Estimation of Variability, Heritability and Genetic Advance of Exotic Rice (*Oryza sativa* L.) Breeding Lines for Short Growth Development

ABSTRACT

This work aims to study the genetic parameters for yield and yield contributing characters in thirty-two early maturing rice (*Oryza sativa* L.) lines. The morphological data were analyzed by different statistical plant breeding software's that ware reliable and faster in analysis. The line CT 18173-1-9-1-3-6-M had the tallest ~~and~~ IR 82489-594-3-2-2 earlier flowering line but BP 10620F-BB4-13-BB8 early maturing one. The highest effective tillers hill^{-1} and yield plant^{-1} was found in BP 10620F-BB4-13-BB8. Number of filled grains panicle^{-1} and number of unfilled grains panicle^{-1} exhibited high Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV). Small differences between GCV and PCV were recorded for all the characters studied which indicated less environmental influence. The characters *viz.,* 1000 seed weight and days to maturity exhibited high heritability and number of filled grains panicle^{-1} measured high genetic advance ~~indicating that simple selection could be effective for improving these characters.~~ Thirty-two lines were assigned into three clusters, ~~and each cluster~~ contained a different number of lines. Among the lines, BP 10620F-BB4-12-BB8 possessed the highest selection score index ~~and~~ IR 79201-49-1-1-1 ~~was~~ the lowest selection index score. The overall evaluation for the lines revealed that the best line was BP 10620F-BB4-12-BB8 and it can be used for future breeding program or farmer's field cultivation.

Keywords: *Genetic advance, Heritability, Clustering, Selection Index and Rice*

1. INTRODUCTION

Rice (*Oryza sativa* L.) is the staple food for about 2.5 billion world's population which may escalate to 4.6 billion by the year 2050 (Maclean, 2002). Rice production have significantly increased for high yielding varieties (HYV), modern varieties and improved agricultural practices during the past century. More than 2,000 modern varieties have been commercially released in twelve countries of South and Southeast Asia over the past 40 years (Cantrell and Hettel, 2004). In Bangladesh at present cropping intensity is 183% (BBS, 2012). It can be increased by further short duration rice nearly 300%. A critical analysis of genetic variability is a prerequisite for initiating any crop improvement program and also for adopting appropriate selection techniques. The selection of lines plays a vital role in developing ideal combinations for breeding. The prediction of genetic advance is a precondition for crop improvement breeding programs especially when large populations are subjected to selection. The progress in breeding for yield and its contributing characters of any crop is polygenically controlled, environmentally influenced and determined by the magnitude and nature of their genetic variability (Wright, 1935; Fisher, 1981). Hence there is a need to study variability. Variability for different traits in the source population is a prerequisite for crop improvement since all attempts of breeding and selection would be futile unless major portion of variability is heritable. It is difficult to judge whether observed variability is highly heritable or not. Moreover, knowledge of heritability is essential for selection based improvement, as it indicates the extent of transmissibility of a character into future generations (Sabesan *et al.* 2009). Mruthunjaya and Mahadevappa (1995) reported that the success of a crop improvement program depends on the definition and assembly of the required genetic variations and selection for yield through high heritable traits. Making of selection indices and their analysis would give the most appropriate selection score of each of two or more characters to be used simultaneously for selection.

2. MATERIALS AND METHODS

Thirty-one early maturing rice lines along with check variety Binadhan-7 were used for the experiments. ~~The study was conducted from July 2012 to November 2012 in the experimental field Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh-2202.~~ The seeds of the rice lines were collected from the International Network for Genetic Evaluation of Rice (*INGER*)~~,~~ International Rice Research Institute (IRRI).

