If this situation continues we have to face hard challenge to feed the numerous hungry mouths of the future. So, we should think of expanding rice production per unit area and increasing productivity or both.

Grain yield is the major factor in determining the improvement of a cereal crop. For efficient utilization of genetic stock in crop improvement, information of mutual association between yield and yield components is necessary. Grain yield in rice is a quantitative character, which is influenced by a number of yield contributing characters. So, the selection for desirable types should not only be based on yield, but other yield components should also be considered. The success of a breeding programme depends largely upon the amount of genetic variability present in the population and the extent to which the desirable traits are heritable. Moreover, knowledge of correlation between yield and its contributing agro-morphological traits are basic requirement to find out guidelines for plant selection. In rice, large amount of genetic variability has been reported (Khatun *et al*., 2015; Ahmed *et al*., 2015; Islam *et al*., 2017; Akter *et al*., 2018; Islam *et al*., 2018) which indicates the potential for genetic improvement. Partitioning of total correlation into direct and indirect effect by path analysis helps in making the selection more meaningful way. The present investigation was, therefore, undertaken to estimate genetic variability, associations among desired traits and their direct and indirect contributions toward grain yield in rice.

MATERIALS AND METHODS

Materials, design and intercultural operations

Forty Boro rice germplasm (Table 1) were collected from the Genebank of Bangladesh Rice Research Institute (BRRI) in which 11 were newly collected from the different districts of Bangladesh. The experiment was conducted at BRRI HQ farm, Gazipur during Boro season 2016-17. The trial was conducted in a randomized complete block design with three replications. Forty-day-old seedlings grown in wet seed bed were transplanted using single seedling hill^{-1} in 2.4 m^2 plot following 20 cm and 20 cm space between rows and plants respectively. Fertilizers were applied @ 80:60:40:12 kg N, P, K and S per hectare. All the fertilizers except N were applied at final land preparation. Nitrogen was applied as urea in three equal splits at 15 days after transplanting (DAT), at 35 DAT and just before flowering. Intercultural operations and pest control measures were done as and when necessary.

Data were collected from the randomly selected ten plants in each replication for leaf length (cm), leaf width (cm), number of effective tiller, panicle length (cm), plant height (cm), days to flowering, days to maturity, filled grains per panicle, 1000 grain weight (TGW) (g), grain length (mm), grain breadth (mm), decorticated grain length (mm), decorticated grain breadth (mm), decorticated grain length breadth ratio and yield hill^{-1} (g).

Statistical analysis

The analysis of variance was done using Statistix 10 software. The calculation of mean, range and standard deviation (SD) was also done for each character. The mean sum of square was estimated for the calculation of genotypic and phenotypic variances (Johnson *et al*., 1955). Genotypic and phenotypic coefficients of variation were estimated by the suggested formula (Burton, 1952). The broad sense heritability and genetic advance was estimated by the suggested formula (Johnson *et al*., 1955 and Lush, 1949). Genetic advance in percentage of mean was calculated for different characters by the given formula (Comstock *et al*., 1952). Phenotypic and genotypic correlations were calculated by using the suggested formula (Falconer, 1964). Path coefficient analysis was estimated according to method modified by Dewey and Lu (1959). After calculating the direct and indirect effect of different traits, the co-efficient of determination (R^2) and residual effect (U) were calculated using the formula suggested by Singh and Choudhury (1985).

Table 1. Information on local name, place of collection and season of the Boro rice germplasm.

