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Assessment of heritability and genetic advance for yield contributing characters in hill rice (*Oryza sativa* L.) genotypes of Manipur

Sophia Longjam and NB Singh

Abstract
A study was conducted on 46 genotypes of hill rice during 2017 with an objective of assessing heritability and genetic advance for yield contributing characters. The experiment was laid out in Augmented Design with two checks at the Research Farm of Department of Genetics and Plant Breeding, College of Agriculture, Central Agricultural University, Imphal, Manipur, India. Analysis of variance among 46 genotypes showed significant difference for all 13 quantitative characters studied. The highest PCV and GCV were recorded for the characters, number of unfilled spikelets per panicle and grain yield per plant. The GCV ranged from 24.20% (number of unfilled spikelets per panicle) to 3.29% (days to 50% flowering). The small differences between PCV and GCV for the traits, plant height, test-weight, days to 50% flowering, spikelet fertility and leaf length represented some degree of environmental influence on the phenotypic expression of these characters. High estimates of heritability were observed for leaf length, spikelet fertility, test-weight, plant height, days to 50%flowering, total number of tillers per plant, panicle length, number of unfilled spikelets per panicle. Genetic advance as percent of mean resulted high for number of unfilled spikelets per panicle, effective tillers per plant, total number of tillers per plant, and grain yield per plant. High heritability with high genetic advance as percent of mean was observed for total number of tillers per plant (h^2=76.89, GAM=25.39), and number of unfilled spikelets per panicle (h^2=60.74, GAM=38.91). Therefore, it helps in indicating possibilities of effective selection for the improvement of these characters.

Keywords: Rice, broad sense heritability, genetic advance as percent of mean, genotypic coefficient of variation, phenotypic coefficient of variation

Introduction

India has an abundant source of genetic diversity for rice in plant architecture and growing habits and in phenotypes such as width, weight, cooking properties, aroma and texture. It is reported that the extensive phenotypic and genotypic variation within the *Oryza sativa* makes itself a powerful tool to study genetic diversity, resulting in the development of methods to enhance health-promoting qualities of rice grain.

Rice, as a paddy field crop, is specifically influenced by water stress (Tao *et al*., 2006; Yang *et al*., 2008) [19, 20]. It is estimated that drought affects 50 per cent of world rice production (Bouman *et al*. 2005) [5]. Also, water deficit is frequently occurring in irrigated areas due to decreasing water tables.

Rice, the principal food grain crop of the North Eastern hilly ecosystem occupies 3.51 million hectares which accounts for more than 80% of the total cultivated area of the region and 7.8 per cent of the total rice area in India. Rice cultivation in the NEH region of India is manifested to different biotic and abiotic stresses that include extreme temperatures at the time of flowering and grain filling stages. Thus, it results to very discouraging numbers in rice productivity and production of the region which contemplates a lower per capita consumption as well. (Ngachan *et al*., 2011) [11]. The states of Arunachal Pradesh, Assam, Manipur, Meghalaya, Mizoram, Nagaland, Sikkim and Tripura which comprises the entire north-eastern hill region of India falls under the agro-climatic sub-Himalayan Zone 2. (Anon, 1999) [2].

The hill rice landraces have spread by the interaction between alteration to the harsh environment and selection imposed by the farmers who determine the cultivation of varieties under a particular agro-ecological condition. It will be compulsive to consider the contact of practices and local culture of farmers on the conservation, exchange and genetic structure of traditional landrace varieties, by following up on the study of rice landraces collected from a unique ecological niche like mountain sides.

Therefore, the validation of distinguishing characters is mandatory to carry out the scientific study and provide an important framework for significant increase in the efficiency of selections made in plant breeding programmes.

