Research Article

Genetic variability and trait association in *Jhum* Rice of Arunachal Pradesh, India

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Abstract

The study comprised of 19 *jhum* rice landraces from different parts of Arunachal Pradesh. The analysis of variance based on 14 quantitative traits revealed significant traits-wise variations across the genotypes. Based on cluster analysis the landraces were grouped into 3 distinct clusters. Principal component analysis (PCA) extracted 5 principal components (Eigen value >1) with 80.5 % of the total variance. About 60.4% of the cumulative variance was exhibited by the first three principal components. Traits like grain yield (GY), plant height (PH), primary branch per panicle (PBP), filled grain per panicle (FGP), test grain weight (TGW) and grain morphology exhibit heavy positive loadings in these first PCs. The value of the phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for most of the traits. The traits exhibits moderate to high PCV, GCV, heritability and genetic advance as a percent of the mean (GAM). High heritability couple with high GAM was exhibited by GY, TGW and PH. While moderate heritability with (GAM) was exhibited by panicle length (PnL), FGP and PBP. Except ligule length (LgL) and flag leaf width (FLW), all the traits displayed positive associations with GY. A high positive significant correlation (P≤ 0.01) was exhibited by grain width (0.716) and TGW (0.583). Path coefficient analysis revealed direct positive effects on GY by girth diameter (GD), flag leaf length (FLL), blade leaf width (BLW), filled grain number per panicle (FGP), TGW, and grain length (GL). The residual effect magnitude of 0.1386 indicated that 99.8 % of the variability was accounted by the traits included in the present study. Thus the study revealed information about the genetic diversity among the *jhum* rice landraces and associated yield contributing traits for future breeding programme.

Keywords correlation, genetic variation, heritability, Jhum rice, path coefficient

Introduction

The state of Arunachal Pradesh is endowed with considerable diversity of rice landraces. Due to its hilly topography, shifting or *jhum* cultivation still prevails and covers about 76 per cent of the total cultivated cropped area. This state is one of the world's biodiversity hotspots of rice germplasms and cultivars vary across the state [1]. Nature has endowed the north

eastern states of India with huge genetic diversity of rice landraces [2-4]. These local rice landraces harbour huge genetic variations of about 60 per cent total variation in India [5]. Here rice is cultivated as rainfed with diverse prevailing climatic conditions up to the altitude of 2000 m above mean sea level. Such a diverse cultivation system of rice in the region promotes genetic diversity and allelic variations [6]. Although the landraces grown in mountain regions are low in yield potential, they possess many desirable traits that can be used for varietal development programmes [7].

The richness in genetic variation of any germplasm is a vital key to integrate favourable alleles for successful crop improvement [8-9]. As the local rice landraces often possess wide genetic diversity [10-11], the systemic characterization would facilitate their effective utilization in cultivar development [12]. The systemic characterization of existing untapped local rice landraces is essential for successful crop improvement programmes [13] and the development of cultivars adaptive to different environments [14-15].

For any breeding programme, a thorough understanding of genetic diversity, and the association of yield contributing traits with grain yield is of utmost importance [16-17]. Grain yield (GY) is a complex attribute which is being influenced by the nature of genes arrangement, effects of the environment, and the extent and nature of genetic diversity [18]. Further, the contribution of each trait to the final output of grain yield could be either direct or indirect [19-21]. Keeping all these factors into account, the study was carried out to evaluate the genetic variability and nature of trait associations among the rice landraces of Arunachal Pradesh.

Methodology

Collection of germplasm and field experiment

Local rice germplasm from different parts of Arunachal Pradesh were collected from seed stocks or fields and farmers' stores. Selected 19 genotypes (Table 1) were subjected to field characterization for two seasons with three replications in Randomised Block Design (RBD) at ICAR Research Complex for North Eastern Hill Region, Arunachal Pradesh Centre, Basar (N270 59.537' and E 940 41.269').

Table 1. List of jhum rice landraces of Arunachal Pradesh included in the present study

SN.	Variety	Village/Place	Latitude (N)	Longitude (E)
1	Bali red	Gori	27° 58' 50.8836''	94° 41' 19.6692''
2	Bali white	Gori	27° 58' 50.8836''	94° 41' 19.6692''
3	Mingpong	Seppa	27° 19' 59.1996''	93° 3' 47.6928''
4	Yali amo	Jomoh	28° 11' 20.724''	94° 37' 27.912''
5	Kimin red	Pagi	27° 55' 50.844''	94° 42' 54.036''
6	Jarli	Sodo Doke	28°02.224'	94°37.939'
7	Kimin white	Dali	28°17'597''	94°50'677''
8	Poore	Dumporijo	27° 59' 32.208''	94° 17' 25.44''
9	Ambher	Tuting	28° 59' 42.648''	94° 53' 22.056''
10	Chipu	Dake	28° 1' 7.356''	94° 34' 42.888''
11	Kecha	Boleng	28°18'25.5468''	94°57'11.7792''
12	Angkear	Sago	27° 55' 50.844''	94° 42' 54.0432''
13	Pumik	Tai	28° 1' 7.356''	94° 34' 42.888''
14	Ampu	Tai	28° 1' 7.356''	94° 34' 42.888''
15	Mukte	Pushi Doke	28° 3' 2.2392''	94° 42' 38.9412''
16	Amchiriri	Tai	28°00.034'	94°31.715'
17	Lemmuk	Pushi Doke	28° 3' 2.2392''	94° 42' 38.9412''
18	Bamtare	Bam	27°58'56.776''	94°41'23.451''
19	Takear	Yumlo Mongku	28° 9' 57.0564''	94° 38' 13.3728''

Sowing was done in the first week of April in upland conditions with spacing 25 x 15cm between rows and plants respectively. Data for different 14 quantitative traits were recorded at different growth stages as per the guidelines of the International Rice Research Institute [22] and five competitive plant samples were selected for various data recording.