Code no.	Local name	Acc. no.	Upazila	District	Season
G1.	Begun Bichi	7358	Sadar	Manikganj	Boro
G2.	Nerica-10	7361	Sadar	Jessore	Boro
G3.	Jhora Dhan-1	7362	Monirampur	Dinajpur	Boro
G4.	Jhora Dhan-2	7363	Sadar	Dinajpur	Boro
G5.	Minikit	7364	Sadar	Rangpur	Boro
G6.	Sada Jamai Babu	7368	Sadar	Satkhira	Boro
G7.	Kajollata	7369	Tala	Satkhira	Boro
G8.	Super Miniket	7370	Tala	Satkhira	Boro
G9.	Ponchog	7372	Tala	Khulna	Boro
G10.	Chandrone	7373	Dumuria	Jamalpur	Boro
G11.	Khaily	7374	Sadar	Jamalpur	Boro
G12.	Lal Swarna	7375	Sadar	Nilphamari	Boro
G13.	Pajam Boro	7376	Sadar	Naranganj	Boro
G14.	Sunwala Dhan	7378	Sadar	Naranganj	Boro
G15.	Sada Boro	7379	Sadar	Naranganj	Boro
G16.	Jirasail	7381	Sadar	Cumilla	Boro
G17.	Tepul	7382	Sadar	Patuakhali	Boro
G18.	Shakti-R	7386	Sadar	Gazipur	Boro
G19.	Khato Vojon	7656	Sadar	Pirojpur	Boro
G20.	Kali Boro-1	7657	Sadar	Pirojpur	Boro
G21.	Lal Vojon	7658	Sadar	Pirojpur	Boro
G22.	Black Vojon	7659	Sadar	Pirojpur	Boro
G23.	Sada Vojon	7660	Sadar	Pirojpur	Boro
G24.	Khami Dhan	7661	Sadar	Pirojpur	Boro
G25.	Abdul Hai	7662	Sadar	Barguna	Boro
G26.	Kalo Boro	7663	Sadar	Barguna	Boro
G27.	Aynasail	7665	Sadar	Sylhet	Boro
G28.	Ayla binni	7666	Sadar	Habigonj	Boro
G29.	Kali Boro-2	NC*	Sadar	Tangail	Boro
G30.	Atasail	NC*	Sadar	Tangail	Boro
G31.	Kajallata	NC*	Sadar	Jashore	Boro
G32.	Suballata	NC*	Sadar	Jashore	Boro
G33.	Unknown-1	NC*	Sadar	Jashore	Boro
G34.	Suballata	NC*	Sadar	Jashore	Boro
G35.	Super miniket	NC*	Sadar	Jashore	Boro
G36.	K-1	NC*	Sadar	Dinajpur	Boro
G37.	Sada Boro	NC*	Sadar	Rajshahi	Boro
G38.	Tulsi Boro	NC*	Sadar	Rajshahi	Boro
G39.	Unknown-2	NC*	Sadar	Rajshahi	Boro
G40.	Dhali Boro	NC*	Sadar	Tangail	Boro

*NC= New collection.

RESULTS AND DISCUSSION

After analyzing the mean performance of these germplasm, it was found that 20 germplasm for leaf length, 20 for leaf width, 13 for effective tiller, 23 for panicle length, 19 for plant height, 16 for days to flowering, 17 for days to maturity, 19 for filled grain per panicle, 20 for 1000 grain weight, 17 for grain length, 18 for grain breadth, 18 for decorticated grain length, 17 for decorticated grain breadth, 17 for decorticated grain length breadth ratio, 20 for yield hill^{-1} were out performed over their grand mean (GM) values, respectively (Table 2). According to the mean performance, of the studied germplasm, it is observed that few of them can be selected for their better performance, such as G28 for the highest yield hill^{-1}, G15 and G16 for similar higher yield, G20 for the highest TGW, G11 for filled grains per panicle, G39 for the shortest days to maturity, G17 for the longest panicle length and G2 for the longest grain length.