Table1. ~~List~~ of ~~Experimental materials~~

Sl. No	Lines Name	Origin	Sl. No	Lines Name	Origin
1	IR 79246-105-2-2-4	IRRI	17	BP 1018F-BB8-13-BB4	INDONESIA
2	IR 73718-26-1-2-5	IRRI	18	IR 79525-20-2-2-2	IRRI
3	BP 10620F-BB4-13-BB8	INDONESIA	19	IR 80285-34-3-3-2	IRRI
4	IR 79538-1-1-1-1	IRRI	20	CT 18173-1-9-1-3-6-M	CIAT
5	IR 76494-28-1-2-2	IRRI	21	BP 10620F-BB4-2-BB4	INDONESIA
6	YN 2883-12-2-1	MYANMAR	22	PSB RC 64	INDIA
7	AD 02207	INDIA	23	IR 08N261	IRRI
8	BP 10620F-BB4-8-BB8	INDONESIA	24	RATNAGIRI 2	INDIA
9	C1-4-11-7P-2P-1P	CIAT	25	MTU-1113	INDIA
10	IR 79201-49-1-1-1	IRRI	26	KARJAT 5	INDIA
11	BP 10620F-BB4-12-BB8	INDONESIA	27	KHAZAR	IRAN
12	IR 82489-594-3-2-2	IRRI	28	IR 59552-21-3-2-2	IRRI
13	CT 18509-10-6-1VI-2	CIAT	29	C 2-9-9-2P-1P-3P	CIAT
14	IR 74052-153-5-3-1-3	IRRI	30	IR 39809-26-3-3	IRRI
15	PSD RC 2	IRRI	31	CT 18148-11-1-1-1-1-M	CIAT
16	IR 08N293	IRRI	32	Binadhan-7	BINA

The experiment was laid out in a RCBD with three replications. The row to row and plant to plant distances were 20 cm and 15 cm respectively. The following data plant height (cm), days to flowering, days to maturity, total tillers and effective tillers hill^{-1}, filled and unfilled grains panicle^{-1}, 1000 seed weight (g), yield plant^{-1} (g) were collected from randomly selected 5 plants of each unit plot. The data was analyzed by using the plant breeding statistical program (PLBSTAT, Version 2N, Utz 2007) for mean performance analysis and least significant difference (LSD). The genotypic and phenotypic variances were calculated as per the formulae proposed by Burton (1952). The genotypic (GCV) and phenotypic (PCV) coefficient of variation was calculated by the formulae given by Burton (1952). Heritability was calculated by the formula given by Hansen *et al.* (1956). For the heritability estimates, the genetic advance (GA) was estimated by the following formula given by Johnson *et al.* (1955). Stat Graphics plus for Windows 3.0 (Statistical Graphics Crop. Rockville, USA) software was used for clustering and ward's dendrogram construction. Selection indices were constructed using the method developed by Smith (1936) based on the discriminate function of Fisher (1936).

3. RESULTS AND DISCUSSION

3.1 Variations and performance of the lines

Analysis of variance resulted in significant variations among the lines for ~~the following characters: plant height, days to 50% flowering, days to maturity, total number of tillers hill^{-1}, effective tillers hill^{-1}, panicle length (cm), filled grains panicle^{-1}, number of unfilled grains panicle^{-1}, yield plant^{-1} (g) and 1000 seed weight~~ (Table 2). These results indicated that there are sufficient scope for further improvement of existing lines through breeding program.

Minimum days to 50 % flowering were observed by the lines IR 82489-594-3-2-2 (64 days). The remaining lines had between 65 to 86 days. Similar results have been reported by Jamal *et al.* (2009) in rice.

The line KARJAT 5 took the highest days to maturity (130 days). In contrast, the line BP 10620F-BB4-13-BB8 took the lowest days to maturity (104 days). This result was in full agreement with Dutta (2001) who observed days to maturity varied between 105 to 130 days in rice lines.

Among the 32 lines, CT 18173-1-9-1-3-6-M had the highest plant height and the line MTU-1113 had the shortest plant height. The results of the present study is supported by the result of different researchers e.g. (Sharma and Sharma, 1983; Talukder, 2004).