Data analysis

The statistical analysis was conducted by the pooling of two years data. All the descriptive statistics with test of significance, Pearson's correlation coefficient and Principal Component Analysis (PCA) were performed by using SPSS version 20.0 [23]. The hierarchical clustering based on the unweighted pair group method with arithmetic mean (UPGMA) using dissimilarity matrix was computed by DARwin 6.0.12 version [24]. The genotypic and phenotypic variance was calculated according to Burton and Devane [25], heritability by Hanson et al., [26], genetic advance by Johnson et al., [27] and path coefficient analysis by Wright [28].

Results and Discussion

Agro-morphological trait variations

The analysis of variance revealed the presence of significant trait variations among the *jhum* rice landraces. The descriptive statistics of 14 traits among the 19 genotypes were presented in (Table 2).

Table 2. Phenotypic trait mean variations among the 19 *jhum* rice landraces

SN.	Traits	PH	GD	LgL	FLL	FLW	BLL	BLW	PnL	PBP	FGP	TGW	GL	GW	GY
1	Bali red	161	7.14	1.76	46.6	2.3	70	2.02	28.6	10.8	160	3.05	7.7	1.83	30.8
2	Baliwhite	157	7.97	1.59	42.4	2.5	65.8	2.24	27.6	15	212	2.7	6.5	1.87	16.8
3	Mingpong	149	7.34	1.48	36.8	2.5	66	2.3	30.4	9.6	174	2.25	6.9	2.02	24.3
4	Yali amo	151	5.71	1.96	45.6	2.28	64.2	2.06	31.6	11.4	243	2.6	7.9	1.74	23.6
5	Kimin red	155	7.26	1.92	51.6	2.5	62.2	2.3	29.5	12.6	238	2.85	7.2	1.73	19.5
6	Jarli	161	7.44	1.4	43	2.4	62	2	27.8	11.2	187	2.55	7.55	1.84	26
7	Kimin white	146	6.84	1.42	45.2	2.38	62.2	2	29.2	10	185	2.85	6.01	1.72	16.8
8	Poore	162	7.97	1.78	48	2.36	69.6	2.08	26.4	8.7	160	1.98	6.2	1.66	9.9
9	Ambher	126	7.5	1.66	41.6	2.2	61.4	2	30.2	8.8	144	1.95	6.55	1.46	7.6
10	Chipu	157	7.41	1.78	38.6	2.3	61	2.2	27.1	13.8	215	2.45	6.5	1.85	25.3
11	Kecha	112	8.37	1.68	36.8	2.4	53.4	2.3	24.6	10.6	212	2.25	6.45	1.61	10.4
12	Angkear	148	6.22	2.1	49.6	2.5	66.6	2.04	32.2	10.2	198	2.9	8.35	1.57	17
13	Pumik	154	8.1	1.62	52	2.6	67	2.28	25	10.8	197	2.6	6.7	1.81	28.3
14	Ampu	134	8.3	1.58	42.2	2.7	57	2.6	28.6	12.6	245	2.7	7.15	1.72	10
15	Mukte	90.2	5.88	1.96	52.6	2.56	69.8	1.36	19.3	10.2	174	2.25	7.05	1.63	8
16	Amchiriri	150	6.68	2.38	43.4	2.4	62.4	2	26.8	9	183	2	6.65	1.75	9.6
17	Lemmuk	162	7.44	1.9	38.2	2.24	55.6	2.2	26.4	9.8	135	2	6.55	1.57	8.1
18	Bamtare	158	7.35	2.12	46.2	2.6	62.6	2.2	31.8	11.8	277	1.95	6.5	1.69	11
19	Takear	54.6	5.36	2.2	47.4	2.62	67.6	2.46	27.6	10.4	162	2.8	8.45	1.59	13
Gmean		**141**	**7.17**	**1.8**	**44.6**	**2.44**	**63.5**	**2.14**	**27.9**	**10.9**	**195**	**2.46**	**6.99**	**1.72**	**16.6**
Min		**54.6**	**5.36**	**1.4**	**36.8**	**2.2**	**53.4**	**1.36**	**19.3**	**8.7**	**135**	**1.95**	**6.01**	**1.46**	**7.6**
Max		**162**	**8.37**	**2.38**	**52.6**	**2.7**	**70**	**2.6**	**32.2**	**15**	**277**	**3.05**	**8.45**	**2.02**	**30.8**
S.E.			**7.28**	**0.52**	**0.15**	**3.79**	**0.12**	**3.75**	**0.14**	**1.21**	**0.78**	**19.3**	**0.11**	**0.08**	**0.16**	**0.67**
C.D.(5%)			**20.4**	**1.45**	**0.41**	**10.6**	**0.34**	**10.5**	**0.4**	**3.39**	**2.18**	**54**	**0.32**	**1.18**	**0.4**	**2**
CV(%)		**11.5**	**16.2**	**18.2**	**19**	**11**	**13.2**	**14.8**	**9.7**	**16**	**22.2**	**6.23**	**10.1**	**7.73**	**5.73**

* . Significant at the 0.05 level, **. Significant at the 0.05 level

Plant height (PH cm), Girth diameter (GD mm), Ligule length (LgLcm), Flag leaf length (FLLcm), Flag leaf width (FLWcm), Blade leaf length (BLL cm), Blade leaf width (BLW cm), Panicle length(PnL cm), Primary branch number per panicle (PBP), Filled grain number per panicle (FGP), Test grain weight of 100 seeds in gram (TGW), Grain length (GL mm), Grain width (GW mm) and Grain Yield per hectare in quintal (GY)