Table 3 presents the estimation of genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as percent of mean. Wide genotypic and phenotypic differences were present for all the traits except leaf width, grain breadth and decorticated grain length breadth ratio. This result presents that there is less/no environmental influence on these traits. High magnitude of genotypic coefficient of variation indicated the presence of substantial amount of genetic variability in the population and there was little influence of the environment on the expression of the studied characters. Phenotypic coefficients of variation were little higher than the genotypic coefficient of variation for all characters as it was expected. This is due to less environmental influences during the expression of the traits. The environmental influence would be added on PCV that made the value higher. Similar findings were also reported by Akter *et al.* (2018). The coefficients of genotypic and phenotypic variability were comparatively high for filled grains panicle^{-1} (30.32 and 30.60), effective tillers plant^{-1} (27.23 and 29.06) and yield hill^{-1} (27.25 and 27.31). These results were in agreement with the findings by Mishra and Verma (2002) and Gour *et al.* (2017).

Heritability of a trait is an index of transmission of characters from parents to its progeny. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population, hence prior knowledge about the heritability of the traits is a prerequisite for the selection programme (Singh *et al.*, 2011). Broad sense heritability explains both fixable (additive) and non-fixable (dominant and epistatic) variances, which helps in estimating the inheritance of a character (Nirmaladevi *et al.*, 2015). On the basis of heritability, the traits can be classified into three categories viz. highly heritable (> 70%), medium heritable (50-70%) and low (<50%) (Burton, 1952). The magnitude of the estimated broad sense heritability in this study ranged from 86.52 for leaf width to 96.70 for days to flowering. Leaf length, panicle length, plant height, days to flowering, days to maturity, filled grain per panicle, 1000 grain weight, grain length, grain breadth, decorticated grain length and decorticated grain length-breadth ratio were highly heritable, all with an estimated H^2>90.00, whereas other characters showed relatively low heritability. High heritability coupled with high genetic advance as percent of mean was observed in leaf length (96.12, 33.87), number of effective tiller (87.81, 40.32), filled grains per panicle (95.17, 36.47), 1000 grain weight (90.56, 35.72) and decorticated grain length breadth ratio (91.17, 31.49) indicating the role of additive gene expression of these traits and have better scope for improvement of these traits through direct selection. Similar results were reported by Gour *et al.* (2017) and Lakshmi *et al.* (2017).

Table 2. Mean performance of 40 Boro rice germplasm.