The minimum panicle length was recorded in YN 2883-12-2-1 while maximum panicle length was recorded in IR 79201-49-1-1-1. Tahir *et al.* (2002) studied genetic variability for different characters in ten rice genotypes variability for various traits. They found that these traits are under the genetic control and could be used in the selection of a desirable trait.

A total number of tillers hill^{-1} of 4 lines were higher in number compared to reaming 28 lines and the highest effective tillers hill^{-1} was found in BP 10620F-BB4-12-BB8 which contains 17.00 tillers hill^{-1} and 13.42 effective tillers hill^{-1}. The lowest total number of effective tillers hill^{-1} recorded YN 2883-12-2-1(5.40). This observation is supported by Zahid *et al.* (2005).

The highest number of grains panicle^{-1} was found in RATNAGIRI 2 (185). Whereas, the lowest grains panicle^{-1} was found in BP 10620F-BB4-13-BB8 (93). Prasad *et al.* (2001) and Tahir *et al.* (2002) reported highly significant variation for the grains panicle^{-1} for different genotypes.

The highest 1000 seed weight of 23.3 g was recorded for BP 10620F-BB4-13-BB8. In contrast, the minimum 1000 seed weight was found in the line KHAZAR (12.7 g). Tahir *et al.* (2002), and Bharali *et al.* (1994) reported the variation of 1000 seed weight.

The highest yield plant^{-1} (29.5 kg) was recorded for BP 10620F-BB4-12-BB8. In contrast, the minimum yield plant^{-1} was found in the line CT 18173-1-9-1-3-6-M (16.6g). The same variability were reported by Zahid *et al.* (2005) who studied twelve genotypes of coarse rice to check their yield performance in Kallar tract and reported highly significant variation for different traits.

Table 2. Mean performance of 32 lines based on different morphological characters

