Indian J. Plant Genet. Resour. 34(2): 185–195 (2021)
DOI 10.5958/0976-1926.2021.00017.6

RESEARCH ARTICLE

Agro-Morphological Characterization, Genetic Variation and Heritability Analysis of Rice Landraces (*Oryza sativa* L.) of Arunachal Pradesh, Northeast India

Letngam Touthang*, Homeshwar Kalita, Badapmain Makdoh, Thejangulie Angami and Raghuveer Singh
ICAR-Research Complex for North Eastern Hilly Region, Arunachal Pradesh Centre, Basar Leparada District-791101, Arunachal Pradesh, India

(Received: 30 January, 2021; Revised: 10 April, 2021; Accepted: 21 June, 2021)

The present study describes characterization of 35 rice landraces collected from different parts of Arunachal Pradesh. High degree of variations was observed for morphological traits. Mean plant height of 127.39 cm, panicle length (25.7 cm), flag leaf length (40.54 cm), flag leaf width (2.10 cm), blade leaf length (58.66 cm), blade leaf width (1.82 cm), ligule length (2.14 cm), test weight (2.44 g) and mean grain yield per hectare of (18.65 q/ha) were recorded respectively. The cluster analysis grouped 35 landraces into 4 clusters (67% dissimilarity) in which *Jhum* and wetland landraces formed distinct clusters. The first three PCA extracted accounted for 81.64% of the total variation based on 12 phenotypic traits. A significant positive association was observed among the traits, and the genetic variability computation revealed higher PCV than GCV. Highest PCV (43.61%), GCV (43.3%), heritability (98.44%) and GAM (88.43%) were recorded for grain yield. The high variability with promising yield potential among the Arunachal Pradesh landraces is expected to be significance immense significance for rice breeding programmes.

Key Words: Agromorphology, Arunachal Pradesh, Characterization, Genetic Variation, Landraces, Rice

Introduction

The state Arunachal Pradesh is one of the world's biodiversity hotspots and the richest biogeographical province of the Himalayan zone (Hussain and Hore, 2008). Due to its remote location coupled with undulating topography, *jhuming* or shifting cultivation still prevails in the state as subsistence farming. The state is endowed with diverse rice germplasms and the cultivars vary from one district to another (Hore, 2005). The state is contiguous with the region from where ecogeographic races of Asian rice cultigens originated, diversified, and disseminated (Chang, 1985). Northeast India is one of the hot spots and important centers of origin of rice inhabited by thousands of indigenous rice landraces (Durai, 2015). These landraces have great genetic diversity and accounted for 60% of all rice grown in India (Longvah and Prasad, 2020). The region has extremely diverse rice-growing climatic conditions up to 2000 m above sea level when compared to other parts of the country. Such a diverse cultivation system is known to promote allelic variation and genetic diversity (Roy *et al.,* 2014a).

There has been interweaving of the rice-based agriculture system of the Indian subcontinent with its socio-cultural fabric, and thousands of landraces with poorly tapped agronomic traits have been nurtured in these bio-culturally diverse North-Eastern states of the country (Chakraborty and Ray, 2019). As the improvement of existing variety depends upon desirable genes that are possibly present in landraces and wild varieties, the importance of landraces can never be denied in the agriculture system (Holden *et al.,* 1993). They possess a valuable gene pool for the future breeding programme (Richharia, 1979; Patra, 2000). The efforts made to understand the existing landrace diversity as well as to improve them were so limited. There is a rich genetic diversity in rice germplasm from different parts of north-eastern India (Bhuyan *et al.,* 2007; Rathi and Sarma, 2012; Choudhury *et al.,* 2013). But the systemic characterization of rice landraces of Arunachal Pradesh is lacking and scanty. Characterization of germplasm is essential to identify desirable traits, effective utilization of genetic resources, and breeding programme. The valuable germplasms has little practical utility until a collection has been properly evaluated and its attributes become known to breeders. Therefore the collection, characterization, and conservation of these valuable rice landraces are important (Sharma *et al.,* 2007; Thomson *et al.,* 2009; Sanni *et al.,* 2012; Sinha *et al.,* 2013).

**Author for Correspondence: Email- letngam111@gmail.com*

Materials and Methods

Collection of germplasm and field experiment

The study comprised of 35 landraces (19 genotypes of *jhum/upland and 16 wetland rice cultivation (WRC)/* lowland) collected from different parts of the state Arunachal Pradesh (Table 1). Field experiment was conducted for two seasons *Kharif* 2015 and *Kharif* 2016 in Randomised Block design (RBD) with two replications using standard checks. Five competitive plants were randomly selected from each germplasm for recording field observations for all the traits. Data for different qualitative and quantitative traits were recorded at different growth stages based on five competitive plant samples following standard evaluation system for rice from the International Rice Research Institute (IRRI 2002).

Table 1. List of rice landraces of Arunachal Pradesh used in the study

Variety	Village/ Place	Latitude (N)	Longitude (E)
Mingpong	Seppa	27° 19' 59.1996"	93° 3' 47.6928"
Yali amo	Jomoh	28° 11' 20.724"	94° 37' 27.912"
Bali red	Gori	27° 58' 50.8836"	94° 41' 19.6692"
Bali white	Gori	27° 58' 50.8836"	94° 41' 19.6692"
Kimin white	Dali	28^{0}17'597"	94^{0}50'677"
Kimin red	Pagi	27° 55' 50.844"	94° 42' 54.036"
Ampu	Tai	28° 1' 7.356"	94° 34' 42.888"
Jarli	Sodo Doke	28^{0}02.224'	094^{0}37.939'
Pumik	Tai	28° 1' 7.356"	94° 34' 42.888"
Kecha	Boleng	28°18'25.5468"	94°57'11.7792"
Bamtare	Bam	27°58'56.776"	94°41'23.451"
Poore	Dumporijo	27° 59' 32.208"	94° 17' 25.44"
Chipu	Dake	28° 1' 7.356"	94° 34' 42.888"
Amchiriri	Tai	28^{0}00.034'	094^{0}31.715'
Angkear	Sago	27° 55' 50.844"	94° 42' 54.0432"
Takear	Yumlo Mongku	28° 9' 57.0564"	94° 38' 13.3728"
Mukte	Pushi Doke	28° 3' 2.2392"	94° 42' 38.9412"
Ambher	Tuting	28° 59' 42.648"	94° 53' 22.056"
Lemmuk	Pushi Doke	28° 3' 2.2392"	94° 42' 38.9412"
Deku amo	Pashighat	28°04'12.00"	94°19'48.00"
Bodong amo	Boleng	28°18'25.5468"	94°57'11.7792"
Amham	Yumlo Mongku	28° 9' 57.0564"	94° 38' 13.3728"
Amkeer	Boleng	28°18'25.5468"	94°57'11.7792"
Pumde	Tai	28^{0}00.060'	094^{0}31.722'
Gejang	Boleng	28°18'25.5468"	94°57'11.7792"
Tinin	Dake	28° 1' 7.356"	94° 34' 42.888"
Taok amo	Daporijo	27^{0}59'9.83"	94^{0}13'18.16"
Amtum	Gori	27° 58' 50.8836"	94° 41' 19.6692"
Pumso	Gori	27° 58' 50.8836"	94° 41' 19.6692"
Amlum	Gori	27° 58' 50.8836"	94° 41' 19.6692"
Deku oval	Pashighat	28°04'12.00"	94°19'48.00"
Riew amo	Boleng	28°18'25.5468"	94°57'11.7792"
Basmati	Pashighat	28°04'12.00"	94°19'48.00"
Mugme	Bam	27°58'56.776"	94°41'23.451"
Ame amli	Tato	28° 30' 29.34"	94° 27' 28.296"