Mean plant height (PH) varied from 54.6 cm (Takear) to 162 cm (Poore) with an average of 141.35 cm (% CV=11.51). Girth diameter (GD) ranged from 5.36 mm (Takear) to 8.37 mm (Kecha) with a mean of 7.17 mm (% CV=16.15). The ligule length (LgL) varied from 1.4 cm (Jarli) to 2.38 cm (Amchiriri) with an average of 1.80 cm (% CV= 18.24). The flag leaf (FLL) value varied from 36.8 cm (Kecha) to 52.6 cm (Mukte) with an average of 44.62 cm (% CV=19). While the flag leaf width (FLW) ranged from 2.2 cm (Ambher) to 2.7 cm (Ampu) with an average of 2.44 cm (% CV= 10.9). Blade leaf length (BLL) varied from 53.4 cm (Kecha) to 70 cm (Bali red) with an average of 63.49 cm (% CV=13.2). While the blade leaf width (BLW) varied from 1.36 cm (Mukte) to 2.6 cm (Ampu) with an average of 2.14 cm (% CV=14.75), panicle length (PnL) varied from 19.34 cm (Mukte) to 32.2 cm (Angkear) with an average of 27.94 cm (% CV=9.7). The number of primary branch per panicle (PBP)

ranged from 8.7 (Poore) to 15 (Bali white) with an average of 10.91 (% CV=15.96). While filled grain per panicle (FGP) varied from 135.2 (Lemmuk) to 277.4 (Bamtare) with an average of 194.74 (% CV=22.15). The test grain weight of 100 seeds (TGW) varied from 1.95 (Bamtare) to 3.05 (Bali red) with an average of 2.46 g (% CV=6.23). Grain length (GL) varied from 6.0 mm (Kimin white) to 8.45 mm (Takear) with an average of 6.99 mm (% CV=10.05). While grain width (GW) ranged from 1.46 mm (Ambher) to 2.02 mm (Mingpong) with an average of 1.72 mm (% CV= 7.73). Among the 19 genotypes, the grain yield per hectare (GY) varied from 7.6 q/ha (Ambher) to 30.8 q/ha (Bali red) with an average of 16.63 q/ha (% CV=5.73). The following 6 genotypes were promising in grain yield potential viz. Bali Red (30.8 q/ha), Pumik (28.3 q/ha), Jarli (26 q/ha), Chipu (25.3 q/ha), Mingpong (24.3 q/ha and Yali amo (23.6 q/ha) respectively (Figure 1).
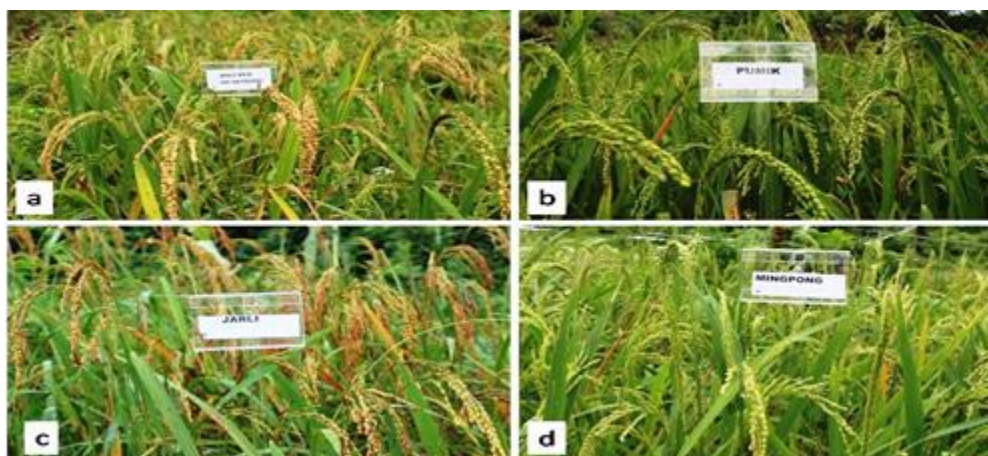
Figure 1. Promising *Jhum* rice landraces (a) Bali red (b) Pumik (c) Jarli (d) Mingpong

For any improvement in breeding programmes, understanding the genetics of quantitative traits is a prerequisite [29]. Despite its rich genetic resources, information on the systematic characterization of rice germplasm of Arunachal Pradesh is fragmented and scanty. In our study the recorded coefficient of variation varied from 5.73% (yield/ha) to 22.2 (FGP). The significant trait variations among the study rice landraces suggest the presence of considerable genetic diversity and scope for further exploitation of desirable traits. In congruence to our study, earlier researchers have also reported the existence of huge genetic variations among the local landraces conserved by the farmers [10-11, 30-31]. Such a broad genetic base of traditional landraces will be of immense help for the future improvement of the breeding programme.