Lines name	DF	DM	PH	TT	ET	PL	FG	UG	SWT	Y/P
IR 79246-105-2-2-4	79.3	109.3	61.6	12.3	10.6	19.6	67.6	77.5	18.1	23.5
IR 73718-26-1-2-5	79.6	108.7	64.6	11.6	10.6	22.6	95.1	55.5	19.5	24.1
BP 10620F-BB4-13-BB8	65.3	104.0	55.0	9.6	9.0	18.3	93.8	24.8	23.3	21.1
IR 79538-1-1-1-1	74.0	106.0	67.3	10.0	8.6	20.3	88.6	61.3	20.8	20.9
IR 76494-28-1-2-2	70.3	105.7	74.6	10.3	9.6	22.3	138	56.0	17.8	23.1
YN 2883-12-2-1	74.6	104.7	72.6	5.3	4.3	22.3	115.5	36.0	17.8	18.3
AD 02207	75.0	114.0	64.3	13.6	10.3	20.3	108.7	46.6	19.8	21.5
BP 10620F-BB4-8-BB8	65.0	105.0	59.6	9.6	7.6	19.3	108.2	25.8	21.7	19.2
C 1 -4- 11-7P-2P-1P	75.6	111.7	61.0	9.3	7.6	22.0	130.2	47.3	16.2	20.3
IR 79201-49-1-1-1	66.3	110.7	60.0	16.3	13.0	22.0	165.3	26.0	16.2	23.1
BP 10620F-BB4-12-BB8	70.6	115.0	60.3	17.0	13.4	21.3	109.3	22.6	22.1	25.6
IR 82489-594-3-2-2	64.0	105.7	70.6	11.7	10.0	22.0	169.2	66.1	17.3	24.0
CT 18509-10-6-1VI-2	78.3	129.0	70.6	10.0	9.00	22.0	140.3	68.0	16.4	21.2
IR 74052-153-5-3-1-3	74.0	111.3	71.3	10.6	7.00	22.6	77.3	42.5	18.2	20.0
PSD RC 2	75.6	112.7	61.3	10.7	8.60	21.0	99.3	24.8	16.6	20.3
IR 08N293	74.6	114.7	74.0	12.3	10.6	24.0	136	42.8	16.9	22.5
BP 1018F-BB8-13-BB4	74.3	115.3	68.0	13.6	12.6	21.6	113.5	73.1	17.6	24.2
IR 79525-20-2-2-2	74.0	113.7	72.6	14.0	11.6	21.6	165.5	50.3	21.6	20.7
IR 80285-34-3-3-2	74.3	114.3	64.3	14.0	11.0	21.0	119.5	36.5	17.2	21.7
CT 18173-1-9-1-3-6-M	64.3	113.7	80.0	8.30	7.0	22.0	118.7	43.1	15.4	16.6
BP 10620F-BB4-2-BB4	71.3	112.0	59.3	11.0	8.30	19.3	140.7	32.0	19.6	19.7
PSB RC 64	77.3	115.0	67.0	12.0	11.0	21.0	99.3	35.3	22.0	23.2
IR 08N261	75.6	123.3	70.6	14.3	12.0	20.3	181.3	25.8	17.8	24.6
RATNAGIRI 2	75.6	123.3	70.6	14.3	12.0	20.3	185.0	30.0	17.8	23.6
MTU-1113	73.6	129.7	53.0	11.6	10.0	20.3	112.7	68.3	19.3	23.7
KARJAT 5	80.0	130.3	59.0	12.3	11.3	21.0	107.8	49.5	14.3	24.1
KHAZAR	86.0	129.0	69.6	13.3	11.3	19.6	80.1	67.5	12.7	24.2
IR 59552-21-3-2-2	73.6	112.7	69.0	10.3	9.00	21.3	92.5	54.8	21.1	20.1
C2-9-9-2P-1P-3P	73.6	114.3	78.6	14.6	13.0	23.6	175.3	54.1	18.5	23.7
IR 39809-26-3-3	79.3	129.0	59.6	12.0	9.60	21.0	89.3	40.0	16.2	22.9
CT 18148-11-1-1-1-1-M	75.0	114.0	67.6	10.6	9.60	22.0	106.0	59.3	17.2	23.9
Binadhan-7	65.3	114.0	65.0	8.30	6.60	21.0	115.3	53.0	19.6	17.0
Mean	73.7	114.7	66.3	11.7	9.80	21.2	120.1	46.7	18.3	21.9
CV %	5.92	1.67	4.90	21.9	20.2	5.99	17.7	24.6	0.61	6.20
LSD 0.05	4.54	3.48	5.33	4.22	3.25	2.07	34.5	19.5	0.18	2.22

DM=Days to 50%flowering, DM=Days to maturity, PH=Plant height (cm), TT=Total number of tillershill^{-1}, ET=Effective number of tillers hill^{-1}, PL=Panicle length (cm), FG=Filled grains panicle^{-1}, UG=Unfilled grains panicle^{-1}, SWT=1000 seed weight (g), Y/P=Yield plant^{-1} (g)

3.2 Estimation of genetic parameters

3.2.1 Variability parameters

Greater variability in the initial breeding material ensures better chances of producing desired forms of a crop plant. The phenotypic co-efficient of variation (PCV) were higher than genotypic co-efficient of variation (GCV) for all the characters studied indicating that they all interacted that less influenced by environment (Table 3). The characters studied in the present investigation exhibited low, moderate and high PCV and GCV values. Among the characters, highest PCV and GCV values were recorded for a number of unfilled grains panicle^{-1}, followed by grain yield plant^{-1} (g) and the lowest PCV and GCV values were recorded for days to maturity. Similar results were obtained by Kumar *et al.* (1994), Rather *et al.* (1998), Madhavilatha *et al.* (2005), Patra *et al.* (2006), Binodh *et al.* (2007), Sabesan *et al.* (2009) and Jayasudha and Sharma (2010).