Code no.	LL (cm)	LW (cm)	ET	PL (cm)	PH (cm)	DF	DM	FG/P	TGW (g)	GL (mm)	GB (mm)	DGL (mm)	DGB (mm)	DGLBR	Y/H (g)
G1	42.40	1.04	12	24.93	123.00	116	142	189	11.60	5.25	2.95	3.55	2.57	1.38	15.29
G2	40.27	1.43	9	24.00	89.07	118	144	146	29.95	9.78	3.03	6.78	2.59	2.62	23.27
G3	38.80	1.14	11	20.53	78.03	118	144	76	20.20	7.55	2.81	5.40	2.54	2.12	13.54
G4	45.33	0.95	15	21.40	84.07	118	143	10	20.40	7.95	2.79	5.35	2.47	2.17	13.81
G5	37.80	1.00	11	24.00	95.43	115	141	177	23.33	9.22	2.17	6.87	1.92	3.58	23.40
G6	28.93	0.75	10	24.93	83.23	110	137	135	22.60	9.40	2.54	6.73	2.32	2.89	22.56
G7	36.07	0.90	9	26.47	96.00	110	136	147	22.20	9.35	2.80	6.61	2.34	2.83	22.37
G8	40.80	1.00	10	23.47	88.80	110	137	152	18.90	9.59	2.29	6.72	2.01	3.35	20.80
G9	38.53	1.24	10	23.47	93.23	120	146	161	29.00	9.48	3.03	7.10	2.65	2.67	23.85
G10	24.53	0.65	20	20.00	104.00	105	132	66	20.07	8.19	3.20	5.80	2.71	2.14	11.30
G11	34.20	1.10	10	25.00	96.67	136	162	204	22.70	7.70	2.88	5.59	2.63	2.13	23.91
G12	42.47	1.20	13	25.07	102.50	124	149	115	16.60	7.53	2.61	5.16	2.62	2.03	21.89
G13	44.13	1.25	12	23.53	117.80	118	144	124	17.80	7.62	2.73	5.23	2.39	2.18	22.27
G14	41.93	1.15	16	18.27	81.13	124	150	103	21.70	7.49	2.66	5.31	2.30	2.31	24.79
G15	44.40	1.23	12	25.00	92.20	118	145	150	22.50	8.28	2.57	5.78	2.25	2.57	25.42
G16	35.93	1.15	8	23.53	88.27	115	141	133	18.12	9.05	2.30	6.38	2.05	3.11	25.36
G17	37.53	1.05	11	31.47	95.80	139	166	88	26.40	8.49	3.26	6.18	2.81	2.19	23.47
G18	45.87	1.09	11	23.47	86.53	130	155	95	28.75	8.87	3.09	5.78	2.33	2.48	23.96
G19	35.60	1.04	13	21.40	74.93	130	157	87	28.20	8.22	3.20	5.82	2.84	2.05	22.69
G20	42.20	1.19	11	24.47	120.13	124	150	146	30.72	7.86	3.48	5.56	2.90	1.92	24.21
G21	33.33	1.14	11	21.93	63.73	116	142	119	26.10	8.07	3.31	5.50	2.77	1.99	20.38
G22	36.80	1.09	12	21.00	111.63	104	133	45	23.80	8.28	2.76	5.93	2.52	2.35	18.82
G23	46.80	1.25	9	27.60	86.33	117	143	115	25.00	8.10	3.21	5.70	2.86	1.99	21.47
G24	44.80	1.24	10	26.87	97.33	116	142	159	14.50	6.18	2.64	4.19	2.32	1.81	15.25
G25	72.27	1.03	10	23.40	111.53	131	157	114	25.30	8.23	3.06	5.33	2.53	2.12	24.10
G26	39.40	0.95	13	20.47	90.70	114	144	94	28.00	8.22	3.16	5.99	2.67	2.24	23.78
G27	36.67	0.99	10	26.33	94.07	127	152	150	21.40	8.57	2.66	6.16	2.21	2.79	17.53
G28	40.93	1.04	9	29.00	89.60	115	141	150	19.90	8.14	2.52	5.80	2.32	2.51	26.43
G29	29.20	0.81	25	19.40	112.40	105	132	147	16.85	8.85	2.63	6.34	2.19	2.89	8.663
G30	45.60	0.97	10	26.40	116.60	116	142	95	20.50	7.91	2.68	5.39	2.41	2.23	16.05
G31	28.26	0.94	13	21.47	83.10	114	140	114	17.30	8.23	2.30	5.96	2.01	2.97	16.16
G32	27.40	0.82	9	21.40	95.00	115	141	180	10.60	8.06	2.18	5.69	1.95	2.93	12.33
G33	32.00	1.05	11	22.40	75.07	113	140	102	23.30	9.63	2.34	6.54	2.15	3.05	11.26
G34	31.47	0.95	7	20.87	75.13	116	142	149	14.30	6.62	2.75	4.36	2.42	1.80	17.01
G35	38.40	1.09	9	25.00	78.00	116	142	122	16.53	9.05	2.24	6.45	2.04	3.16	15.49
G36	34.47	1.09	12	25.40	92.27	116	141	134	16.50	9.03	2.07	6.54	1.83	3.57	16.89
G37	29.67	1.03	11	20.40	101.13	102	130	67	20.40	7.41	2.79	5.55	2.40	2.31	15.87
G38	22.00	0.72	13	19.13	98.00	105	132	66	25.03	7.63	2.75	5.42	2.40	2.26	5.85
G39	43.20	1.07	10	25.47	110.67	93	120	131	29.53	9.42	3.06	6.66	2.68	2.49	24.14
G40	31.40	0.74	16	19.40	95.67	108	135	62	26.40	8.01	3.20	6.22	2.76	2.26	14.95
GM	38.05	1.04	11.65	23.44	94.22	116.43	142.81	122.85	21.83	8.26	2.76	5.84	2.42	2.46	20.24
CV	4.40	6.30	10.15	5.08	4.99	3.91	3.76	4.14	4.54	5.91	6.58	5.58	4.48	6.45	9.82