Cluster analysis
Based on 14 phenotypic traits, the UPGMA Hierarchical clustering grouped the 19 *jhum* rice landraces of Arunachal Pradesh into 3 major clusters (Figure 2). Cluster-I comprised of 13 genotypes with 34 % dissimilarity. This major cluster-I was further grouped into 2 sub- clusters. The first sub-clusters comprised of 10 genotypes viz. Jarli, Bali red, Kimin white, Pumik, Chipu, Bali white, Mingpong, Angkear and Yali amo with 32 % dissimilarity. While the second sub-cluster consisted of three genotypes namely Kecha, Ampu and Bamtare with 33 % dissimilarity. The second major cluster-II comprised of genotypes such as Amchiriri, Poore, Lemmuk and Ambher with 28 % dissimilarity. Whereas the third major cluster-III comprised of only two genotypes Mukte and Takear with 36 % dissimilarity. Among all the 19 genotypes Lemmuk and Ambher with 21 % dissimilarity were found to be most related. These two genotypes were from higher altitude locations. The genotypes in cluster-I displayed higher mean values of traits like plant height, panicle length, filled grain per panicle and yield (Table 3). The genotypes in cluster-II have shorter grain lengths, tall plant height and the lowest yield potential. While the genotypes in cluster-III have comparatively longer grain
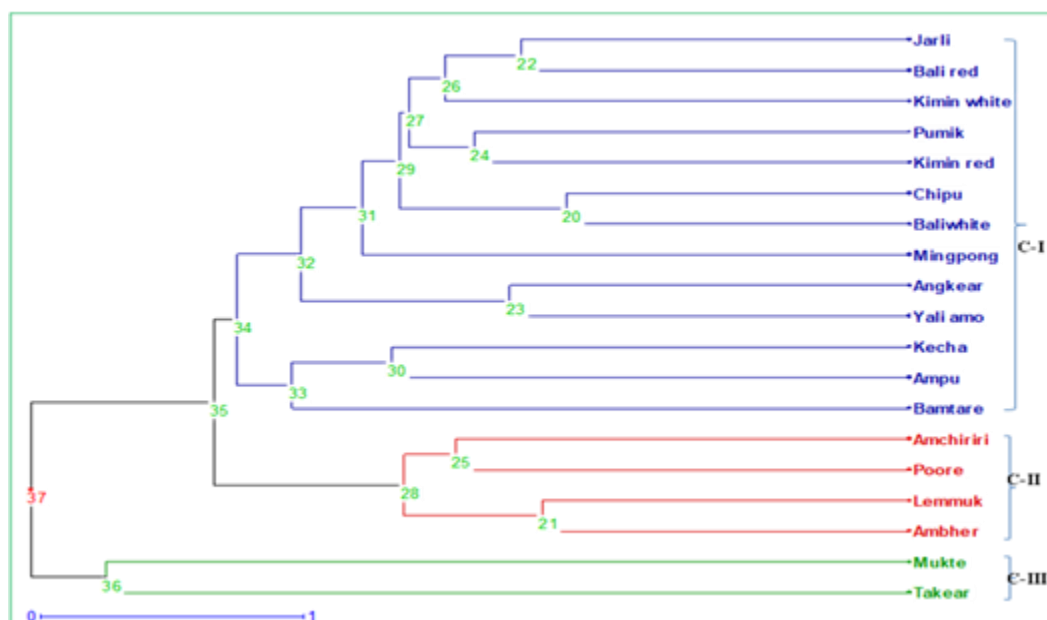
Figure 2. Grouping of 19 *jhum* rice landraces based on unweighted pair group method with arithmetic means (UPGMA) hierarchical clustering method

Table 3. Cluster means of phenotypic traits

Traits	C-I	C-II	C-III
PH	149.37	149.78	72.4
GD	7.34	7.4	5.62
LgL	1.72	1.93	2.08
FLL	44.35	42.79	50
FLW	2.46	2.3	2.59
BLL	63.08	62.25	68.7
BLW	2.2	2.07	1.91
PnL	28.77	27.46	23.47
PBP	11.57	9.08	10.3
FGP	211.03	155.3	167.8
TGW	2.59	1.98	2.53
GL	7.03	6.49	7.75
GW	1.77	1.61	1.61
GY	19.98	8.8	10.5

Plant height (PH cm), Girth diameter (GD mm), Ligule length (LgLcm),
Flag leaf length (FLLcm), Flag leaf width (FLWcm), Blade leaf length (BLL cm),
Blade leaf width (BLW cm), Panicle length(PnL cm), Primary branch number per panicle (PBP),
Filled grain number per panicle (FGP), Test grain weight of 100 seeds in gram (TGW),
Grain length (GL mm), Grain width (GW mm) and Grain Yield per hectare in quintal (GY)

lengths and shorter plant height with higher mean values of flag leaf and blade leaf characteristics. In the present study, the grouping pattern of genotypes does not congruent with their geographical place of collection. A similar trend has also been reported in previous studies by several researchers [7, 32-34]. The grouping of rice based on phenotypic traits have also been reported earlier by Kumar et al., [35] on *jhum* rice germplasm of Northeast India, Sinha et al., [36] in West Bengal rice, Ahmed et al., [37] in Bangladesh rice genotypes and Roy et al., [7] in hill rice landraces of Northeast India into japonica and indica types.

Principal component analysis (PCA)
Principal component analysis (PCA) using 14 phenotypic characters extracted five principal components (Eigen value > 1) with a total phenotypic variance of 80.5 percent (Table 4). About 61.4

% of the total variation was displayed by the first three principal components. The PCA discerns the important traits with greater influence with their degree of contribution to the total variations [38]. In order to visualize the nature of trait variations critically, the degree of traits contributions in the first three principal components are most crucial [39-40]. The grouping pattern by scoring of PCA biplot with PC1 and PC2 among the 19 genotypes was similar to cluster analysis (Figure 3).

