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Morphological characterisation of rice accessions of semi deep water ecology

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The present investigation was carried out to evaluate the magnitude and nature of genetic variability of 569 rice germplasm accessions with semi deep water ecology, commonly known as *asra*, at the Regional Agricultural Research Station (RARS), Karimganj, Assam Agricultural University, Assam (India). These accessions were recognised as having flood tolerant characteristics. The first five principal components explained approximately 76.71% of the total variation. Principal component analysis revealed that traits such as number of panicles per hill, spikelet fertility, days to 50% flowering, number of chaffs per panicle, and plant height were the principal discriminatory quantitative traits. It is recommended that the genetic variation prevailing in the assessed *asra* rice germplasm accessions can be efficiently utilised for the enhancement of the genetic gain. The divergent extreme phenotypes in the accession can also be utilised to develop the mapping population for the identification of quantitative trait loci for flood tolerance. The rice accessions were grouped into three different clusters for both quantitative and qualitative traits. The hybridization among the selected germplasm of different clusters is expected to produce the maximum number of transgressive segregants. This will lead to area expansion with higher productivity of this crop in predominantly flood prone areas.

Keywords: Asra rice, Cluster analysis, Correlation, Genetic variability, Principal component analysis

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Rice (*Oryza sativa* L.), the world's second most extensively grown cereal crop, feeds more than half of the world's population, especially in Asian nations[1]. Rice genetic resources are quite abundant in India. Farmers all around the nation used to grow a variety of landraces or native varieties, which were especially useful in the unfavourable ecosystem. Assam, in North-eastern India, is a rice-growing state. The state's diverse microclimate has resulted in the emergence of several unique indigenous rice cultivars[2]. Mostly, indigenous rice varieties and landraces have higher nutritional and medicinal properties, fragrance, grain length, and are more resilient to abiotic and biotic stress[3]. However, the indigenous rice supply is rapidly diminishing owing to overexploitation, human-induced environmental changes, plant genetic alteration, and aggressive promotion and mono-cropping of HYV[4]. *Asra* is a semi-deep-water native rice that is cultivated in low land areas during the monsoon period (April-May) and post-monsoon period (November-December), mostly in the catchment areas of rivers and wetlands that stay wet for most of the cropping season because of the heavy rains and long-term storage of rain water in these areas[5].

It is a long duration crop (240 to 270 days), customarily grown broadcast or transplanted in lowland areas experiencing a water depth of less than 100 cm. *Asra* rice cultivars are popular in the Karimganj area, which is on the border between Assam and Bangladesh. They are also cultivated in some flood-prone areas of Bangladesh. Almost 30% of the district is usually under water for 6 months or more every year. *Asra* rice is grown in areas where all other rice varieties like winter rice would result in a chance crop production due to rapid submersion of such areas due to irregular rainfall during June and July[6]. Traditional rice cultivars under *asra*, which can grow fast by elongating internodes in response to increasing water levels, may be the best choice for this region in terms of making efficient use of land resources and sustainable rice production.

Most of the traditional varieties and landraces have endured through many generations of natural and

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human assisted processes and have adapted to the local environment. Such landraces, on the other hand, have limited crop production potential and are unable to meet the existing population-based consumption demands. It is widely established that the importance of these landraces and the genetic diversity they possess are critical components for the development of better adapted and higher producing cultivars. In many instances, the variability of genetic enhancement programmes is underutilised due to lack of proper characterization and accessibility of the genetic potential of individuals. To promote the use of rice germplasm, plant breeders need to understand the pattern of variability existing within the germplasm pool and group them accordingly. Assessments of genetic distance and the classifying of germplasm into heterotic groups for selecting parental associations with significant genetic diversity form the cornerstone of every hybridization programme initiation. Multivariate analysis may be used to estimate genetic distance, which is essential for figuring out how much heterogeneity in the population panel can be used.

As a multifaceted, multi-attribute quantitative trait, grain yield does not respond properly to natural selection. Indirect selection requires an understanding of genetic diversity and the association between grain yield and its attributes[7]. Genetic variation of the genotype has been extensively studied using multivariate statistical methods. Multivariate statistical approaches like principal component analysis (PCA) are used to determine the plant traits that demonstrate the distinctiveness of certain genotypes[8]. For new varieties, PCA helps to discover attributes that are the most variable, while correlating these traits to yield is a powerful tool for developing new varieties more efficiently and effectively. Knowledge of genetic variations involved in the inheritance of quantitative attributes, such as yield and its attributes, is important in enhancing the genetic gain and selecting an appropriate selection approach.