Data Analysis

The statistical analysis was conducted by the pooling of two-year data. All descriptive statistics with test of significance, Principal Component Analysis (PCA) and Multidimensional scale analysis and Pearson's correlation coefficient (r) were performed by using SPSS version 20.0 (IBM Corp. Released 2011. IBM SPSS Statistics for Windows, Version 20.0. Armonk, NY: IBM Corp.). Unweighted Pair Group Method with Arithmetic Mean (UPGMA) hierarchical clustering based on dissimilarity matrix to assess the phenotypic diversity among the rice landrace was computed in the DARwin software version 6.0.12 (Perrier and Jacquemoud, 2006) DARwin software http://darwin.cirad.fr/). The phenotypic and genotypic variance was estimated according to Burton and Devane (1953), heritability as per Hanson *et al.* (1956), and genetic advance was estimated using the formula suggested by Johnson *et al.* (1955).

Results and Discussion

Traits Variability Among the Landraces

From the analysis of variance, it was observed that the landraces have a significant variation of agro-morphological traits. Among the 35 landraces, the traits under study showed significant variations (Table 2). Plant height (PH) ranges from 54.6 cm to 161.60 cm with a mean of 127.39 cm and 22.20 CV%. Panicle length (PnL) ranges from 10 to 32.20 cm with a mean of 25.70 cm (%CV=17.53). Girth diameter (GD) ranges from 0.42 cm to 0.83 cm with a mean of 0.64 cm (%CV=19.19). The number of primary branches per panicle (PBR) ranges from 8.70 to 15 with a mean of 11.49 (%CV=13.32). Flag leaf length (FLL) ranges from 24.84 to 52.60 cm with a mean of 40.54 (%CV=18.53) and Blade leaf (BLL) ranges from 34.84 cm to 70.00 cm with mean of 58.66 cm (%CV=14.25) respectively. Flag leaf width (FLW) recorded mean of 2.10 cm (%CV=20.46) and blade leaf width (BLW) recorded mean of 1.82 cm (%CV=23.82) respectively.

Table 2. Agromorphological variation of rice landraces (*Jhum* and WRC)

Trait	Range	Minimum	Maximum	Mean	SEM (±)	Std. Deviation	CV(%)	C.D. (5%)
PH	107.00	54.60	161.60	127.39*	5.93	28.28	22.20	16.45
PnL	22.20	10.00	32.20	25.70*	1.22	4.50	17.53	3.40
GD	4.2	4.2	8.4	6.4	0.4	1.2	181.9	1.1
PBR	6.30	8.70	15.00	11.49*	0.75	1.53	13.32	2.08
FLL	27.76	24.84	52.60	40.54*	3.55	7.51	18.53	9.84
FLW	1.56	1.14	2.70	2.10*	0.10	.42	20.46	0.27
BLL	35.16	34.84	70.00	58.66*	3.85	8.36	14.25	10.67
BLW	1.72	.88	2.60	1.82*	0.12	.43	23.82	0.33
LgL	2.48	1.40	3.88	2.14*	0.15	.58	27.51	0.42
FGP	206.80	70.60	277.40	172.47*	18.09	42.93	24.89	50.14
TW	1.10	1.95	3.05	2.44*	0.14	.31	13.07	0.40
YLH	30.30	5.00	35.30	18.65*	0.71	8.10	43.43	2.04

*significant at the 0.05 level SEM: Standard error of mean

Plant height (PH cm), Panicle length(PL cm), Girth diameter (GD mm), Primary branch number per panicle (PBR), Flag leaf length (FLLcm), Flag leaf width (FLWcm), Blade leaf length (BLLcm), Blade leaf width (BLWcm), Ligule length (LgLcm), Filled grain number per panicle (FGP), Test weight 100 seeds in gram (TW), Yield per hectare in quintal (YLH).

Although all the landraces under study have cleft type ligule, a significant variation in ligule length (LgL) was observed which ranges from 1.40 cm to 3.88 cm with a mean of 2.14 cm (%CV=27.51). The number of filled grain per panicle (FGP) recorded a mean of 172.47 per panicle which ranges from 70.60 to 277.40 per panicle (%CV=24.89). The highest variation was recorded in yield potential which ranges from as low as 5q per ha to 35.30 q/ha with a mean of 18.65 q/ha (%CV=43.43) respectively. Among the *jhum* landraces, six genotypes 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 were identified as promising (Fig. 1). While among WRC, Amham (35.3 q/ha), Amlum (31 q/ha), Pumde (29 q/ha), Riew Ammo (28 q/ha), Tinin (27.6 q/ha) and Amtum (26.0 q/ha) respectively were found to be promising (Fig. 2). The agro-morphological characterization of germplasm variety is fundamental to provide information for plant breeding programmes (Lin, 1991). It is the basic foundation for crop improvement to facilitate the utilization of germplasm by breeders (Upadhyaya *et al.*, 2008) and the genetic analysis of quantitative traits is one of the prerequisite for planning a breeding programme (Khatun *et al.*, 2015). Rice is not