Table 4. Principal component scores from correlation matrix

| Traits	PC1	PC2	PC3	PC4	PC5
PH	0.343	-0.034	0.285	0.158	-0.493
GD	0.388	-0.247	-0.023	-0.248	0.02
LgL	-0.334	0.068	-0.261	0.194	-0.388
FLL	-0.269	0.318	0.044	-0.26	-0.308
FLW	-0.009	0.267	-0.387	-0.436	0.039
BLL	-0.222	0.313	0.352	-0.174	-0.135
BLW	0.303	0.058	-0.385	0.175	0.286
PnL	0.174	0.153	-0.093	0.621	-0.199
PBP	0.314	0.24	-0.21	-0.181	-0.073
FGP	0.236	0.212	-0.392	-0.07	-0.441
TGW	0.081	0.453	0.032	0.043	0.317
GL	-0.196	0.398	-0.082	0.312	0.246
GW	0.341	0.217	0.27	-0.166	-0.018
GY	0.245	0.349	0.374	0.086	0.091
Eigen values	**3.45**	**3.16**	**1.99**	**1.5**	**1.16**
Variance %	**24.67**	**22.57**	**14.2**	**10.72**	**8.31**
Cumulative %	**24.67**	**47.25**	**61.45**	**72.17**	**80.47**
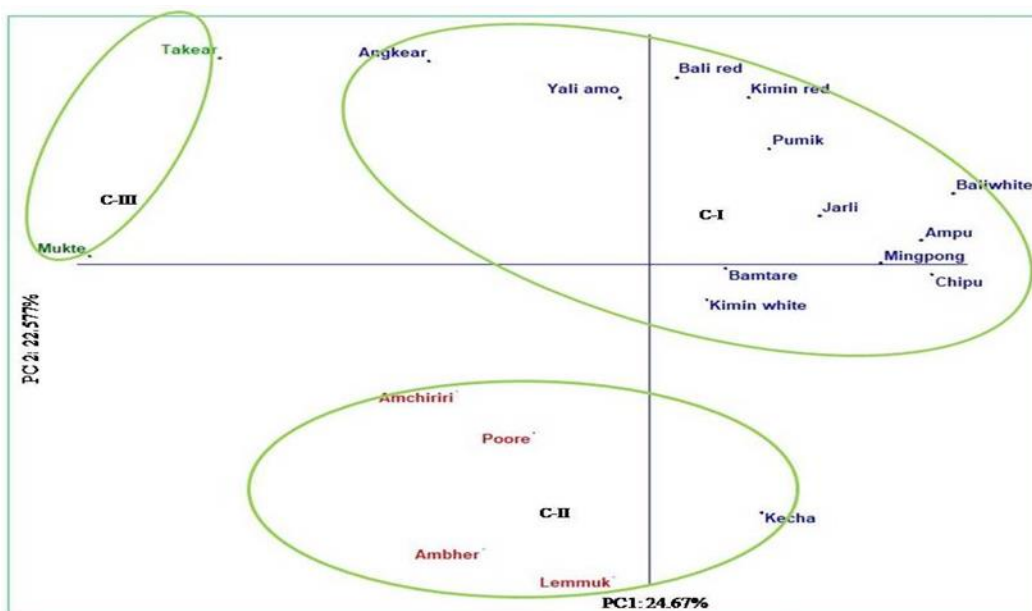
Figure 3. PCA biplot representation of 19 *jhum* rice landraces

Genotypes from cluster-I mostly occupied the right side of the biplot. While cluster-II and Cluster-III are mainly confined to the left side of the biplot. A similar cumulative variance of 79.05% was reported earlier in rice landraces of West Bengal by Sinha et al., [41] in jhum rice landraces of Northeast India (56%) by Kumar et al., [35] and in the hill rice landraces of Northeast India (76.4%) by Roy et al., [7]. The first principal components explained about 24.7 % of the total phenotypic

variation and the traits like PH, GD, BLW, PnL, PBP, FGP, GW and GY have high positive loadings respectively. While traits like LgL, FLL, BLL and GL have high negative loadings. The second component (PC2) accounted for an additional variance of 22.5 % and traits like FLL, FLW, PBP, FGP, TGW, GL, GW and GY have high positive loadings. Whereas traits like PH and GD exhibited negative loading. Similarly, an additional cumulative variance of 14.2 %, 10.7 % and 8.3 % were accounted to PC3, PC4 and PC5 respectively. A similar finding of high positive loading of traits like leaf length, leaf breadth, panicle length, and plant height in the first principal component was reported earlier by Roy et al., [34]. Thus the 14 quantitative traits variations in the present study were robust enough to discern the *jhum* rice genotypes into distinct groups.

Components of genetic variability
Understanding the nature of the relationship between yield and other attributes is essential for effective selection [42]. It will be deceptive to select a genotype based only on their phenotypic variance due to the presence of considerable environmental effects [43]. Thus, it is necessary to split the variation into genotypic and environmental components [44]. In our study, the variation of phenotypic and phenotypic coefficient of variation (PCV) were found to be comparatively greater than their corresponding genotypic variance and genotypic coefficient of variation (GCV) (Table 5). This reflects the impacts of the environment on the nature of trait variation among the genotypes.

Table 5. Components of genetic variations for quantitative traits among the 19 *jhum* rice landraces

Traits	Mean	Fratio	PV	GV	PCV	GCV	h²b	GA	GAM
PH	141.35	14.97	1004.71	739.93	22.42	19.24	73.65	48.09	34.02
GD	7.17	2.8	1.82	0.48	18.83	9.68	26.43	0.74	10.25
LgL	1.8	3.41	0.16	0.05	22.22	12.67	32.55	0.27	14.9
FLL	44.62	1.71	82.03	10.19	20.3	7.15	12.42	2.32	5.19
FLW	2.44	1.38	0.08	0.01	11.4	3.03	7.08	0.04	1.66
BLL	63.49	1.56	78.17	7.88	13.92	4.42	10.08	1.84	2.89
BLW	2.14	3.21	0.14	0.04	17.72	9.82	30.69	0.24	11.2
PnL	27.94	6.17	14.94	7.6	13.83	9.86	50.85	4.05	14.49
PBP	10.91	4.59	5.21	2.17	20.91	13.52	41.78	1.96	18
FGP	194.75	3.79	2896.88	1036.41	27.64	16.53	35.78	39.67	20.37
TGW	2.46	11.53	0.15	0.12	15.61	14.31	84.04	0.66	27.02
GY	16.63	130.67	59.73	58.82	46.47	46.11	98.48	15.68	94.27