In light of the significance of the aforementioned aspects, this study was conducted to assess the genetic variability across 569 *asra* rice accessions for yield and its attributes, the degree of correlation between attributes, and identify plant attributes that reflect the dissimilarities among specified genotypes.

Materials and Methods

The experimental materials comprised 569 accessions of *asra* rice germplasm available at Regional Agricultural Research Station (RARS), Assam Agricultural University, Karimganj, Assam (India) rice gene bank and five checks *viz.*, Badal, IET-21858, MSE- 9, Manoharsali and Maguri Bao. The details of materials include (red, white, and amber-coloured kernel landraces, breeding lines, germplasm, traditional cultivars, and improved cultivars) collected from different states of India, including 89 exotic collections from Bangladesh, which were presented in Supplementary Table 1. For easy identification and retrieval, each accession was named as AG1 to AG569. The experiment was carried out at Research Farm of the RARS, Karimganj, India (24º50′ N latitude and 92 º20′ E longitude at an elevation of 16 m above MSL) during the *kharif* seasons of 2017-18 and 2018-19 using an augmented design introduced by Federer[9-11].

For evaluating a large number of genotypes, an augmented design is typically preferable. Checks are used to produce a standard design that can be easily replicated. There are extra plots that are generated in each replication and test entries are allocated to these plots in an incomplete block design[12]. Partition the field into blocks to handle the predicted variability of the experiment environment. It was done such that the checks were replicated in each block, but the accessions to be assessed were not repeated and occurred only once during the study[13]. Analysis of unreplicated germplasm was facilitated by suppressing impacts from replicated checks. The replicated checks' error term was considered in the statistical significance test.

Each plot had four rows of four metres each, with a 50 cm gap between them. Two to three seedlings per hill were transplanted at 20 cm row spacing and 15 cm plant spacing. The crop was grown using a regular set of procedures. A total of nine quantitative characters were measured on five randomly selected plants in each plot (Table 1). The morphological traits of *asra* rice genotypes were recorded and presented in Supplementary Table 2. Detailed description and oobservations were also noted on eighteen qualitative traits (Table 1, Supplementary Table 3 and Supplementary Table 4) as per IRRI[14]. The observations recorded during both years were pooled and statistically analyzed using R-software (R Studio) with Augmented RCBD[15] and FactoMineR packages[16] with some general commands.

Results and Discussion

Variability analysis

The genetic material must have a sufficient amount of genetic variation in order to facilitate efficient

Table 1 — List of quantitative and qualitative traits considered for recording observations in 569 accessions of *asra* rice germplasm.

Sl. No.	Traits	Sl. No.	Traits	Sl. No.	Traits
A	Quantitative traits:				
1	Days to 50% flowering	4	Number of panicles/hill	7	Number of chaffs/ panicle
2	Plant height (cm)	5	Panicle length (cm)	8	Spikelet fertility (%)
3	Stem thickness (mm)	6	Number of filled grains/ Panicle	9	Grain yield/plant (g)
B	Qualitative traits:				
1	Basal leafs heath color	7	Leaf auricles	13	Culm attitude
2	Intensity of green color in leaf	8	Anthocyan in coloration of auricles	14	Attitude of flag leaf blade
3	Anthocyanin coloration of leaf blade	9	Leaf collar	15	Color of stigma
4	Anthocyan in coloration of leaf sheath	10	Anthocyan in coloration of collar	16	Distribution of awns on panicles
5	Intensity of anthocyan in coloration in leaf sheath	11	Shape of ligule	17	Panicle exertion
6	Leaf pubescence	12	Color of ligule	18	Lemma and palea color