LL= Leaf length (cm), LW= Leaf width (cm), NET= Number of effective tiller, PL= Panicle length (cm), PH= Plant height (cm), DF= Days to flowering, DM= Days to maturity, FG/P= Filled grain per panicle, TGW= 1000 grain weight (g), GL= Grain length (mm), GB= Grain breadth (mm), DGL= Decorticated grain length (mm), DGB= Decorticated grain breadth (mm), DGLBR= Decorticated grain length breadth ratio, Y/H=yield hill^{-1} (g), GM= Grand mean, CV= Coefficient of variation

Table 3. Range, phenotypic variance (V_p), genotypic variance (V_g), genotypic and phenotypic coefficient of variation (GCV and PCV), heritability (h^2_b), genetic advance (GA), genetic advance in percent of mean (GAMP) of 40 Boro rice germplasm.

	Range	Vg	Vp	GCV	PCV	h_b^2	GA	GAM (%)
LL (cm)	22-72.27	69.21	72.01	21.86	22.30	96.12	12.89	33.87
LW (cm)	0.65-1.43	0.03	0.03	15.40	16.56	86.52	0.24	22.64
NET	6.93-24.67	10.06	11.46	27.23	29.06	87.81	4.70	40.32
PL (cm)	18.27-31.47	8.21	8.45	12.22	12.40	94.18	4.46	19.04
PH (cm)	63.73-123	185.67	193.59	14.46	14.77	95.91	21.08	22.38
DF	93-139	84.60	85.71	7.90	7.95	96.70	14.44	12.40
DM	120-166	77.50	78.68	6.16	6.21	95.50	13.80	9.67
FG/P	45-204.33	1387.01	1412.93	30.32	30.60	95.17	47.31	36.47
TGW (g)	10.6-30.72	25.84	25.96	23.29	23.34	90.56	8.01	35.72
GL (mm)	5.25-9.78	0.89	0.91	11.41	11.57	93.27	1.47	17.79
GB (mm)	2.07-3.48	0.13	0.13	12.90	13.00	93.52	0.56	20.23
DGL (mm)	3.55-7.10	0.55	0.56	12.68	12.77	92.47	1.16	19.87
DGB (mm)	1.83-2.90	0.08	0.09	11.45	12.30	86.74	0.41	16.85
DGLBR	1.38-3.58	0.25	0.25	20.22	20.51	91.17	1.78	31.49
Y/H (g)	5.85-26.43	30.43	30.56	27.25	27.31	89.55	6.70	35.96

LL= Leaf length (cm), LW= Leaf width (cm), NET= Number of effective tiller, PL= Panicle length (cm), PH= Plant height (cm), DF= Days to flowering, DM= Days to maturity, FG/P= Filled grains per panicle, TGW = 1000 grain weight (g), GL= Grain length (mm), GB= Grain breadth (mm), DGL= Decorticated grain length (mm), DGB= Decorticated grain breadth (mm), DGLBR= Decorticated grain length breadth ratio, Y/H= Yield/hill(g), Vg= Genotypic variance, Vp= Phenotypic variance, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, h^2_b= heritability, GA= Genetic advance, GAMP= Genetic advance in percent of mean

Heritability estimates (above 60%) along with genetic advance (above 20%) would be helpful in predicting gain under selection than heritability estimates alone. In this study, the estimation of genetic advance in the percent of mean were very high for number of effective tiller (40.32), filled grain per panicle (36.47), TGW (35.72), yield hill^{-1} (35.96) and whereas moderate for, leaf length (33.87) and decorticated grain length- breadth ratio (31.49). Similar results were reported by Mishra and Verma (2002) and Bornare *et al.* (2014). The characters, which exhibited high heritability, suggests that the selection will be more effective whereas the traits showing low heritability indicates that the selection will be influenced by the environmental factors. These results matched with Islam *et al.* (2016) and Lakshmi *et al.* (2017).