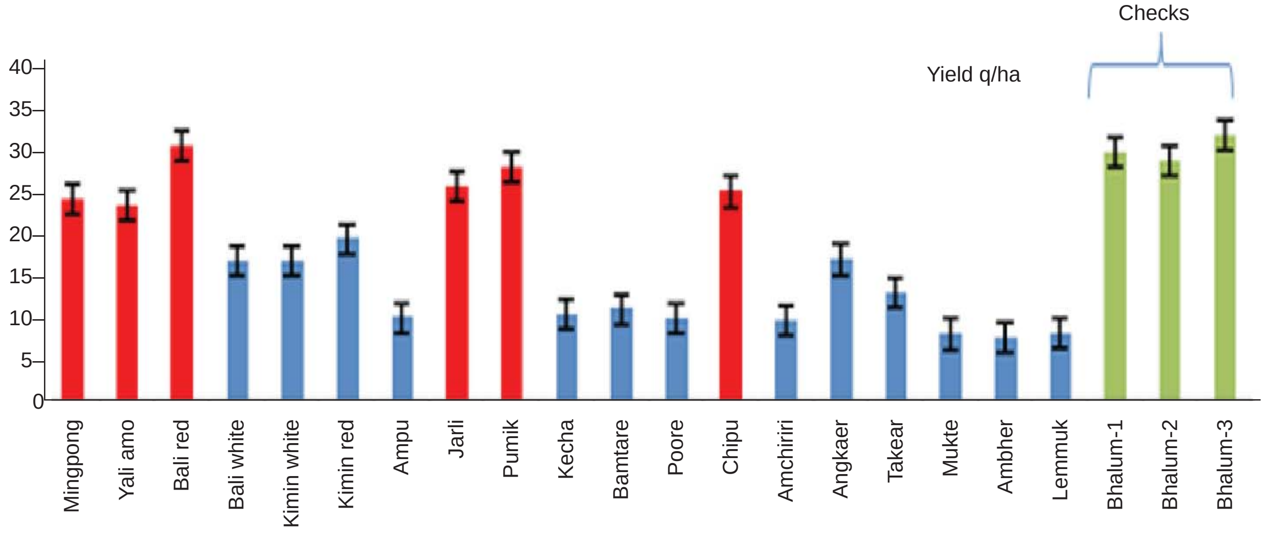

Fig. 1. Yield variation of *jhum* landraces

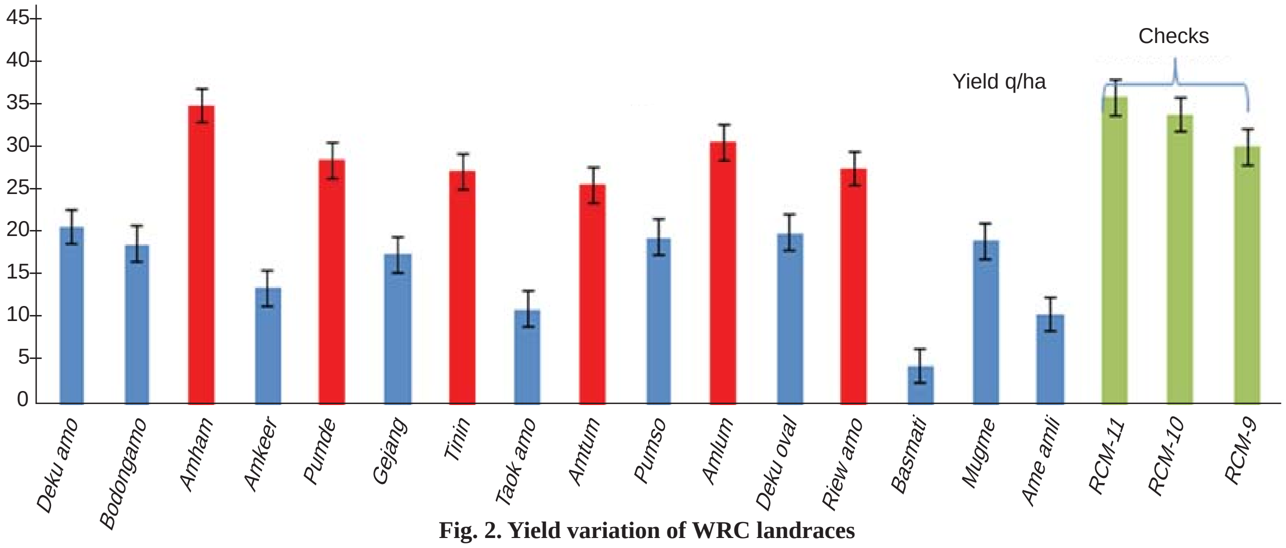

Fig. 2. Yield variation of WRC landraces

only stapled food to these hill dwellers. The tribal farming communities have selected and maintained numbers of landraces with deep-rooted socio-cultural attachment and many indigenous cultivars of rice are being conserved and cultivated by the resource-poor farmers. The farmers in the region usually classify hill rice cultivars based on agronomic traits (Roy *et al.,* 2016). Although the state Arunachal Pradesh is endowed with large varieties of rice germplasms which vary place to place (Hore, 2005), its systemic characterization informations are scanty and fragmented.

Similar to earlier reports (Subudhi *et al*,. 2012**;** Singh, 2013), the coefficient of variation of morphological traits ranges widely (5.4% to 23.45%) and little variation on qualitative traits. In general the *jhum* landraces were taller with lower average yield in compare to WRC genotypes. Tall stature, droopy or deflex flag leaf nature of *jhum* rice landraces as compare to erect flag leaf nature of lowland/WRC landraces could be one of the main variations in yield concerning efficiency and longevity of photosynthates accumulation during grain filling. In spite of low average yield as a whole, the study observed at par yield potential of identified promising landraces against check varieties. As the rice landraces maintained by farmers harbour wide genetic variability (Fukuoka *et al.*, 2006; Ram *et al*,. 2007; Rana *et al.*, 2007), these landraces with broad genetic base will be of immense help for future improvement breeding programme.

Diversity Pattern by Cluster Analysis

Based on 12 agro morphological traits, UPGMA Hierarchical clustering grouped the 35 rice landraces into four clusters with 67% dissimilarity (Fig. 3). Cluster-I comprised of 15 WRC genotypes with a characteristic of erect flag leaf with slender grain. Cluster-III comprised of 18 genotypes of *jhum* landraces with deflex or droopy flag leaf with bold and short-grain characteristics. These two clusters (I&II) were further grouped into four sub-clusters each with 66% and 65% dissimilarity respectively. The mean plant height, GD, FLL, and width, BLL, and width were lower in cluster-I as compare to cluster III. Bali red, a popular landaces of *jhum* formed distinct sub-cluster. While Takear constituted cluster-II and Amham constituted cluster-IV respectively. This revealed that Amham and Takear were distinct from the rest of the landraces and will be useful for future breeding programme. The highest PH of 146 cm, GD (7.27 mm), and grain number per panicle were recorded in cluster-III (Table 3). While highest PnL (29.2 cm), PBR (13), and yield (35.3 q/ha) were recorded in cluster-IV. The highest means of FLL, FLW, BLL, BLW, and TW were recorded in cluster-II. While the highest LgL was recorded in Cluster-I and have the lowest mean value of traits like BLL, BLW, FGP, and PH. The highest inter-cluster genetic dissimilarity of 98.1 was recorded in between Cluster-III and II (Table 4) and lowest in between Cluster-IV and III (32.3).