Materials and Methods

The experimental materials comprised of 46 rice genotypes, maintained at Rice Research Station, Wangbal, Thoubal (Manipur) and Department of Agriculture, Agartala (Tripura), India. Forty-four local genotypes *viz.* Shangao Chingphou, Satao Agounu Chingphou, Tare Shang Chingphou, Lamjang Chingphou, Bodzii Ro, Mozha Ro, Nyozhiro, Kono-A Ro, Nepunibuii Ro, Oromon-O, Keibuji Ro, Telpnibu, Sangailobi, Pawnba Maizawn, Maivarsa, Zongambu, Paemba Malvar, Maizawl, Sunpawber, Buman Senhnoi, Satsudhbu, Changnum, Sengbmam, Kahaola, Keibu Chiro, Lamyanbu, Seventhei, Kosam, Chakia Mao, Koum bumlii Anand, Kiophou, Chedo, Chemp selak, Sajei, Changat, Changphai, Chedanand, Chakia 58, Leithangnu, Kahara, Disha Phou, Kongrush, Kholiro and Sengbu were evaluated and two genotypes *viz.* Oromon-A, a local accession, and Sahbhagi Dhan, a drought tolerant rice variety of Tripura, were used as checks.. Seeds of the accession, Sahbhagi Dhan was obtained from Department of Agriculture, Agartala (Tripura), India. The genotypes were grown in Augmented Block Design with two checks at Research Farm of Genetics and Plant Breeding, College of Agriculture, Central Agricultural University, Imphal, Manipur, India during *Kharif*, 2017. Each genotype was sown in a plot comprising four rows, each having 2.4 meter length at spacing of 20 cm X 15 cm. The seeds were soaked for 24 hrs, incubated for 48 hrs for proper germination and were directly sown in the field. Thirteen quantitative characters were recorded on five randomly selected plants in each plot. The characters studied were plant height, leaf length, leaf width, days to 50% flowering, panicle length, total number of tillers per plant, effective tillers per plant, total number of spikelets per panicle, number of filled spikelets per panicle, number of unfilled spikelets per panicle, spikelet fertility(%), test weight and grain yield per plant**.** The one-way analysis of variance (ANOVA) was performed using the Statistical Analysis System Software (SAS 9.3). The genotypic and phenotypic coefficients of variation were determined according to the formula suggested by Burton and de Vane (1953) [6]. Estimate of Heritability in broad sense (h^2_{bs}) was also determined with the formula suggested by Johnson *et al*. (1955) [10]. From the heritability, estimation of genetic advance (GA) was done according to the formula given by Burton (1952) and the range of genetic advance as percent of mean was classified as suggested by Johnson *et al*. (1955) [10].

Result and Discussion

The analysis of variance of 13 different characters of 46 hill rice showed differences among the genotypes which revealed that there was genetic variation among the genotypes studied. Plant height, leaf length, leaf width, days to 50% flowering, panicle length, total number of tillers per plant, effective tillers per plant, total number of spikelets per panicle, number of filled spikelets per panicle, number of unfilled spikelets per panicle, spikelet fertility(%), test weight and grain yield per plant differed significantly across 46 rice genotypes (Table 1). This suggested the selection of superior and diverse genotypes for use in escalating the genetic yield potential of rice.

Days to 50% flowering, plant height, tillers per plant, effective tillers per plant, panicle length, spikelet fertility (%) and grain yield were reported to be significantly different. This is in agreement with work of Jayasudha *et al.* (2010) [9]. There are significant differences for plant height, length of panicle, filled grains per panicle, unfilled grains per panicle, days to 50% flowering, test weight as reported by Shahriar *et al*. (2014) [16]. Leaf length, leaf width, plant height, panicle length, effective tillers per plant, filled grains per panicle, total grains per plant, spikelet fertility%, test weight and grain yield per plant were significantly different as reported by Singh *et al*. (2014) [17]. Days to 50% flowering, tillers per plant, plant height, grains per panicle, fertile grains per panicle, test weight, grain yield per plant were significantly different as found out by Prasad Bhatt *et al*. (2016) [13].

Co-efficient of variation of 13 different quantitative characters of hill rice were presented along with the mean per se performance of 46 genotypes of hill rice. (Table 2). High PCV and GCV was recorded for the characters, number of unfilled spikelets per panicle, grain yield per plant and effective tillers per plant.(Shahriar *et al.*, 2014, Singh *et al.*, 2015) [16, 18]. Similar findings of high PCV and GCV are seen in the work of Pandey *et al*. (2009) [12] and Behera *et al*. (2018) [3] for grain yield per plant, and Abebe *et al*. (2017) [1] for number of unfilled grain per panicle and grain yield.

Heritability

In this study, high category of heritability was recorded for the characters leaf length (95.78%), spikelet fertility (92.83%), test weight (88.65%), plant height (88.06%) and days to 50% flowering (84.86%) given as in Table 3. Similar findings are seen in the works of Singh *et al*. (2014) [17] for days to 50% flowering, leaf length, spikelet fertility%, test weight, plant height, Prasad *et al*. (2017) [13] for plant height and days to 50% flowering.