Table 4 presents the genotypic and phenotypic correlations of coefficient among the traits. The results revealed that genotypic correlations of coefficient values are always higher than the phenotypic correlations of coefficient value. Leaf length, days to flowering, days to maturity and TGW showed highly positive significant correlation present with yield hill^{-1} and these results agreed with Devi *et al.* (2017), Naseer *et al*. (2015), Vanisree *et al*. (2013) and Gour *et al*. (2017). Panicle length showed positive significant correlation with yield. In this circumstance, these traits would be effective in the direct selection process and meets with the findings of Reddy *et al*. (2013). Number of effective tiller showed significant negative correlation with yield so that this trait must be discarded from the direct selection. Similarly, plant height and decorticated grain length breadth ratio showed non-significant negative correlation with yield and matched with Moosavi *et al*. (2015) and Rawte and Saxena (2017). On the other hand, filled grain per panicle, grain length, grain breadth, decorticated grain length and decorticated grain breadth showed positive non-significant correlation with yield. Therefore, direct selection based on these traits would not be effective.

Leaf length, leaf width, days to flowering and TGW showed positive direct effect on yield and made the total correlation positive and significant (Table 5). Similar results were observed by Ashok *et al*. (2016) and Chuchert *et al*. (2016). Therefore, direct selection based on these traits would be effective for the yield improvement of Boro germplasm. Days to maturity projected negative direct effect on yield but made the total correlation positive and highly significant. Therefore, direct selection based on days to maturity would not hamper the yield improvement. Number of effective tiller showed negative direct effect on yield and made the total correlation negative and significant. This finding was in accordance with Prasad *et al*. (2013). Therefore, this trait has no effect on further yield improvement strategy of the studied germplasm. However, panicle length, grain length and grain breadth had negative direct effect on yield but made the total correlation positive and non-significant. This result agreed with Ketan and Sarkar (2014). Filled grain per panicle, decorticated grain length and decorticated grain breadth showed positive direct effect on yield and made the total correlation positive non-significant. Therefore, direct selection based on these traits would not hamper the yield improvement. Plant height and decorticated grain length- breadth ratio showed negative direct effect on yield along with negative non-significant total correlation which is agreed with Chuchert *et al*. (2016) and Reddy *et al*. (2013). Therefore, these traits must be discarded. Besides, the residual effect was found 0.3594, indicating 64.06% variability was estimated by the studied 14 yield contributing traits. The rest amount of variability (35.94%) would be controlled by other yield contributing traits which were not included in this study.

Table 4. Genotypic correlation coefficient (r_g) and phenotypic correlation coefficient (r_p) of 40 Boro rice germplasm.