3.2.2 Heritability

Heritability is classified as low (below 30%), medium (30-60%) and high (above 60%). Heritability in broad sense indicates days of 50% flowering, days to maturity, plant height, 1000 seed weight (g) and yield plant^{-1} (g) were high heritable and that measured 75.6, 92.9, 78.7, 99.7 and 70.8% respectively (Table 3). High heritability values indicate that the less influenced by the environment in their expression. It indicates the scope of genetic improvement of these characters through selection. Similar results had been reported by Sarawgi *et al.* (2000), Bhandarkar *et al.* (2002), Kuldeep *et al.* (2004), Sabesan *et al.* (2009) and Jayasudha and Sharma (2010). On the other hand, the total number of tillers hill^{-1}, number of effective tillers hill^{-1}, panicle length (cm), number of filled grains panicle^{-1}, number of unfilled grains panicle^{-1} were medium heritable (Table 3).

3.2.3 Genetic advance

Genetic advance is a useful indicator that can be expected as result of exercising selection of the population. Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al.* 1955). The genetic advance was highest for number of filled grains panicle^{-1} and lowest for panicle length (cm). The genetic advance as percent of mean was highest in case of number of unfilled grains panicle^{-1}, while lowest recorded by days to maturity (Table 3). In this study high heritability along with high genetic advance was noticed for the traits, number of filled grains panicle^{-1} and number of unfilled grains panicle^{-1}. Similar results were also reported by Singh and Singh (2005), Sarkar *et al.* (2007), Anbanandan *et al.* (2009), Sabesan *et al.* (2009) and Jayasudha and Sharma (2010). Other characters (viz: days to 50% flowering, plant height, number of tillers hill^{-1}, effective tillers hill^{-1}, panicle length, 1000 seed weight, yield plant^{-1} showed high heritability along with moderate or low genetic advance which can be improved by intermitting superior lines of segregating population developed from combination breeding.

Table 3. Estimation of genetic parameters of 32 rice lines based on different morphological traits related to yield

Characters	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	Heritability (%)	GA	GA (%)
DF	84.8	82.4	10.9	10.2	87.0	27.6	19.6
DM	94.3	92.6	8.76	7.7	78.3	3.60	14.1
PL	96.7	95.8	12.1	11.6	91.1	26.1	22.8
TT	97.8	97.1	9.00	8.20	82.5	23.7	15.4
ET	96.9	95.9	21.0	20.2	92.2	5.5	40.0
PL	98.0	96.4	21.9	20.9	91.5	5.4	41.3
FG	201.1	177	31.2	31.0	98.7	78.6	63.4
UG	112.8	109.5	51.6	51.4	99.1	28.0	105.5
SWT	145.3	131.3	19.6	19.2	95.7	9.40	38.7
Y/P	3.4	1.10	37.8	37.5	98.7	24.4	76.9

DM=Days to 50%flowering, DM=Days to maturity, PH=Plant height (cm), TT=Total number of tillers hill^{-1}, ET=Effective number of tillers hill^{-1}, PL=Panicle length (cm), FG=Filled grains panicle^{-1}, UG=Unfilled grains panicle^{-}1, SWT=1000 seed weight (g), Y/P=Yield plant^{-1} (g)

3.3 Nature and magnitude of genetic diversity

The knowledge on the nature and magnitude of genetic diversity governing the inheritance of quantitative characters like yield and its components is essential for effecting genetic improvement. Using Euclidean distance following Ward's method, the ~~lines~~ were grouped into distinct clusters. ~~The lines~~ were grouped into three clusters (Table 4). Cluster I and II had maximum ~~no.~~ of lines and the cluster III contained only nine lines.