Genetic advance

Genetic advance gives information on the improvement required in the genotypic value of the new population over original population. The value of genetic advance as percent of mean (GAM) were calculated high for number of unfilled spikelets per panicle (38.91%), grain yield per plant (27.12%), total number of tillers per plant (25.39%), effective tillers per plant (21.35%). High genetic advance as percentage of means were reported in the works of Abebe *et al*., 2017 [1] for grain yield per plant and number of unfilled grain per panicle, Rahman *et al*., 2014 [14] for effective tillers per plant. The estimates of genetic advance as a percent of mean provide more reliable information regarding the selection in improving the traits. The heritability with high genetic advance as per cent of mean under the control of additive gene action would be effective for selecting superior varieties. High heritability with high genetic advance as percent of mean was observed for total number of tillers per plant (h^2=76.89, GAM=25.39), and number of unfilled spikelets per panicle (h^2=60.74, GAM=38.91). Therefore, it helps in indicating possibilities of effective selection for the improvement of these characters.

Table 1: Analyses of variance of 13 different characters in hill rice.

S. No.	Characters	Mean sums of squares					
		Blocks (eliminating tests+controls) (df=10)	Entries (ignoring blocks) (df=45)	Tests (df=43)	Controls (df=1)	Tests vs. Controls (df=1)	Error (df=10)
1.	LL	0.63	87.35**	52.52**	330.34**	1342.09**	0.38
2.	LBW	0.01	0.04*	0.042*	0.34**	0.006	0.005
3.	PH	6.42	276.87**	177.83**	850.89**	3961.60**	3.70
4.	DF	2.63	68.45**	45.75**	1078.00**	35.03*	1.20
5.	PL	0.99	12.51**	10.77**	1.09	98.42**	0.67
6.	NTPP	0.40	11.55**	8.73**	144.33**	0.17	0.34
7.	EFTP	0.79	8.81*	6.25*	127.68**	0.24	0.89
8.	FS	321.23	1385.39*	1356.10*	1472.72*	2557.28*	162.92
9.	UFS	10.61	125.91**	122.23**	142.54*	267.76*	7.64
10.	NOS	307.28	1117.98*	1083.89*	2531.64*	1170.07*	228.14
11.	SFP	15.46*	243.98**	234.92**	44.87*	832.77**	1.87
12.	TGW	1.18*	14.81**	11.52**	162.25**	9.13**	0.19
13.	GYPP	12.52	66.85*	64.51*	222.45*	11.68	6.06

*, ** Significant at 5% and 1% respectively.

df- degree of freedom. LL- leaf length, LBW-leaf blade width, PH-plant height, DF- days to 50% flowering, PL-panicle length, NTPP-total number of tillers per plant, EFTP-effective tillers per plant, FS- number of filled spikelets per panicle, UFS- number of unfilled spikelets per panicle, NOS- total number of spikelets per panicle, SFP -spikelet fertility(%), TGW-test weight and GYPP -grain yield per plant

Table 2: Mean per se performance of 46 genotypes of hill rice.