		LW (cm)	ET	PL (cm)	PH (cm)	DF	DM	FG/P	X (g)	GL (mm)	GB (mm)	DGL (mm)	DGB (mm)	DGLBR	Y/H(g)
LL (cm)	r_g	0.520**	-0.278	0.359*	0.259	0.407**	0.396*	0.109	0.187	-0.079	0.209	-0.216	0.182	-0.249	0.529**
	r_p	0.479**	-0.227	0.361*	0.250	0.407**	0.398*	0.114	0.185	-0.067	0.212	-0.205	0.173	-0.243	0.519**
LW (cm)	r_g		-0.466**	0.366*	-0.065	0.382**	0.370*	0.245	0.191	-0.011	0.092	-0.074	0.141	-0.127	0.552**
	r_p		-0.354*	0.357*	-0.057	0.367*	0.351*	0.243	0.178	0.006	0.093	-0.059	0.145	-0.125	0.509**
ET	r_g			-0.547**	0.214	-0.218	-0.202	-0.351*	-0.025	-0.078	0.150	-0.016	0.102	-0.072	-0.379*
	r_p			-0.465**	0.189	-0.173	-0.158	-0.299*	-0.013	-0.047	0.160	0.006	0.107	-0.066	-0.355*
PL (cm)	r_g				0.152	0.352*	0.330*	0.395*	0.024	0.113	-0.018	0.077	0.035	0.042	0.343*
	r_p				0.152	0.357*	0.336*	0.397*	0.027	0.124	-0.008	0.086	0.044	0.041	0.339*
PH (cm)	r_g					-0.156	-0.150	0.089	-0.071	-0.248	0.163	-0.216	0.159	-0.234	-0.159
	r_p					-0.149	-0.144	0.086	-0.068	-0.236	0.161	-0.207	0.144	-0.224	-0.153
DF	r_g						0.995**	0.204	0.141	-0.134	0.206	-0.189	0.192	-0.219	0.418**
	r_p						0.994**	0.209	0.143	-0.122	0.210	-0.181	0.184	-0.214	0.416**
DM	r_g							0.164	0.178	-0.134	0.238	-0.180	0.227	-0.236	0.419**
	r_p							0.169	0.179	-0.120	0.242	-0.170	0.217	-0.231	0.416**
FG/P	r_g								-0.314	-0.006	-0.305*	-0.022	-0.322*	0.199	0.186
	r_p								-0.307	-0.001	-0.294*	-0.016	-0.289*	0.193	0.185
TGW (g)	r_g									0.448**	0.653**	0.443**	0.589**	-0.089	0.404**
	r_p									0.441**	0.649**	0.440**	0.549**	-0.088	0.403**
GL (mm)	r_g										-0.206	0.962**	-0.275	0.778**	0.218
	r_p										-0.196	0.953**	-0.244	0.757**	0.216
GB (mm)	r_g											-0.203	0.961**	-0.725**	0.195
	r_p											-0.195	0.896**	-0.711**	0.194
DGL (mm)	r_g												-0.247	0.789**	0.181
	r_p												-0.225	0.778**	0.181
DGB (mm)	r_g													-0.781**	0.235
	r_p													-0.773**	0.213
DGLBR	r_g														-0.028
	r_p														-0.025

*Significance at the 5% level and **Significance at the 1% level.

LL= Leaf length (cm), LW= Leaf width (cm), NET= Number of effective tiller, PL= Panicle length (cm), PH= Plant height (cm), DF= Days to flowering, DM= Days to maturity, FG/P= Filled grains per panicle, TGW= 1000 grain weight (g), GL= Grain length (mm), GB= Grain breadth (mm), DGL= Decorticated grain length (mm), DGB= Decorticated grain breadth (mm), DGLBR= Decorticated grain length breadth ratio, Y/H= Yield hill^{-1}(g)

Table 5. Partitioning of genotypic correlation into direct (bold phase) and indirect components of 40 Boro rice germplasm.