selection and increased adaptability. Kurlovich[17] argues that qualitative characters are essential for accurate plant description, and these traits are influenced primarily by the socio-economic environment, consumer preferences, and natural selection[18]. As seen in Supplementary Fig. 1 (a-r), the frequency distribution for eighteen qualitative characteristics is shown. This research documented the varied characteristics of these morphological characters. A majority of the germplasm accessions were found to possess green basal leaf sheath colour (80%), medium intensity of green colour in leaf (80%), green anthocyanin colouration of leaf blade (83%), absence of anthocyanin colouration of leaf sheath (87%), very weak intensity of anthocyanin colouration in leaf sheath (84%), medium pubescence on leaf blade surface (42%), presence of leaf auricles (98%), colourless auricle (92%), presence of leaf collar (98%), absence of anthocyanin colouration in collar (96%), acute ligule (78%), white ligule colour (93%), spreading culm (52%), semi erect flag leaf blade (36%), white stigma (85%), awns on panicle tips only (80%), well exerted panicle (81%) and straw coloured lemma and palea (60%). A minority of the germplasm accessions were reported to have purple basal leaf sheath colour (1%), dark intensity of green colour in leaf (8%), purple anthocyanin colouration of leaf blade (<1%), presence of anthocyanin colouration of leaf sheath (6%), very strong intensity of anthocyanin colouration in leaf sheath (0%), absent pubescence on leaf blade surface (2%), absence of leaf auricles (2%), purple auricle (1%), absence of leaf collar (2%), presence of anthocyanin colouration in collar (4%), truncate ligule (2%), purple ligule colour (1%), erect culm (15%), drooping flag leaf blade (4%), purple stigma (<1%), awns on panicle whole length (9%), partly exerted panicle (81%) and purple spots/ furrows on straw and brown (tawny) coloured lemma and palea (2%). The *asra* germplasm with purple stigma is due to an accumulation of anthocyanin pigments that can help in the regulation of drought tolerance. Likewise, so many desirable traits can be exploited in introgressive breeding programmes as they have a huge reservoir of diverse favourable alleles.

All attributes except the number of effective tillers per hill showed extremely significant (p 0.01) variation across germplasm accessions using analysis of variance (ANOVA) of nine quantitative attributes (Table 2). The skewness and kurtosis estimates of nine traits are shown (Table 3). It is possible to learn about the pattern of gene action[19] and the number of genes that influence a trait's distribution from a study of skewness and kurtosis[20]. According to the general theory, non-additive gene action and environmental influences are responsible for traits with skewed distributions. Negative skewness is linked to duplicate (additive x additive) gene interactions, while positive skewness is linked to complementary gene interactions. Regardless of whether they have an increasing or decreasing influence on the characteristic, the genes influencing the skewed distribution trait tend to be primarily dominant[21].

Almost normal distributions were observed for plant height, stem thickness and panicle length. There was a positive skewness in the attributes such as

Table 2 — Analysis of variance (block adjusted) for nine quantitative traits in 569 accessions of *asra* rice germplasm

Source of variation	d.f.	Days to 50% flowering	Plant Height (cm)	Stem thickness (mm)	No. of panicles/ hill	Panicle length (cm)	No. of filled grains/ panicle	No. of chaffs/ panicle	Spikelet fertility (%)	Grain yield/plant (g)
Treatment (ignoring Blocks)	573	51.38**	619.3**	1.3 **	26.3^{ns}	8.2 **	2045.2**	572.17**	122.58**	361.93**
Treatment: Check	4	2428.16**	13548.8**	9.56**	237.13**	14.16**	6215.66**	5610.2**	650.77**	4898.99**
Treatment: Testvs. Check	1	685.84**	29775.08 **	6.1 **	1828.23**	0.00017^{ns}	5837.17*	1412.55**	45.5^{ns}	2455.41**
Treatment: Test	568	33.53**	476.92**	1.23**	21.64^{ns}	8.17**	2009.16**	535.21**	119**	326.29**
Block (eliminating Treatments)	22	2.31^{ns}	144.71**	1.5 **	53.1**	6.5 **	2016.53**	129.34^{ns}	21.14^{ns}	354**
Residuals	88	1.87	65.75	0.53	21.93	3.05	914.7	170.59	44.23	169.29
Mean		138.90±0.24	174.84±0.94	7.26±0.05	14.15±0.22	28.34±0.13	146.33±1.92	32.57±0.97	82.03±0.46	41.67±0.76

ns p>0.05; *p<=0.05;**p<=0.01

Table 3 — Estimates of genetic parameters of nine quantitative traits in 569 accessions of *asra* rice germplasm