Genotype	LL	LBW	PH	DF	PL	NTPP	EFTP	FS	UFS	NOS	SFP	TGW	GYPP
Sajei	22.11	1.27	86.74	75.23	18.64	5.95	5.14	62.73	17.86	80.59	79.74	19.59	5.83
Nepunibuii-Ro	34.61	1.17	106.34	73.23	26.94	5.95	3.81	122.73	14.86	137.59	88.13	23.67	11.60
Kosam	32.36	0.67	101.44	70.23	22.64	7.95	5.14	72.73	41.86	114.59	63.86	21.69	7.98
Sengbmam	44.71	0.97	81.74	79.23	25.74	8.62	8.48	161.73	11.86	173.59	91.27	27.71	27.85
Telpnibu	42.56	1.19	98.13	74.73	20.79	5.45	4.15	91.23	6.86	98.09	92.62	23.23	8.20
Tare Shang	38.76	1.34	97.63	87.73	23.39	2.78	4.15	34.23	2.86	37.09	92.55	24.21	2.58
Oromon-O	33.51	0.99	93.03	72.73	18.39	7.45	6.48	43.23	12.86	56.09	78.91	20.15	5.06
Zongambu	32.61	1.69	96.63	87.73	26.79	7.45	6.15	90.23	26.86	117.09	77.62	23.99	13.18
Changnum	20.91	0.72	56.25	73.23	18.85	3.96	4.82	64.23	11.36	75.59	85.53	22.80	7.52
Mozha Ro	39.61	0.92	93.65	76.23	20.93	8.62	7.15	92.23	9.36	101.59	90.99	31.49	19.97
Chedo	35.01	0.42	91.25	84.23	17.88	5.29	4.48	52.23	12.36	64.59	81.54	25.74	6.55
Maivarsa	29.16	1.12	91.75	76.23	12.95	2.96	3.15	36.23	24.36	60.59	58.92	23.86	8.17
Changat	27.04	0.82	100.27	73.73	21.44	11.79	10.99	93.73	7.86	101.59	91.64	26.05	25.57
Lamjang Chingphou	38.49	1.17	98.87	78.73	22.14	5.12	3.99	166.73	3.86	170.59	97.91	23.66	14.18
Kholiro	46.94	0.82	92.77	85.73	24.34	6.79	5.32	128.73	8.86	137.59	93.40	22.67	14.81
Chakia Mao	25.29	0.97	65.17	61.73	19.51	5.12	4.65	84.73	17.86	102.59	81.53	23.61	9.64
Leithangnu	37.39	1.02	55.96	89.23	15.74	5.78	3.65	39.73	40.86	80.59	35.24	21.33	6.70
Bodzii-Ro	26.99	0.97	79.76	70.23	24.64	6.45	5.31	104.73	12.86	117.59	88.24	22.33	12.63
Koum bumlii Anand	43.94	1.07	93.36	85.23	25.74	8.45	5.98	178.73	2.86	181.59	99.53	21.61	23.46
Kiophou	46.64	1.12	120.76	90.23	22.34	5.45	3.65	38.73	48.86	87.59	30.36	34.28	4.66
Keibu chiro	26.34	0.87	81.26	88.23	22.29	9.95	5.82	105.23	25.86	131.09	78.84	28.48	18.94
Satsudhbu	46.14	1.42	102.96	69.23	18.94	8.95	5.49	121.23	10.86	132.09	90.44	22.42	16.32
Seventhei	41.34	1.37	100.76	76.23	30.14	6.62	3.82	136.23	10.86	147.09	91.22	27.27	16.03
Chemp selak	26.14	0.97	83.36	71.23	20.54	14.62	9.49	124.23	8.86	133.09	92.01	21.94	23.49
Kono-A-Ro	41.21	1.17	111.28	85.23	28.55	12.45	9.15	178.73	8.36	187.09	98.09	24.39	24.33
Changphai	28.11	1.32	98.88	88.23	26.35	7.12	3.49	103.73	13.36	117.09	88.87	30.63	12.25
Maizawl	40.51	1.12	126.08	88.23	17.85	9.45	7.15	34.73	34.36	69.09	39.39	24.18	5.33
Sunpawber	42.86	1.07	88.48	74.23	21.35	5.45	3.49	42.73	39.36	82.09	44.35	24.71	8.45
Chedanand	39.24	0.99	103.63	83.23	24.95	5.46	5.65	99.73	14.36	114.09	87.73	24.44	12.91
Pawnba Maizawn	29.89	0.94	101.93	86.23	24.15	6.12	3.98	135.73	19.36	155.09	88.59	30.08	14.68
Lamyanbu	32.24	1.14	99.93	71.23	23.45	8.12	7.31	127.73	16.36	144.09	89.70	25.65	21.51
Dishaphou	43.59	1.04	99.33	86.23	22.25	8.12	6.31	119.73	3.36	123.09	99.18	27.37	18.62
Satao angounu chingphou	21.06	1.32	64.81	84.23	15.97	3.28	2.15	34.73	11.36	46.09	80.93	28.75	3.44
Sangailobi	40.61	1.37	95.01	71.23	19.07	2.62	1.81	55.73	23.36	79.09	75.78	28.77	5.94
Sengbu	36.11	0.82	96.31	83.23	18.67	13.95	9.81	87.73	4.36	92.09	95.38	26.50	25.02
Paemba malvar	35.46	1.17	97.41	84.23	22.37	3.95	2.81	108.73	0.36	109.09	99.23	22.11	5.44
Keibuji Ro	42.26	0.97	90.71	88.73	15.39	12.62	10.99	27.23	3.36	30.59	90.66	26.02	8.62
Kahaola	31.21	1.02	91.31	80.73	19.59	6.29	4.32	85.23	15.36	100.59	86.11	21.28	7.98
Nyozhiro	37.91	0.77	99.21	90.73	18.29	10.18	8.99	63.23	13.36	76.59	84.38	33.91	20.26
Kahara	32.56	0.52	87.81	70.73	13.69	9.62	8.32	30.23	8.36	38.59	81.91	34.36	9.50
Buman Senhnoi	44.21	0.99	72.77	78.23	20.04	5.95	4.14	86.73	2.86	89.59	95.04	23.47	8.59
Chakia-58	26.16	0.99	72.27	78.23	19.74	16.95	14.81	47.73	19.86	67.59	73.25	22.99	20.50
Shangao chingphou	27.61	1.29	82.97	70.23	20.11	4.95	4.14	78.73	4.86	83.59	92.83	23.13	7.77