Similar to the present investigation, grouping of rice genotypes based on various phenotypic traits have been reported earlier by Kumar *et al.* (2013) on jhum rice germplasm of Northeast India, Sinha *et al.* (2013) in West Bengal rice, Ahmed *et al.* (2016) in Bangladesh rice genotypes and Roy *et al.* (2016) in hill rice landraces of Northeast India into *japonica* and *indica* types. Out

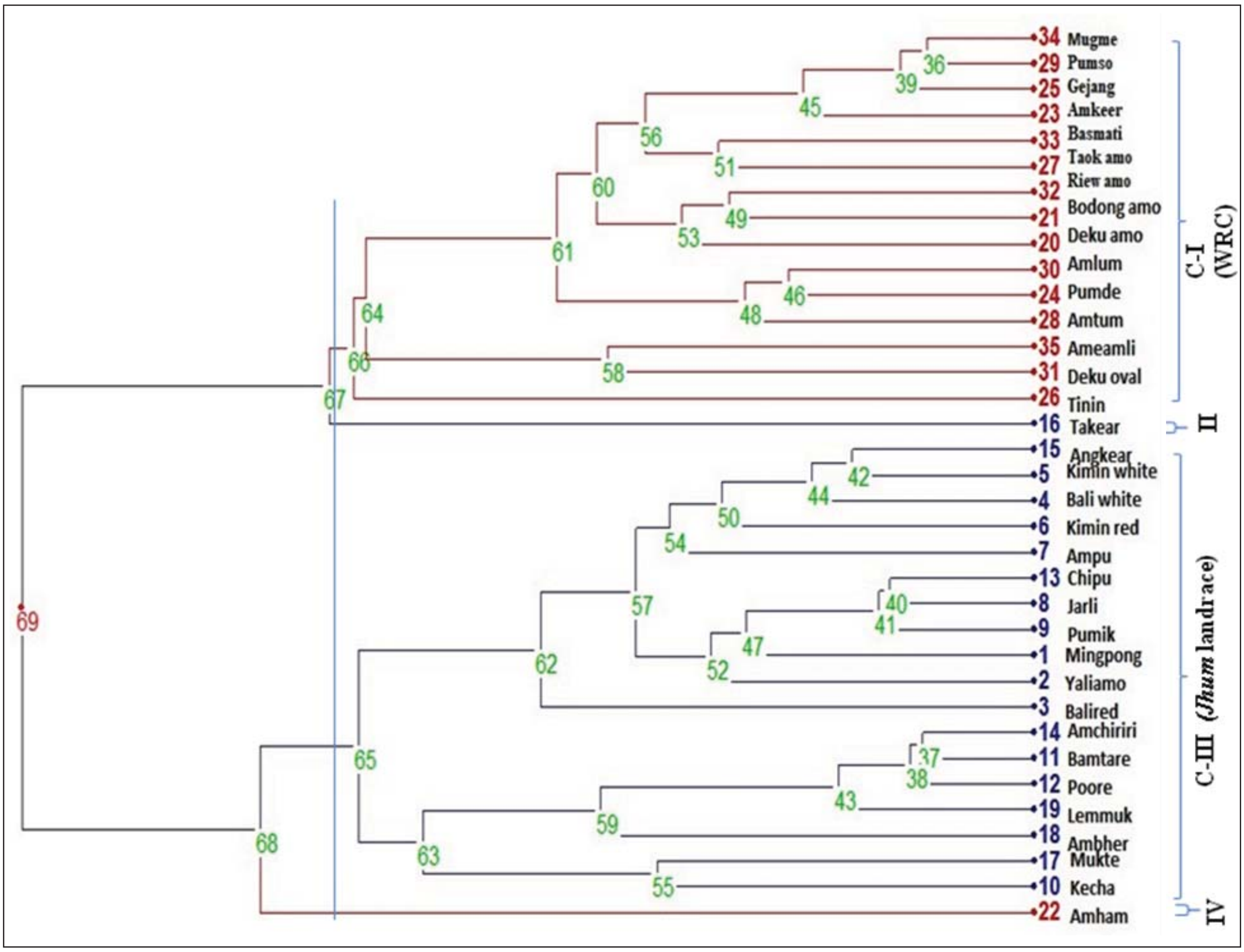

Fig. 3. Grouping of 35 rice landraces based on unweighted pair-group method with arithmetic means (UPGMA) hierarchical clustering method

Table 3. Inter cluster means of agromorphological traits

	PH	PnL	GD	PBR	FLL	FLW	BLL	BLW	LgL	FGP	TW	YLH	Genotypes
Cluster-I	110	22.7	5.48	12	36	1.7	52	1.4	2.54	142	2.42	20.1	15
Cluster-II	54.6	27.6	5.36	10	47	2.6	68	2.5	2.2	162	2.8	13	1
Cluster-III	146	28	7.27	11	44	2.4	63	2.1	1.78	197	2.44	16.8	18
Cluster-IV	122	29.2	5.97	13	39	2.1	61	1.7	2.6	205	2.67	35.3	1

Table 4. Genetic distance between groups and between cluster

	Dissimilarity matrix			
	Euclidean Distance			
	Cluster-I	Cluster-II	Cluster-III	Cluster-IV
Cluster-I	0.000			
Cluster-II	62.654	0.000		
Cluster-III	67.178	98.117	0.000	
Cluster-IV	66.761	83.791	32.318	0.000

of the 35 landraces, landraces like Amham (WRC), Takear (*jhum*) and Bali red (*Jhum*) which deviated distinctively from their respective group with promising yield potential would be useful for future breeding programme. *Jhum* landraces generally have bold seed, panicle well exerted, and droopy or deflex flag leaf with tall plant height. Whereas, the landraces of WRC generally have erect flag leaf with slender grain with shorter plant height characteristics.

Principal Component Analysis (PCA)

Principal component analysis (PCA) resolved three principal components (Eigenvalue >1) with cumulative total phenotypic variance of 81.64% (Table 5). The first principal component (PC1) explained 56.55% of the total variance and the traits like LgL, PH, BLL, FLL, FLW, BLW, PBR, and FGP have high positive loadings respectively. While traits like TW, PnL, Yield, and GD have negative loadings. The second component (PC2) accounted the additional variance of 16.70% in which traits like PBR, Yield, TW, LgL, FLL, BLL, and FLW have high positive loadings respectively. Whereas traits like FGP, PnL, PH, GD, and BLW have been negatively loaded. The third principal component (PC3) accounts additional variance of 8.38% with high positive loading of TW, GD, PnL, FGP, BLW, and Yield respectively. Whereas traits like LgL, PH, and PBR were negatively loaded in the third component. Similar to cluster analysis, the PCA biplot grouped the landraces (*Jhum*/upland and WRC) into different coordinates (Fig. 4.). The *Jhum* landraces with higher values for PH, PnL, GD, FLL, FLW, BLL, and BLW occupied the right half of biplot. While WRC landraces occupied the left half of biplot having a higher value for traits such as PBR, LgL, and Yield.