Characters	Skewness	Kurtosis	σ^2G	σ^2P	GCV (%)	PCV (%)	$h^2_{b.s.}$ (%)	GA (%)	GA as per cent of mean
Days to 50% flowering	-0.33**	4.34**	31.66	33.53	4.05	4.17	94.44	11.28	8.12
Plant height (cm)	-0.18 ns	3.82**	411.17	476.92	11.60	12.49	86.21	38.84	22.22
Stem thickness (mm)	-0.05 ns	3.14ns	0.70	1.23	11.54	15.28	57.04	1.31	17.98
No. of panicles/hill	0.36**	2.87ns	-	21.64	-	32.87	-	-	-
Panicle length (cm)	0.17ns	3.22ns	5.12	8.17	7.99	10.09	62.68	3.70	13.04
No. of filled grains/panicle	0.52**	3.80**	1094.46	2009.16	22.61	30.63	54.47	50.37	34.42
No. of chaffs/panicle	1.91**	10.26**	364.62	535.21	58.63	71.04	68.13	32.51	99.84
Spikelet fertility (%)	-1.26**	5.23**	74.76	119	10.54	13.3	62.83	14.14	17.24
Grain yield/plant (g)	0.55**	3.46*	157	326.29	30.07	43.35	48.12	17.93	43.03

ns p>0.05; *p<=0.05;**p<=0.01

number of panicles per plant, number of chaffs per panicle, number of filled grains per panicle and grain yield per plant and negative skewness for days to 50% flowering and spikelet fertility (Table. 3). On the other hand, most of the traits under study showed leptokurtic distribution.

The evaluations of genotypic variance (σ2G), phenotypic variance (σ2P), genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability in broad sense (h2b.s.), genetic advance (GA) and genetic advance as percentage of mean for all the nine quantitative traits are presented in (Table 3). There was a strong correlation between high GCV and PCV values and greater heritability estimates and % genetic advance for attributes such as the number of grains filled in a panicle, the number of chaffs in a panicle, and the grain yield per plant, all of which were found in the study. Similarly, Rahman *et al.*[22] achieved the same findings. On the other hand, plant height, stem thickness and spikelet fertility showed medium estimates of these parameters, while days to 50% flowering and panicle length reported low GCV and PCV estimates. Similar results were also obtained by Islam *et al.*[23] while working with 113 aromatic and fine rice germplasm. Similarly, the findings of Mishra *et al.*[24], Kumari *et al.*[25], Tiwari *et al.*[26] and Pandey *et al.*[27] also support the current findings, who also identified significant variation among the genotypes they analysed.

Character association analysis

The degree to which variables are associated with one another is measured by correlation. It is the direction and strength of association between yield and its attributes, as well as between the attributes themselves, that determines the efficacy of selection for yield, a complex quantitative character. Pearson's correlation coefficient was calculated for nine quantitative variables among 569 *asra* rice germplasm accessions and reported in (Table 4). In the present investigation, the results revealed that grain yield per plant indicated a highly significant (p≤0.01) and positive correlation with stem thickness, number of panicles per plant, number of filled grains per panicle and spikelet fertility indicating the importance of these traits while undertaking indirect selection for grain yield per plant based on component traits. Similarly, the findings of Verma *et al.*[28] also support

Table 4 — Pearson's correlation coefficient among nine quantitative traits in 569 *asra* rice germplasm

Characters	Days to50% flowering	Plant height (cm)	Stem thickness (mm)	No. of panicles/ hill	Panicle length (cm)	No. of filled grains/ panicle	No. of chaffs/ panicle	Spikelet fertility (%)	Grain yield/plant (g)
Days to50% flowering									
Plant height (cm)	0.079*								
Stem thickness (mm)	0.107**	0.247**							
No. of panicles/hill	-0.081*	-0.187**	-0.122**						
Panicle length (cm)	-0.041^{NS}	0.147**	0.104**	-0.050^{NS}					
No. of filled grains/panicle	-0.051^{NS}	0.042^{NS}	0.173**	-0.006^{NS}	0.225**				
No. of chaffs/panicle	0.180**	0.198**	0.164**	-0.111**	0.184**	0.028^{NS}			
Spikelet fertility (%)	-0.153**	-0.164**	-0.073^{NS}	0.088*	-0.073^{NS}	0.351**	-0.872**		
Grain yield/plant (g)	0.062^{NS}	0.050^{NS}	0.183**	0.140**	0.001^{NS}	0.267**	-0.072^{NS}	0.183**	

ns p>0.05; *p<=0.05;**p<=0.0

the current findings. Similarly, days to 50% flowering showed a highly significant positive correlation with stem thickness, number of chaffs per panicle and significant positive correlation with plant height. On the other hand, it showed a highly significant negative correlation with spikelet fertility and a significant negative correlation with the number of panicles per plant. Plant height showed a highly significant positive correlation with stem thickness, panicle length, number of chaffs per panicle and highly significant negative correlation with the number panicles per plant and spikelet fertility. Stem thickness showed a highly significant positive correlation with panicle length, number of chaffs per panicle and number of filled grains per panicle and highly significant negative correlation with the number of panicles per plant. The number of panicles per plant showed a highly significant negative correlation with the number of chaffs per panicle.