Phenotypic variance (PV), Genotypic variance (GV), Phenotypic coefficient of variation (PCV), Genotypic co-efficient of variation (GCV), Heritability in broad sense (h2b), Genetic advance (GA), Genetic advance in percent of mean (GAM), Plant height (PH cm), Girth diameter (GD mm), Ligule length (LgLcm), Flag leaf length (FLLcm), Flag leaf width (FLWcm), Blade leaf length (BLL cm), Blade leaf width (BLW cm), Panicle length(PnL cm), Primary branch number per panicle (PBP), Filled grain number per panicle (FGP), Test grain weight of 100 seeds in gram (TGW) and Grain Yield per hectare in quintal (GY)

Similar findings of low GCV than PCV were reported earlier by Roy and Shil [45]. The highest PCV was recorded in yield (46.47%) followed by FGP (27.64%), PH (22.42%), LgL (22.2%), PBP (20.91%) and FLL (20.3%) respectively. While the lowest PCV value of 11.4 was rescored in flag leaf width. This moderate to high PCV revealed the influences of environmental factors in the phenotypic traits variation among the rice landraces under study. The GCV estimation among the 14 traits revealed that yield (46.11%) variations are highly under genetic control. Moderate GCV values were recorded in PH (19.24 %), FGP (16.53 %), TGW (14.31 %), PBP (13.52 %) and LgL (12.67 %) respectively. While low GCV value was observed in traits like PnL (9.86 %), BLW (9.82 %), GD (9.68 %), FLL (7.15 %), BLL (4.42 %) and BLW (3.03 %) respectively. High broad sense heritability was observed in yield (98.48 %), test weight (84.04 %) and PH (73.65 %) respectively. While traits like PnL (50.85 %) and PBP (41.78 %) showed moderate heritability. Low heritability values were observed in FGP (35.78 %), LgL (32.55 %), BLW (30.69 %), GD (26.43 %), FLL (12.42 %), BLL (10.08 %) and FLW (7.08 %) respectively. The analysis of genetic advance as percent of the mean (GAM) revealed that traits like yield (94.27 %), PH (34.02 %), TGW (27.02 %) and FGP (20.37 %) have high genetic advance respectively. The moderate genetic advance was recorded in PBP (18 %), LgL (14.9%), PnL (14.49 %), BLW (11.2 %) and GD (10.25 %) respectively. Whereas low genetic advance

was observed in FLL (5.19 %), BLL (2.89 %) and FLW (1.66 %) respectively. According to Jonhson et al., [27] the levels of PCV, GCV and GA were ranked as low, (<10%), moderate (10-20%) and high (>20%) respectively. Similarly, broad sense heritability (h2b) was classified as low (40%), moderate (40–60%) and high (>60%) respectively [46]. Moderate to high PCV and GCV recorded in GY, FGP, PBP, FLL and TGW in our study suggested that these traits have greater genetic diversity [9, 47] with more genetic control [29, 48-49] and can be used for selection criterion for genetic improvement [8, 47]. Whereas traits like GD, FLL, FLW, BLL, BLW and PnL have low GCV values. This suggests the low level of variation among these traits [9, 47] and the selection using the variation of such traits would not be rewarding and effective [50]. Similar values of PCV and GCV in PnL and other traits were also reported in previous findings [47]. According to Deshmukh et al., [51] the differences between the value of PCV and GCV were ranked as low (<10%), moderate (10–20%) and high (> 20%) respectively. The least difference between PCV and GCV was recorded in GY (0.36 %) followed by TGW (1.3 %) and PH (3.18 %) respectively. This indicates the influence of additive gene action on such traits expression [50]. Similarly, results of negligible PCV and GCV difference in phenotypic traits of rice were also reported in the previous findings [50, 52]. The degree of heritability of a specific trait indicates the extent of it transmissibility to the next generation during the selection programme [53]. It is desirable to have a high value of both heritability and genetic advance for predicting genetic gain in the breeding programme [27]. Since the value of heritability alone is not robust enough as the sole selection criteria, considering both high heritability and genetic advance would be more effective [54-55]. Thus traits with high heritability couple with high genetic advance would be desirable for effective selection due to additive gene action [56]. In our investigation, high heritability couple with high GAM were observed in traits like GY, TGW and PH. This suggests that the inheritance of these traits are governed by more of additive gene action and selection be rewarding. Similar findings of high h2b and GAM on yield attributes in rice were also reported by earlier researchers [29, 47, 50, 57]. In congruence with the present study, Singh et al., [30] and Saha et al., [49] also reported high h2b and high GAM in traits like grain yield, PH and FGP. While PnL and PBP shown moderate h2b couple with GAM indicating the influence of both additive and non-additive gene action. Similar results of moderate h2b and GAM in rice were reported earlier by several researchers [47, 50]. The low h2b and GAM recorded in traits like GD, LgL, FLL, FLW, BLL and BLW indicates the traits variations are more of non-additive gene and environmental effects. Hence it may not be effective to use such traits criterion for the selection of genotypes. The traits variability, h2b, and GAM in the present investigation indicates the presence of huge genetic variations and opportunity for improvement breeding of the local *jhum* rice landraces. Similar trends of high PCV, GCV, heritability, and GAM were reported by Kumar et al., [35] in *jhum* rice germplasm of Northeast India, Tuhina-Khatun et al., [29] on upland rice and Saha et al., [49] in Bangladesh rice germplasm and Faysal et al., [50] in Aman rice genotypes respectively.

Pearson's correlation coefficient
Except for ligule length and flag leaf width, all the remaining 12 quantitative traits exhibit a positive correlation with grain yield (Table 6). A comparatively highest significant positive correlation (P≤ 0.01) with grain yield was displayed by 100 seed test weight and grain width. A similarly positive significant correlation (P≤ 0.01) was found between PH with GD; FLL with BLL; and FGP with PBP. While significant negative correlation was observed between LgL with GD and GL with GD. Due to the impacts of environmental effects on the variations of quantitative traits, the selection criterion of desirable phenotypes only on grain yield should be avoided [58] and the nature of the association between grain yield and other yield contributing traits needs to be critically examined [47]. Hence the selection for augmenting yield should be based on the correlation coefficient of all the quantitative attributes that has desirable impacts on grain yield, heritability and genetic advance [17, 47]. The interrelationship between traits displayed a positive significant correlation between PH and GD (P ≤ 0.05), BLL with FLL (P ≤ 0.01), FGP with PBP (P ≤ 0.01) and GL with TGW (P ≤ 0.05).