Kongrush	41.91	1.04	101.17	74.23	22.84	10.28	7.48	99.73	37.86	137.59	72.33	22.08	17.81
Oromon-A	21.86	0.94	69.42	70.73	18.47	5.05	3.57	109.91	13.91	123.82	88.29	27.12	10.69
Sahbhagi Dhan	29.61	1.19	81.85	84.73	18.91	10.18	8.39	93.55	8.82	102.36	91.14	21.69	17.05
Lowest range	20.91	0.42	55.96	61.73	12.95	2.62	1.81	27.23	0.36	30.59	30.36	19.59	3.44
Highest range	46.94	1.69	126.08	90.73	30.14	16.95	14.81	178.73	48.86	187.09	99.53	34.36	27.85
Mean	32.12	1.05	86.59	78.76	20.42	7.54	5.90	92.92	14.21	107.14	84.69	24.93	13.27
CV%	1.93	7.05	2.22	1.391	4.02	7.69	16.03	13.74	19.46	14.10	1.62	1.74	18.55
SE.d(a)	0.26	0.03	0.82	0.47	0.35	0.25	0.40	5.44	1.18	6.44	0.58	0.18	1.05
SE.d(b)	0.87	0.10	2.72	1.55	1.16	0.82	1.34	18.05	3.91	21.36	1.93	0.61	3.48
SE.d(c)	1.07	0.13	3.33	1.90	1.42	1.00	1.64	22.11	4.79	26.16	2.37	0.75	4.26
SE.d(d)	0.77	0.09	2.39	1.36	1.02	0.72	1.17	15.87	3.44	18.78	1.70	0.54	3.06
CD 5%(a)	0.59	0.07	1.83	1.04	0.78	0.55	0.90	12.13	2.63	14.35	1.30	0.41	2.34
CD 5%(b)	1.95	0.23	6.06	3.45	2.58	1.83	2.98	40.22	8.71	47.59	4.31	1.36	7.76
CD5%(c)	2.39	0.29	7.43	4.23	3.16	2.24	3.65	49.26	10.67	58.29	5.28	1.67	9.50
CD5%(d)	1.71	0.20	5.33	3.03	2.27	1.61	2.62	35.36	7.66	41.84	3.79	1.20	6.82

Table 3: Estimate of mean, range, PCV, GCV, broad sense heritability (h^2_{bs}) and genetic advance as percent of mean for 13 characters of hill rice

S. No	Characters	Mean	Range		PCV	GCV	h^2	GA	GAM
			Min.	Max.	%	%	%	(k=2.06)	(k=2.06)
1.	LL	32.12	20.91	46.94	9.38	9.18	95.78	5.95	18.54
2.	LBW	1.05	0.42	1.69	9.42	6.25	44.00	0.09	8.55
3.	PH	86.59	55.96	126.08	6.43	6.04	88.06	10.12	11.68
4.	DF	78.76	61.73	90.73	3.57	3.29	84.86	4.93	6.26
5.	PL	20.42	12.95	30.14	6.67	5.33	63.77	1.79	8.78
6.	NTPP	7.54	2.62	16.95	16.01	14.04	76.89	1.92	25.39
7.	EFTP	5.90	1.81	14.81	22.02	15.10	47.00	1.26	21.35
8.	FS	92.92	27.23	178.73	18.17	11.90	42.87	14.93	16.07
9.	UFS	14.21	0.36	48.86	31.05	24.20	60.74	5.53	38.91
10.	NOS	107.14	30.59	187.09	16.62	8.80	28.06	10.31	9.62
11.	SFP	84.69	30.36	99.53	6.03	5.81	92.83	9.78	11.55
12.	TGW	24.93	19.59	34.36	5.15	4.85	88.65	2.35	9.42
13.	GYPP	13.27	3.44	27.85	26.26	18.58	50.08	3.60	27.12

LL- leaf length, LBW-leaf width, PH-plant height, DF- days to 50% flowering, PL-panicle length, NTPP-total number of tillers per plant, EFTP -effective tillers per plant, FS- number of filled spikelets per panicle, UFS- number of unfilled spikelets per panicle, NOS- total number of spikelets per panicle, SFP -spikelet fertility(%), TGW-test weight and GYPP -grain yield per plant, PCV-phenotypic coefficient of variation, GCV-genotypic coefficient of variation, h^2_{bs}- Broad sense heritability, GA-genetic advance, GAM- genetic advance as percent of mean

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