Table 5. Component Score Coefficient Matrix

Traits	Component		
	PC1	PC2	PC3
FGP	.003	–.006	.300
TW	–.235	.299	.599
PnL	–.020	–.045	.303
YLH	–.011	.362	.028
PH	.218	–.124	–.193
GD	–.036	–.262	.400
PBR	.032	.381	–.129
FLL	.198	.068	–.123
FLW	.174	.009	–.038
BLL	.199	.025	–.104
BLW	.108	–.052	.125
LgL	.229	.194	–.259
Eigen values	6.786	2.005	1.006
Variance (%)	56.554	16.706	8.383
Cumulative (%)	56.554	73.260	81.643

PCA discerns the important characters which have a greater impact on the total variables and the degree of contribution (Sanni *et al.*, 2008). The first three principal components are often the most important in reflecting the

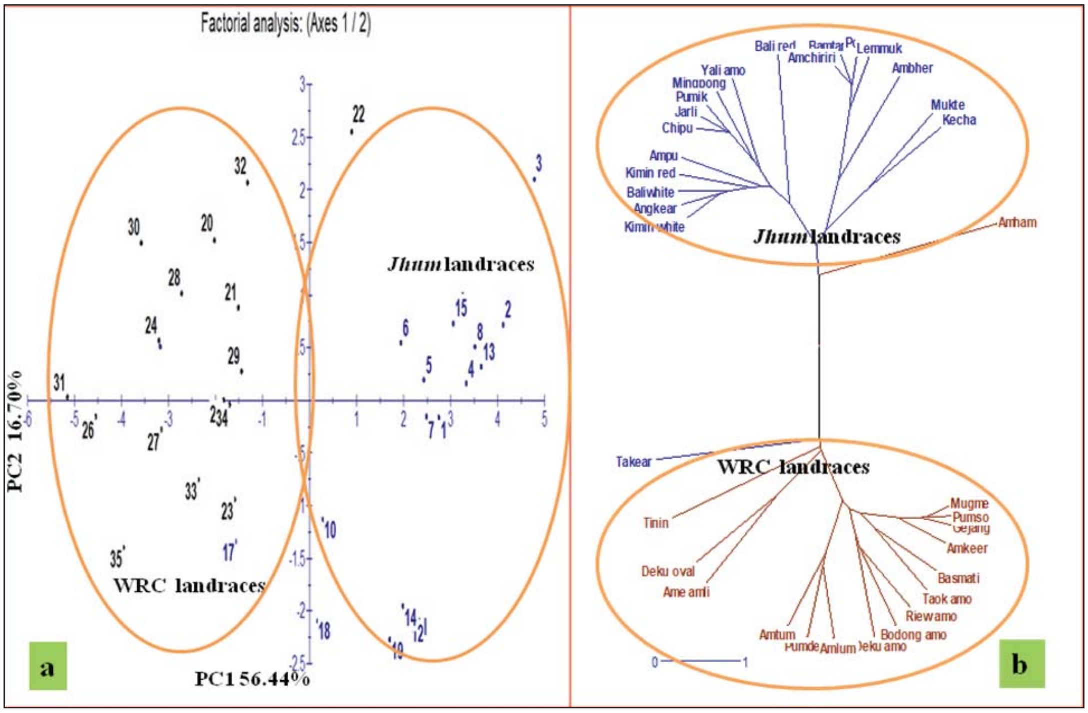

Fig. 4. a. A representation of 19 jhum landraces and 16 WRC landraces on the first two principal component scores, b. Representation of population structure of *jhum* and WRC landraces

variation patterns (Clifford and Stephenson, 1975; Guei *et al.*, 2005). The total cumulative variance revealed by the first three PCA (81.64%) in the present study was higher than the total variance of 79.05%, 56% and 76.4% reported by (Sinha *et al.*, 2013; Kumar *et al.* (2013; Roy *et al.*, 2016) respectively. High positive loading of traits like PH, PBR, FGP, LgL, flag leaf area, and blade leaf area in the first principal component followed by yield and test weight in the second component reflects the high variation of these traits among the landraces. Roy *et al.* (2014b) have also reported high positive loading of traits like leaf length, leaf breadth, plant height, and panicle length in the first principal component. A similar trend was reported by Ibrahim *et al.* (2019).

Correlation among the Traits (Pearson's co-efficient)

Pearson's correlation (r) measured the strength of the association between the two characters. The correlations among the traits in the present study showed a significant positive association among the traits. The grain yield showed positive correlation with TW, PnL, PBR, BLL, BLW, PH, FLL, FLW and LgL (Table 6). The number of primary branches per panicle positively correlates with FLL, FLW, BLL, and BLW. Similar significant positive associations were revealed between FLL with BLW, Grain number per panicle with test weight, PH with GD, TW with PBR etc. Negative correlations were found between PH with PBR, FLL, BLL, FLW, LgL, and TW. Panicle length with FLL, FLW, BLL, and LGL. Flag leaf area and BLL with FGP respectively. The significant positive correlation associations among yield contributing traits show an ample scope for genetic architecture enhancement of the landraces in the future breeding programme. The significant positive correlation of 100-grain weight with grain yield in the present study was in agreement with the earlier reports by (Efendi *et al.*, 2015; Ibrahim *et al.*, 2019). Thus the manipulation of these traits would have a high positive impact on yield enhancement. Except for girth diameter and the number of grain per panicle, all the traits show a positive correlation with yield. A significant positive correlation of yield with LgL observed in the study was also in agreement with Ibrahim *et al.* (2019). A similar finding of negative correlation of yield with the number of filled grain per panicles have also reported by Saha *et al.* (2019). The positive association of plant height with yield in the present study was in agreement with earlier reports (Mohaddesi *et al.*, 2010; Roy *et al.*, 2014b). But this was in contrast with negative associations reported by (Akinwale *et al.*, 2011; Sarawgi *et al.*, 2013). The positive association of plant height with yield in the present study may be due to its ecological needs of landraces to survive against harsh climatic conditions and to have high competitive growth with luxuriant weeds growth. But according to Karine *et al.* (2014),

Table 6. Correlation among agromorphological traits of 35 landraces

	PH	PnL	GD	PBR	FLL	FLW	BLL	BLW	LgL	FGP	TW	YLH
PH	1	.										
PnL	.507**	1										
GD	.718**	.564**	1									
PBR	-.070	.009	-.350*	1								
FLL	-.377*	-.318	-.730**	.474**	1	.						
FLW	-.508**	-.419*	-.932**	.452**	.844**	1						
BLL	-.113	-.130	-.618**	.498**	.851**	.859**	1					
BLW	.085	.079	-.380*	.523**	.812**	.665**	.928**	1				
LgL	-.321	-.271	-.780**	.524**	.936**	.943**	.964**	.866**	1			
FGP	.422*	.464**	.589**	.069	-.226	-.412*	-.056	.085	-.216	1		
TW	-.088	.203	.055	.342*	.168	.039	.170	.279	.152	.381*	1	.
YLH	.054	.131	-.150	.327	.306	.292	.416*	.565**	.392*	-.024	.460**	1