	LL (cm)	LW (cm)	NET	P L (cm)	PH (cm)	DF	DM	FG/P	X(g)	GL (mm)	GB (mm)	DGL (mm)	DGB (mm)	DGLBR	Y/H(g)
LL (cm)	**0.5256**	0.0653	0.0227	-0.0164	-0.0579	0.1199	-0.0653	0.0208	0.0331	0.0434	-0.0801	-0.2664	0.0134	0.1712	0.5293**
LW (cm)	0.2658	**0.1291**	0.0471	-0.0165	0.0196	0.1109	-0.0599	0.0460	0.0291	0.0031	-0.0350	-0.0859	0.0107	0.0874	0.5515**
ET	-0.1368	-0.0549	**-0.0873**	0.0237	-0.0464	-0.0595	0.0307	-0.0627	-0.0032	0.0389	-0.0584	-0.0196	0.0077	0.0480	-0.3798*
PL(cm)	0.1890	0.0468	0.0452	**-0.0457**	-0.0343	0.1042	-0.0548	0.0745	0.0039	-0.0673	0.0055	0.1015	0.0028	-0.0287	0.3426
PH (cm)	0.1344	-0.0080	-0.0179	-0.0069	**-0.2265**	-0.0453	0.0243	0.0166	-0.0128	0.1408	-0.0617	-0.2675	0.0115	0.1597	-0.1593
DF	0.2138	0.0485	0.0176	-0.0161	0.0348	**0.2947**	-0.1639	0.0387	0.0222	0.0749	-0.0789	-0.2337	0.0142	0.1515	0.4183**
DM	0.2085	0.0469	0.0163	-0.0152	0.0335	0.2931	**-0.1648**	0.0312	0.0279	0.0746	-0.0911	-0.2220	0.0177	0.1619	0.4185**
FG/P	0.0582	0.0315	0.0290	-0.0181	-0.0200	0.0606	-0.0273	**0.1884**	-0.0488	0.0026	0.1146	-0.0249	-0.0233	-0.1365	0.1861
TGW (g)	0.0987	0.0240	0.0017	-0.0011	0.0157	0.0418	-0.0293	-0.0586	**0.1568**	-0.2573	-0.2481	0.5552	0.0433	0.0615	0.4043**
GL (mm)	-0.0395	-0.0006	0.0058	-0.0053	0.0552	-0.0382	0.0219	-0.0007	0.0698	**-0.5778**	0.0770	1.2039	-0.0198	-0.5338	0.2179
GB (mm)	0.1105	0.0118	-0.0134	0.0006	-0.0367	0.0611	-0.0394	-0.0567	0.1022	0.1170	**-0.3804**	-0.2519	0.0711	0.4990	0.1948
DGL (mm)	-0.1114	-0.0088	0.0007	-0.0036	0.0482	-0.0548	0.0291	-0.0037	0.0693	-0.5538	0.0763	**1.2562**	-0.0181	-0.5443	0.1813
DGB (mm)	0.0941	0.0184	-0.0098	-0.0017	-0.0347	0.0658	-0.0367	-0.0584	0.0902	0.1525	-0.3578	-0.3005	**0.0753**	0.5387	0.2354
DGLBR	-0.1299	-0.0163	0.0064	-0.0018	0.0522	-0.0639	0.0385	0.0371	-0.0145	-0.4453	0.2741	0.9873	-0.0596	**-0.6926**	-0.0283

Residual Effect= 0.3594. LL= Leaf length (cm), LW= Leaf width (cm), NET= Number of effective tiller, PL= Panicle length (cm), PH= Plant height (cm), DF= Days to flowering, DM= Days to maturity, FG/P= Filled grain per panicle, TGW= 1000 grain weight (g), GL= Grain length (mm), GB= Grain breadth (mm), DGL= Decorticated grain length (mm), DGB= Decorticated grain breadth (mm), DGLBR= Decorticated grain length breadth ratio, Y/H= Yield hill^{-1}(g)

CONCLUSIONS

Presence of genetic variability is an utmost requirement for the improvement of economically important traits like yield in rice. Boro rice germplasm possessed adequate amounts of variability for yield and its associated traits. High heritability coupled with high genetic advance as percent of mean was observed in leaf length, number of effective tiller, filled grains panicle^{-1}, TGW and decorticated grain length- breadth ratio. Finally, it can be concluded that the G28, G20, G11, G17 and G2 are the elite germplasm and these germplasm can directly be selected for the future yield improvement on the basis of yield and other major yield contributing characters. Moreover, G39 (Unknown-2) can be used as early maturing Boro rice germplasm along with its higher grain yield in future breeding programme.

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