Table 4. Clustering pattern of 32 rice lines and the member present in each cluster

Cluster number	Number of lines	Percent	Sl. no of lines
I	12	37.5	1, 2, 31, 17, 7, 19, 22, 13, 25, 26, 30, 27
II	11	34.3	3, 8, 21, 4, 28, 14, 9, 15, 6, 20, 32
III	9	28.1	5, 12, 16, 29, 18, 10, 11, 23, 24

3.3.1 Ward's dendrogram

Dendrogram grouped ~~of~~ 32 lines of rice into three clusters (Fig 1). Binadhan-7 as control line is grouped in cluster II. with lowest (0.00) genetic distance, IR 79246-105-2-2-4, IR 73718-26-1-2-5, CT 18148-11-1-1-1-1-M, BP 1018F-BB8-13-BB4, AD 02207, BP 1018F-BB8-13-BB4, IR 80285-34-3-3-2, PSB RC 64, CT 18509-10-6-1VI-2, MTU-1113, KARJAT 5, KHAZAR, IR 39809-26-3-3 were grouped in cluster I. IR 76494-28-1-2-2, IR 82489-594-3-2-2, IR 08N293, C 2-9-9-2P-1P-3P, IR 79525-20-2-2-2, IR 79201-49-1-1-1, BP 10620F-BB4-12-BB8, IR 08N261, RATNAGIRI 2 were grouped on cluster III.

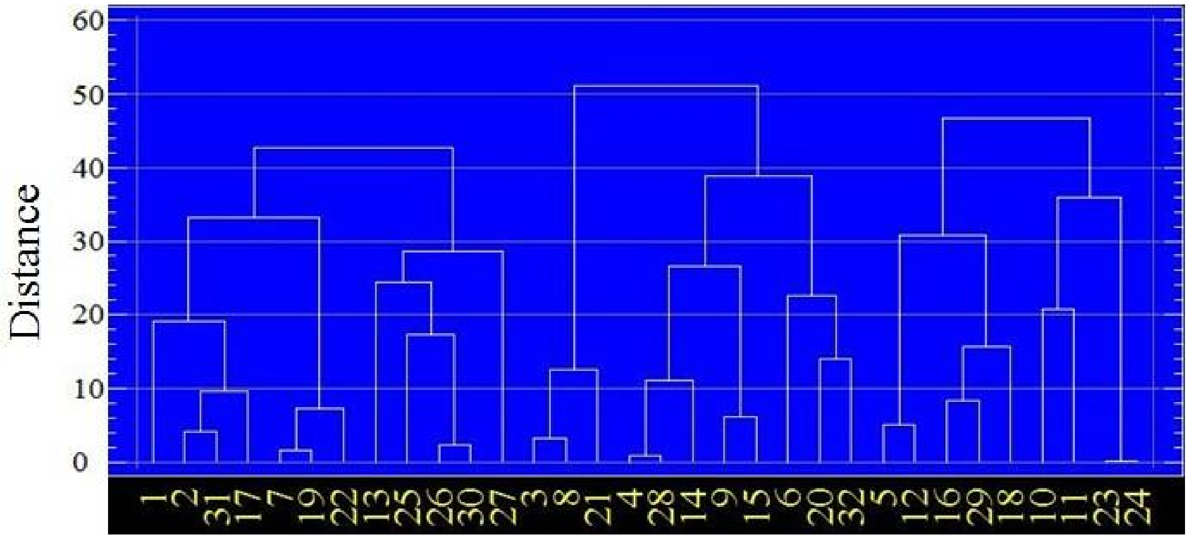

Fig.1. Dendrogram based on summarized data on differentiation among 32 lines of rice according to Ward's method

3.3.2 Characterization of individual clusters

The mean values of each cluster for eleven characters are presented in Table 5. There was a wide range of variation in the cluster mean values for all the characters. The mean values of all characters ~~for the respective character~~ were categorized into low (L), intermediate (I) and high (H) classes. Cluster II required minimum 70.8 days for 50% flowering and 109.8 days for maturity. Cluster I required maximum 77.6 days for 50% flowering, 119.8 days for maturity and cluster III showed intermediate values (71.6-114). In case of plant height, cluster I showed low value (64.1) and cluster III showed high value (70.2). Cluster II, showed intermediate values (65.6). With regard of total number of tillers hill^{-1}, cluster II showed low value (9.39) and cluster III showed high value (13.8). With regard of effective number of tillers hill^{-1}, cluster II exhibited low value (7.64) and cluster III showed high value (11.7). For panicle length (cm) cluster III showed low value (21.9) and cluster II showed high value (20.8). Number of filled grains panicle^{-1}, cluster III showed high value (158.3) and cluster I showed low value (103.3). Number of unfilled grains panicle^{-1}, cluster I showed high value (56.4) and cluster II showed low value (40.5). With regards to 1000 seed weight, cluster II demonstrated high value (19.1) and cluster I showed low value (17.5). With regards to yield plant^{-1}, cluster III showed high value (23.4) and cluster II showed low value (19.4).