Table 6. Correlation among 14 quantitative traits in 19 *jhum* rice landraces

Traits	PH	GD	LgL	FLL	FLW	BLL	BLW	PnL	PBP	FGP	TGW	GL	GW	GY
PH	1													
GD	0.475*	1												
LgL	-0.27	-0.581**	1											
FLL	-0.142	-0.394	0.328	1										
FLW	-0.348	-0.007	0.099	0.392	1									
BLL	-0.086	-0.436*	0.157	0.650**	0.179	1								
BLW	0.053	0.412	-0.13	-0.352	0.305	-0.405	1							
PnL	0.38	-0.078	0.02	-0.137	-0.114	-0.065	0.411	1						
PBP	0.189	0.224	-0.174	-0.057	0.28	-0.134	0.337	0.086	1					
FGP	0.202	0.123	0.088	0.112	0.448*	-0.23	0.312	0.333	0.638**	1				
TGW	-0.053	-0.225	-0.186	0.35	0.257	0.26	0.2	0.213	0.431	0.179	1			
GL	-0.345	-0.633**	0.347	0.338	0.223	0.332	0.054	0.264	0.027	0.022	0.561**	1		
GW	0.453*	0.218	-0.402	-0.184	0.156	0.225	0.172	0.081	0.418	0.237	0.261	-0.078	1	
GY	0.405	0.005	-0.359	0.088	-0.079	0.329	0.101	0.236	0.32	0.123	0.583**	0.296	0.716**	1

*. Correlation is significant at the 0.05 level
**. Correlation is significant at the 0.01 level
Plant height (PH cm), Girth diameter (GD mm), Ligule length (LgLcm), Flag leaf length (FLLcm), Flag leaf width (FLWcm), Blade leaf length (BLL cm), Blade leaf width (BLW cm), Panicle length(PnL cm), Primary branch number per panicle (PBP), Filled grain number per panicle (FGP), Test grain weight of 100 seeds in gram (TGW), Grain length (GL mm), Grain width (GW mm) and Grain Yield per hectare in quintal (GY)

This suggests that the stronger the stem, the more resistant will be the plant from lodging in sloppy areas of the hill. Likewise the number of primary branches, the better will be the grain yield per panicle and the longer the grain more will be the test weight of the grain. Hence the selection of desirable genotypes using these traits criterion would be promising for augmenting the yield of *jhum* rice. Similar results were reported in previous findings [47]. The positive correlation between the flag leaf and blade leaf area was also in congruence with Roy et al., (2014b). A significant negative interrelationship was observed between LgL with GD and GL with GD. While the rest of the inter traits exhibited non significant negative relationship. Similar trends of correlations among the quantitative traits in rice were reported by several researchers [34, 49, 59].

Analysis of path coefficient
The analysis of path coefficient is necessary for revealing the direct and indirect effects of traits on GY [8, 47, 58]. In our study, GY was measured as a dependent variable and associated traits like PH, GD, LgL, FLL, FLW, BLL, BLW, PnL, PBP, FGP, GL and GW were used as independent variables (Table 7). The direct effects of traits were represented in bold phase along the diagonal of the table and the residual effects of other independent variables magnitude was found to be negligible (0.1198).

The direct effect of PH on GY was negative (-0.1172) and the indirect effect was found to be positive through GW, FLW, GD, LGL and FGP (Table 6). Hence the overall genotypic correlation (0.405) was positive and insignificant. Flag leaf (FLL) showed a positive direct effect on GY (0.4783). While the indirect effects were negative through FLW, GW, GD, LgL and BLL. Thus the overall value of correlation was positively non significant. The direct effect of FLW on GY was negative(-0.608) and the overall correlation also negative (-0.790). The direct effect of BLW on GY was positive (0.1469) with a positive value of overall correlation (0.101). Whereas BLL showed a negative direct effect (-0.0663) with overall positive correlation (0.329). The indirect effect of BLL through FLL on GY was found to be positive. The direct effect of PnL on GY was negative with negligible magnitude (-0054). It displayed indirect positive effects through GL, FLW, GW, BLW, FGP, TGW and BLL respectively. Thus the overall correlation (0.236) of PnL on yield was positive. The direct effect of PBP on GY was negative (-0.0768) and the indirect effects were positive through traits like GW, FGP, TGW, BLW and GL respectively. As a result, the overall correlation magnitude was found to be positive (0.320). FGP showed direct positive effect on GY (0.119). However, the overall positive correlation was low (0.123) due to the negative indirect effect through the traits like PnL, GL, PH and PBP respectively. The test grain weight of 100 seeds (TGW) direct effect on GY was positive (0.1284).