**. Correlation is significant at the 0.01 level (2-tailed). *. Correlation is significant at the 0.05 level (2-tailed).
Plant height (PH cm), Panicle length (PL cm), Girth diameter (GD mm), Primary branch number per panicle (PBR), Flag leaf length (FLLcm), Flag leaf width (FLWcm), Blade leaf length (BLL cm), Blade leaf width (BLWcm), Ligule length (LgLcm), Filled grain number per panicle (FGP), Test weight 100 seeds in gram (TW), Yield per hectare in quintal (YLH)

high yielding types of rice should be of short stature. Similarly, the tall stature of *jhum* landraces in the present study has low yield capacity than the shorter stature of WRC landraces. Plant height had a significant positive correlation with PnL and the number of filled grains per panicle reported in the present study was supported by (Roy *et al.*, 2014b; Srijan *et al.*, 2016 and Saha *et al.*, 2019). A significant positive correlation of filled grain per panicle with PnL was also reported by Roy *et al.* (2014b). Both the flag leaf and blade leaf area have a negative association with plant height. The negative correlation of the flag leaf area with plant height was also reported by Saha *et al.* (2019). As most of the landraces have droopy leaf characters, the photosynthetic efficiency would have been affected and become an unnecessary load to the culm could be one of the reasons. But both have a significant positive correlation between them and with the number of primary branches per panicle. The positive correlation of the flag leaf area and blade leaf area was in accordance with Roy *et al.* (2014b).

Genetic Variability, Heritability and Genetic Advance

The study revealed that the phenotypic variance of all traits was higher than the genotypic variance. Similarly, the phenotypic coefficient of variation (PCV) was also slightly higher than the genotypic coefficient of variation (GCV) in all the traits under study (Table 7). The highest PCV was recorded in Yield (43.60%) followed by FGP (32.55%), LgL (31.04%), BLW (27.21%), FLL (25.5%), PH (24.07%), FLW (22.59%) and GD (22.47%) respectively (Table 8). The lowest PCV of (14.31%) was recorded in test weight. Traits like PnL, BLL, and PBR recorded PCV<20% respectively. Similarly, the highest GCV was recorded in yield (43.26%) followed by LgL (26.55%), BLW (22.89%), FGP (22.57%), PH (21.7%) respectively. The lowest GCV of 11.61% was recorded in the number of primary branches per panicle. Traits like FLW, GD, PnL, FLL, BLL, and test weight have GCV>20% respectively. The traits under study were highly heritable in which heritability value under ranges from 38.8% (PBR) to 98.4% (Yield). Heritability values of 81.3%, 71.4%, and 48.1% were recorded in plant height, PnL, and the number of grain per panicle respectively. The genetic advance as percent of the mean (GAM) ranges from 14.9% (PBR) to 88.4% (Yield).

Variability of any trait is measured by the Genotypic coefficient of variation and the extent of the environmental influence on any traits are indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation. Existence of large differences reflect about the high influence of environment, while small differences reveal high genetic influence. High heritability coupled with high genetic advance is more helpful in forecasting genetic

Table 7. Components of variation for agronomic traits among 35 landraces

	G Mean	Fratio	PV	GV	PCV%	GCV%	h^2%	GA	GAM%
PH	127.394	22.7	941	765	24.08	21.7	81.27	51.35	40.31
PnL	25.7097	13.47	26.3	18.8	19.97	16.9	71.38	7.548	29.36
GD	6.4147	7.609	2.08	1.18	22.47	17	56.93	1.691	26.35
PBR	11.4966	4.168	4.6	1.78	18.66	11.6	38.78	1.714	14.9
FLL	40.5486	4.482	107	43.9	25.5	16.3	41.05	8.746	21.57
FLW	2.1006	18.18	0.23	0.17	22.6	19.9	77.45	0.758	36.06
BLL	58.6697	4.713	129	55.1	19.38	12.7	42.61	9.981	17.01
BLW	1.8234	13.11	0.25	0.17	27.22	22.9	70.77	0.724	39.68
LgL	2.1404	14.66	0.44	0.32	31.04	26.6	73.2	1.002	46.81
FGP	172.477	5.632	3152	1516	32.55	22.6	48.09	55.62	32.25
TW	2.4456	5.035	0.12	0.08	14.32	11.7	66.86	0.482	19.72
YLH	18.6543	127.3	66.2	65.1	43.61	43.3	98.44	16.5	88.43

*GAM: Genetic Advance as percent of mean

Plant height (PH cm), Panicle length (PL cm), Girth diameter (GD mm), Primary branch number per panicle (PBR), Flag leaf length (FLLcm), Flag leaf width (FLWcm), Blade leaf length (BLL cm), Blade leaf width (BLWcm), Ligule length (LgLcm), Filled grain number per panicle (FGP), Test weight 100 seeds in gram (TW), Yield per hectare in quintal (YLH) gain (Johnson *et al.,* 1955). Selection based on the only yield is often unwise. So it is necessary to know the association between yield and its components (Akhtar *et al.,* 2011). Higher PCV than the corresponding GCV for all the traits in the present study revealed an influence of the environmental effects. However the PCV (43.6%) with GCV (43.3%) recorded in yield revealed that it is highly under genetics factor. Similar findings of higher PCV than GCV were reported earlier by (Bhadru *et al.*, 2012; Khatun *et al.,* 2015; Saha *et al.,* 2019).

The PCV, GCV, heritability, and GAM recorded in the present study were moderate to high among the traits. Traits like yield per hectare, FGP, plant height, FLL, and BLW have high PCV (>20%). Traits with PH, and BLW have high GCV (>20%). Traits with moderate GCV (10-20%) were FLW, GD, PnL, FLL, BLL, 100 seed weight, and PBR. Likewise, GAM was high (>20%) for all the traits except 100 seed weight, BLL, and PBR. Kumar at al. (2013) have reported a similar trend of high PCV, GCV, heritability, and GAM from the study of jhum rice germplasm of Northeast India, Khatun *et al.* (2015) on upland rice and Saha *et al.* (2019) on Bangladesh rice germplasm. However, PCV and GCV in the present study were higher than the earlier study of Akinwale *et al.* (2011) on African rice and Kumar *et al.* (2018) from 12 traits of improved lines. High heritability and high GAM on grain per plant, plant height, and yield were also reported by Khatun *et al.* (2015) and Kumar *et al.* (2018). The present study also observed a small difference in PCV and GCV which ranges from 0.34% (yield) to 9.9% (grain number per panicle). This represented some degree of environmental influence on the phenotypic expression of these characters. A similar small difference was reported earlier by Khatun *et al.* (2015). This suggests that traits like yield, PnL, PH, FLW, and test weight were highly genetic control, and selection based on these characters would be effective for future crossing programmes.