Table 5. Cluster mean for 10 yield and yield related characters of 32 rice lines

Characters	I	II	III
Days to 50%flowering	77.6 (H)	70.8 (L)	71.6 (I)
Days to maturity	119.8 (H)	109.8 (L)	114 (I)
Plant height (cm)	64.1 (L)	65.6 (I)	70.2 (H)
Total number of tillers hill^{-1}	12.2 (I)	9.30 (L)	13.8 (H)

Effective number of tillers hill^{-1}	10.6 (I)	7.60 (L)	11.7 (H)
Panicle length (cm)	21.0 (I)	20.8 (L)	21.9 (H)
Number of filled grains	103.3 (L)	107.3 (I)	158.3 (H)
Number of unfilled grains	56.4 (H)	40.5 (L)	41.5 (I)
1000 seed weight (g)	17.5 (I)	19.1 (H)	18.4 (L)
Yield plant^{-1} (g)	23.2 (I)	19.4 (L)	23.4 (H)

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

3.4 Selection index

Selection index was constructed to identify suitable lines among 32 lines of rice in order to recommend for cultivation. Following simultaneous selection model was found by considering 10 characters. Here, among the 32 lines BP 10620F-BB4-12-BB8 possessed the highest selection score (7636) and rank as the best followed by IR 79246-105-2-2-4, IR 73718-26-1-2-5, BP-10620F-BB4-13-BB8, IR 79538-1-1-1-1, IR 79538-1-1-1-1, IR 76494-28-1-2-2, YN 2883-12-2-1, AD 02207, BP 10620F-BB4-8-BB8 and C1 -4- 11-7P-2P-1P with 6813, 5952, 5869 5828 5952, 5869, 4759, 4228, -167 and -231 respectively (Table 6).

The expected genetic gain (ΔG) was 143 at 5% selection intensity i.e. 4-5 highest scoring lines from these 32 rice lines might be recommended for cultivation for better yield.

Table 6. Selection best rice 10 lines considering ten characters

Sl. No	Lines Name	Selection Score	Rank
1	BP 10620F-BB4-12-BB8	7636	1
2	IR 79246-105-2-2-4	6813	2
3	IR 73718-26-1-2-5	4716	3
4	BP 10620F-BB4-13-BB8	5828	4
5	IR 79538-1-1-1-1	5952	5
6	IR 76494-28-1-2-2	5869	6
7	YN 2883-12-2-1	4759	7
8	AD 02207	4228	8
9	BP 10620F-BB4-8-BB8	-167	9
10	C1 -4- 11-7P-2P-1P	-231	10

4. CONCLUSION

The overall results showed that BP 10620F-BB4-13-BB8 was early maturing among the studied rice lines. BP 10620F-BB4-12-BB8 yielded a maximum total number of tillers hill^{-1}, effective number of tillers hill^{-1}, 1000 seed weight (g) and yield plant^{-1}. On the basis of overall results BP 10620F-BB4-12-BB8 was exhibited better performances than that of other exotic lines. ~~However, among the tested lines, IR 79201-49-1-1-1 resulted in higher panicle length. BP 10620F-BB4-12-BB8 also possessed the highest selection score index and it was in cluster III.~~ The origin of this line was Indonesia by considering overall performance it can be recommended for farmer cultivation after appropriate variety release proceeding.

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