Table 7. Path coefficient analysis representing direct and indirect effects relationship of quantitative traits and grain yield

Trait	PH	GD	LgL	FLL	FLW	BLL	BLW	PnL	PBP	FGP	TGW	GL	GW
PH	**-0.1172**	0.0751	0.0447	-0.0681	0.2117	0.0057	0.0078	-0.0021	-0.0145	0.0241	-0.0068	-0.1368	0.3814
GD	-0.0557	**0.158**	0.096	-0.1886	0.0041	0.0289	0.0606	0.0004	-0.0172	0.0147	-0.0289	-0.2508	0.1839
LgL	0.0317	-0.0918	**-0.1653**	0.1571	-0.0602	-0.0104	-0.019	-0.0001	0.0134	0.0104	-0.0239	0.1376	-0.3384
FLL	0.0167	-0.0623	-0.0543	**0.4783**	-0.2381	-0.0431	-0.0517	0.0007	0.0044	0.0133	0.045	0.134	-0.1551
FLW	0.0408	-0.0011	-0.0164	0.1873	**-0.608**	-0.0119	0.0448	0.0006	-0.0215	0.0533	0.033	0.0886	0.1317
BLL	0.0101	-0.0689	-0.026	0.3109	-0.1088	**-0.0663**	-0.0595	0.0004	0.0103	-0.0274	0.0334	0.1316	0.1895
BLW	-0.0062	0.0652	0.0214	-0.1685	-0.1854	0.0269	**0.1469**	-0.0022	-0.0259	0.0371	0.0256	0.0215	0.145
PnL	-0.0445	-0.0123	-0.0033	-0.0655	0.069	0.0043	0.0604	**-0.0054**	-0.0066	0.0396	0.0274	0.1048	0.0684
PBP	-0.0222	0.0354	0.0288	-0.0271	-0.17	0.0089	0.0495	-0.0005	**-0.0768**	0.076	0.0553	0.0107	0.3519
FGP	-0.0237	0.0195	-0.0145	0.0534	-0.2723	0.0152	0.0458	-0.0018	-0.049	**0.119**	0.0229	0.0086	0.1994
TGW	0.0062	-0.0356	0.0308	0.1675	-0.1565	-0.0173	0.0293	-0.0012	-0.0331	0.0213	**0.1284**	0.2225	0.2203
GL	0.0404	-0.1	-0.0574	0.1617	-0.1359	-0.022	0.008	-0.0014	-0.0021	0.0026	0.072	**0.3964**	-0.0661
GW	-0.053	0.0345	0.0664	-0.088	-0.095	-0.0149	0.0253	-0.0004	-0.0321	0.0282	0.0336	-0.0311	**0.8428**

Residual effect: 0.11983

Plant height (PH cm), Girth diameter (GD mm), Ligule length (LgLcm), Flag leaf length (FLLcm), Flag leaf width (FLWcm), Blade leaf length (BLL cm), Blade leaf width (BLW cm), Panicle length(PnL cm), Primary branch number per panicle (PBP), Filled grain number per panicle (FGP), Test grain weight of 100 seeds in gram (TGW), Grain length (GL mm) and Grain width (GW mm)

Negative indirect effects were displayed through PnL, BLL, PBP, GD, and FLW respectively. However, the indirect effects were also positive through GL, GW, FLL, LgL, BLW, FGP and PH respectively. Hence, the overall correlation of TGW with GY was highly positive (0.583) and significant (P ≤ 0.01). Grain length (GL) exhibited a direct positive effect (0.3964) on GY but the indirect effects were negative through PnL, PBP, BLL, GW, GD and FLW. Hence the overall correlation was positive with a low magnitude (0.296). The highest significant (P≤0.01) magnitude of direct positive effect on GY was exhibited by GW (0.8428). The indirect effects were also positive through LgL, GD, TGW, FGP and BLW. While the negative indirect effects through PnL, BLL, GL, PBP, PH, FLL and FLW were in low magnitude. Hence it exhibited the highest overall significant (P ≤0.01) positive correlation (0.716) with GY.

Similar to the present study, the direct positive effect of FLL and FGP on GY have been reported by Faysal et al., [50]. The direct positive impact on GY through TGW was also in congruence with Hasan-Ud-Daula and Sarker [47] in advance breeding lines of rice, Faysal et al., [50] in Aman rice and Pratap et al., [60] in rice germplasm lines. In general, most of the *jhum* rice landraces exhibit deflexes or droopy flag leaf nature. This could limit the activities of photosynthesis. The direct negative effect of FLW on GY suggests that wider leaf width could be one of the possible reasons for the deflexed or droopy flag leaf among the jhum rice landraces.

A direct positive effect of FGP on GY reported earlier by Hasan-Ud-Daula and Sarker [47] was also in congruence with the present finding. Similarly, the negative direct effect of PH on GY in our study was in congruence with previous researchers [47, 50]. But the indirect impact of PH on GY was positive through filled grain per panicle (FGP) and grain width (GL). This suggests the short stature plant type would be effective in yield improvement. So direct selection on PH would be ineffective. The short stature nature of rice are generally preferred for yield improvement [61].

Similar to the present finding, a direct negative effect of PL and PBP was reported in a previous study by Faysal et al., [50]. The residual effect of 0.119 indicates that 99.8 % of the variability among 19 *jhum* rice landraces was contributed by the studied 14 traits. Similar residual effects of 0.138 and 0.130 were reported earlier by Hasan-Ud-Daula and Sarker [47] and Faysal et al., [50] respectively. Hence giving special consideration to important yield contributing traits with direct positive impacts on GY would be rewarding for breeding high yielding varieties.

Conclusion

The *jhum* rice genotypes in the present study have huge genetic variations. The PCV, GCV, heritability and GAM in most of the important yield contributing characters was moderate to high. High

heritability couple with high GAM was found in GY, TGW and PH. While moderate heritability with GAM was recorded in PnL, FGP and PBP. Among all the traits desirable highly significant positive correlation (P≤ 0.01) with GY was exhibited by grain width (0.716) and TGW (0.583). The direct effect on GY by the traits such as GD, FLL, BLW, FGP, TGW, and GL was positive. Considering all the analysis of genetic parameters, the selection of desirable genotypes for further yield improvement of jhum rice using traits like FGP and TGW would be rewarding and effective. Further, the promising genotypes identified in the present study would be of immense help for the selection of parental lines in future breeding programmes.

Conflict of interest

All the authors have no conflict of interest.

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