The high estimates of heritability and genetic advance observed for the above characters were closed in agreement with the earlier reports in rice by (Islam *et al.*, 2004; Manna *et al.,* 2006; Singh *et al.,* 2007; Sarangi *et al.,* 2009; Akinwale *et al.,* 2011; Kumar *et al.,* 2013). Neha and Verma. (2018) and Saha *et al.* (2019) also reported high heritability with high GAM in yield, plant height, number of grain per panicle, PnL, flag leaf, and blade leaf similar with the present study. The relatively high value of heritability and genetic advance observed in the present study indicated that superior genotype could be selected in the segregating population derived from hybridization between selective parents

Conclusion: As these valuable landraces from Arunachal Pradesh possess vast treasured huge genetic variability, most of the untapped landraces in the present study would be of great value to complement and broaden the gene pool in rice breeding. Promising landraces identified in the present study are expected immense help for their popularization.

Acknowledgment: The authors would like to thanks the Director of ICAR Research Complex for North Eastern Hilly Region (NEHR), Umiam, Meghalaya, India for providing all the facilities. Thanks are also due to the local donor farmers and key informants for kind cooperation in the identification and collection of germplasm. The study was conducted under the institute project and no funding was received.

References

Ahmed MSU, M Khalequzzaman, MK Bashar and AKM Shamsuddin (2016) Agro-Morphological, Physico-Chemical, and Molecular Characterization of Rice Germplasm with Similar Names of Bangladesh. *Rice Sci.* **23(4):** 211-218.

Akhtar N, MF Nazir, A Rabnawaz, T Mahmood, ME Safdar, M Asif and A Rehman (2011) Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza sativa* L.). *J Anim Plant Sci.* **21(4):** 660-664.

Akinwale MG, G Gregorio *et al.* (2011) Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *Afr. J Plant Sci* **5(3):** 207-212. http://www.academicjournals.org/ajps.

Bhadru D, VT Rao, YC Mohan and D Bharathi (2012) Genetic variability and diversity studies in yield and its component traits in rice (*Oryza sativa* L.). SABRAO *J Breed. Genet.* **44(1):** 129-137.

Bhuyan N, BK Bora and RN Sarma (2007) Genetic diversity analysis in traditional lowland rice (*Oryza sativa* L.) of Assam using RAPD and ISSR markers. *Curr. Sci.* **93:** 967-972.

Burton GW and EH Devane (1953) Estimating heritability in tall fescue (*Festuca arundanacea*) from replicated clonal material. *Agron J* **45:** 478-481.

Chakraborty D and A Ray (2019) Population genetics analyses of North-East Indian indigenous rice landraces revealed divergent history and alternate origin of aroma in aus group. *Plant Genet. Resour Characterisation Util* 17**(5):** 437-447. doi:10.1017/S1479262119000273.

Chakravorty A, PD Ghosh and PK Sahu (2013) Multivariate analysis of phenotypic diversity of land races of rice of West Bengal. *J. Exp. Agric. Int.* **3(1):** 110-123.

Chang TT (1985) Crop history and genetic conservation: Rice a case study. Iowa State *J. Res.* **59:** 425-455.

Choudhury B, ML Khan and S Dayanandan (2013) Genetic structure and diversity of indigenous rice (*Oryza sativa*) varieties in the Eastern Himalayan region of Northeast India. S*pringe Plus* **2:** 228.

Clifford HT and W Stephenson (1975) An Introduction to Numerical Classification. *Academic Press, London,* 229.

Durai A A, JMS Tomar, P Devi, A Arunachalam and H Mehta (2015) Rice Diversity – The Genetic Resource Grid of North-East India. *Indian J. Plant Genet. Resour.* **28:** 205-2012.

Efendi, E Kesumawaty, S Zakaria, Bakhtiar and Syafruddin (2015) Morpho agronomic performance of rice (*Oryza sativa* L.) landraces under organic cultivation of SRI methods. *Int. J. Agric. Res.* **10(2):**74 82. https://scialert.net/fulltext/?doi=ijar.2015.74.82.

Fukuoka S, TD Suu, K Ebanna, LN Trinh, T Nagamine and K Okuno (2006) Diversity in phenotypic profiles in landraces populations of Vietnamese rice: A case study of agronomic characters for conserving crop genetic diversity on farm. *Genet Resour. Crop Evol.* **53:** 753-761.

Guei RG, KA Sanni, FJ Abamu and I Fawole (2005) Genetic diversity of rice (*Oryza sativa* L.). *Agronomic Africana* **5:** 17-28.

Hanson CH, HF Robinson and CE Comstock (1956) Biometrical studies of yield in segregating populations of Korean laslpedegza. *Agron J* **48:** 268-72.

Holden J, J Peacock and T Williams (1993) Gens, Crops and the Environment. Cambridge University Press Cambridge.

Hore DK (2005) Rice diversity collection, conservation and management in northeastern India. *Genet Resour. Crop Evol.* **52:** 1129-1140.

Hussain S and DK Hore (2008) Collection and conservation of major medicinal plants of Arunachal Pradesh. *Indian For.* **134(12):** 1663-1679.

IBM Corp. Released (2011) IBM SPSS Statistics for Windows, Version 20.0. Armonk, NY: IBM Corp.

Ibrahim S, T Alex, Maxwell d. A, N Daniel and A Richard (2019) Genetic diversity analyses of rice germplasm using morphological traits. *J Plant Breed. Crop Sci.* **11(4):**128-136. doi:10.5897/jpbcs2018.0786.

IRRI (2002) Standard Evaluation System for Rice. Los Baños: IRRI.

Islam MS, MH Kabir and MK Bashar (2004) Inheritance of plant height in aromatic rice. *J. Subtrop. Agric. Res. Dev.* **2(3):** 67-71.

Johnson HW, H F Robinson and RE Comstcock (1955) Estimates of genetic and environmental variability in soybean. *Agron.* **47:** 314-18.

Karine M, DL Champlain, MFM Noel, T Zephirin, NP Alain, F Zephyrin, B Genevieve and W Noe (2014) Agro-morphological characterization of two rice (*Oryza sativa* L.) varieties from Japan and four NERICA varieties in an agro-ecological zone of the town of Younde (Cameroon), comparative study of their performance. *Int. J. Curr. Res.* **6(11):** 9941-9946.

Khatun M T, MM Hanafi, M Rafii Yusop, MY Wong, FM Salleh and J Ferdous (2015) Genetic Variation, Heritability, and Diversity Analysis of Upland Rice (*Oryza sativa* L.) Genotypes Based on Quantitative Traits. *Biomed. Res. Int*. **2015:** 1-7. doi:10.1155/2015/290861.

Kumar A, A Pandey and A Pattanayak (2013) Evaluation of rice germplasm under Jhum cultivation in North East India and breeding for aluminium tolerance. *Indian J Genet. Plant Breed.* **73(2):** 153-161.

Lin MS (1991) Genetic base of japonica rice varieties released in Taiwan. *Euphytica* **56:** 43-4.

Longvah T and VSS Prasad (2020) Nutritional variability and milling losses of rice landraces from Arunachal Pradesh, Northeast India. *Food Chem.* **318:** 126385. doi:10.1016/j.foodchem.2020.126385.

Manna M, MD Nasim Ali and BG Sasmal (2006) Variability, correlation and path coefficient analysis in some important traits of lowland rice. *Crop Res.* **31(1):** 153-156.

Mathure S, A Shaikh, N Renuka, K Wakte, N Jawali, R Thengane and A Nadaf (2011) Characterization of aromatic rice (*Oryza sativa* L.) germplasm and correlation between their agronomic and quality traits. *Euphytica* **179:** 237-246.

Mohaddesi A, A Abbasian, S Bakhshipoor and SM Mohammad (2010) Study of effects of nitrogen fertilizer and planting distance on yield and yield components of promising rice line. *J Crop Ecophysiol.* **2(3):** 198-203.

Neha Singh and OP Verma (2018) Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) under salt stressed soil. *J. Pharmacogn. Phytochem.* **7(3):** 3114-3117.

Patra BC (2000) Collection and characterization of rice genetic resources from Keonjhar district of Orissa. *Oryza* **34:** 324-326.

Perrier X and JP Jacquemoud-Collet (2006) DARwin software http://darwin.cirad.fr/.

Ram SG, T Venkatesan and KK Vinod (2007) Genetic diversity among cultivars, landraces and wild relatives of rice as revealed by microsatellite markers. *J. Appl. Genet.* **48:** 337-345.

Rana RB, C Garforth, B Sthapit and D Jarvis (2007) Influence of socio-economic and cultural factors in rice varietal diversity management on-farm in Nepal. *Agric. Human Values* **24:** 461-472.

Rathi S and RN Sarma (2012) Microsatellite diversity in indigenous glutinous rice landraces of Assam. *Indian J. Biotechnol*. **11:** 23-29.

Ratho SN (1984) Genetic divergence in scented varieties of rice. *Indian J. Agric. Sci.* **54:** 699-701.

Richharia RH (1979) An aspect of Genetic Diversity in Rice. *Oryza* **16:** 1-31.

Roy S, A Banerjee, A Pattanayak, SS Roy, RS Rathi, AK Misra, SV Ngachan and KC Bansal (2014a) Chakhao (delicious) rice landraces (*Oryza sativa* L.) of North-east India: collection, conservation and characterization of genetic diversity. *Plant Genet. Resour.* **12:** 264-272. doi: 10.1017/S1479262113000580.

Roy S, BC Marndi, B Mawkhlieng, A Baneerji, RM Yadav, AK Mishra and KC Bansal (2016) Genetic diversity and structure in hill rice (*Oryza sativa* L.) landraces from the North-Eastern Himalayas of India. *BMC Genet.* **17(1):** 1-15. doi: 10.1186/s12863-016-0414-1.

Roy S, RS Rathi, AK Misra, BP Bhatt and DC Bhandari (2014b) Phenotypic characterization of indigenous rice (*Oryza sativa* L.) germplasm collected from the state of Nagaland, India. *Plant Genet. Resour.* **12(1):** 58-66. doi:10.1017/S1479262113000282.

Saha SR, L Hassan, MA Haque, MM Islam and M Rasel (2019) Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces. *J Bangladesh Agric Univ.* **17(1):** 26-32 doi:10.3329/jbau.v17i1.40659.

Sanni KA, I Fawole, A Ogunbayo, D Tia, EA Somado, K Futakuchi, M Sie´, FE Nwilene and RG Guei (2012) Multivariate analysis of diversity of landrace rice germplasm. *Crop Sci.* **52:** 494-504.

Sanni KA, I Fawole, RG Guei, DK Ojo and EA Somado (2008) Geographical patterns of phenotypic diversity in *Oryza sativa* landraces of Côte d'Ivoire, *Euphytica* **160:** 389-400.

Sarangi DN, B Pradhan, P Sial and CHP Mishra (2009) Genetic variability, correlation and path-coefficient analysis in early rice genotypes. *Environ. Ecol.* **27(1A):** 307-312.

Sarawgi AK, RLV Subba, M Parikh, B Sharma and GC Ojha (2013) Assessment of variability of rice (*Oryza sativa* L.) germplasm using morphological characters. *J. Rice Sc.* **6(1):** 14-28.

Sharma RC, NK Chaudhary, B Ojha, L Yadav, MP Pandey and SM Shrestha (2007) Variation in rice landraces adapted to the lowlands and hills in Nepal. *Plant Genet. Resour.: Characterization and Utilization* **5:** 120-127.

Singh Y, DR Pani, D Khokhar and US Singh (2013) Agro-morphological characterization and molecular diversity analysis of aromatic rice germplasm using RAPD markers. *Oryza.* **50 (1):** 26-34.

Sinha AK and PK Mishra (2013) Agro-morphological characterization and morphology based genetic diversity analysis of landraces of rice variety (*Oryza sativa* L.) of Bankura district of West Bengal. *Int. J. Curr. Res.,* **5(10):** 2764-2769.

Srijan A, Kumar SS, CD Raju and R Jagadeeshwar (2016) Character association and path coefficient analysis for grain yield of parents and hybrids in rice (*Oryza sativa* L.). *J. Appl. Nat. Sci.,* **8(1):** 167-172.

Subudhi HN, S. Samantaray, D Swain and ON Singh (2012) Collection and agro-morphological characterization of aromatic short grain rice in eastern India. *Afr. J. Agric. Res.* **7(36):** 5060-5068.

Thomson MJ, NR Polato, J Prasetiyono, KR Trijatmiko, TS Silitonga and SR McCouch (2009) Genetic diversity of isolated populations of Indonesian landraces of rice (*Oryza sativa* L.) collected in East Kalimantan on the Island of Borneo. *Rice* **2:** 80-92.

Tripathi MP, BR Sthapit, LP Subedi, SK Sah and S Gyawali (2013) Agro-morphological variation in ''Jhinuwa'' rice landraces (*Oryza sativa* L.) of Nepal. *Genet. Resour. Crop Evol.* doi: 10.1007/s10722-013-9992-1.

Upadhyaya HC, Gowda and D Sastry (2008) "Plant Genetic Resources Management: Collection, Characterization, Conservation and Utilization *J. SAT Agric. Res.* **6 (December):** 16p.