Highly significant positive correlations were also observed for panicle length with the number of filled grains per panicle and the number of chaffs per panicle; number of filled grains per panicle with spikelet fertility. On the other hand, highly significant negative correlation was observed between the number of chaffs per plant and spikelet fertility. Kumar *et al.*[29] also reported a highly significant positive correlation of grain yield per plant with the number of filled grains per panicle and spikelet fertility and some other traits in a set of 264 aromatic long grain accessions of rice. The present findings are also in conformity with that of Sarawgi *et al.*[30], that there was no significant correlation of grain yield per plant with days to 50% flowering, plant height and panicle length while working with 408 accessions of dwarf and medium duration rice germplasm.

Table 5 — Eigen values and their variation in nine quantitative traits in 569 *asra* rice germplasm

Principal component axes	Eigen value	Variance (%)	Cumulative variance (%)
I	2.098	23.312	23.312
II	1.731	19.229	42.541
III	1.119	12.432	54.973
IV	1.021	11.339	66.313
V	0.936	10.401	76.714
VI	0.771	8.563	85.277
VII	0.707	7.855	93.132
VIII	0.575	6.386	99.518
IX	0.043	0.482	100.000

Principal component analysis

In a principal component analysis, each component is evaluated for its contribution to the overall variance and its relevance. The individual effect of a particular attribute on the overall variance may be quantified using proper vectors, where each coefficient of a PC reflects the degree to which each original variable is related to each principal component (PC). The attributes that contribute the most to the principal components will be more useful in distinguishing between accessions. It was determined that 569 *asra* rice germplasm had a broad genetic diversity that was explained by the principal component analysis findings. In this investigation, nine quantitative attributes were evaluated using principal component analysis and are displayed in Table 5. As per the standard established by Brejda *et al.*[31], the principal components with eigenvalues more than one and explained at least five percent of the total variability were reflected as the best representatives of attributes. Only four of the nine principal components had eigenvalue (>1) and contributed 66.3% of the total variance of all the traits studied. Eigenvalues,

Table 6 — Eigen values, percent of total variation and contribution of different traits to the principal components

Principal components	I	II	III	IV
Eigen values	2.098	1.731	1.119	1.021
Percent variance	23.312	19.229	12.432	11.339
Cumulative % total variance	23.312	42.541	54.973	66.313
Contribution of different quantitative traits to principal components:				
Days to 50% flowering	3.161	1.014	47.109	4.763
Plant height (cm)	3.958	10.799	8.564	6.193
Stem thickness (mm)	1.379	21.671	3.294	0.346
No. of panicles/plant	1.327	2.843	3.035	72.251
Panicle length (cm)	2.287	16.887	19.572	2.232
No. of filled grains/panicle	2.804	29.876	0.001	1.323
No. of chaffs/panicle	39.701	0.495	0.489	0.489
Spikelet fertility (%)	42.316	2.736	0.239	1.066
Grain yield/plant (g)	3.066	13.679	17.696	11.337

percent of total variance and contribution of different traits to these four principal components are presented in (Table 6). The PC I exhibited 23.3%, while PC II, PC III and PC IV exhibited 19.2, 12.4 and 11.3% variability among the accessions, respectively.

The contributions of various attributes to total variation were calculated for each principal component. The first principal component (PC I) accounted for 23.3% of total variance, with spikelet fertility (42.3%) and the number of chaffs per panicle (39.7%) also playing a role. The number of filled grains per panicle (29.9%), stem thickness (21.7%), and panicle length (16.9%) were the major contributors to the second principal component (PC II), which accounted for 19.2% of total variability. Similarly, the third and fourth principal components accounted for 12.4% and 11.3% of the total variability. Days to 50% flowering (47.1%) and panicle length (19.6%) were the major contributing traits to PC III, while number of panicles per hill (72.3%) was the major contributor to PC IV. Kumar *et al.*[29] also reported that number of filled grains per panicle and panicle length and some other traits were the principal discriminatory traits while working with 264 aromatic long grain rice accessions. Similarly, Sanni *et al.*[32] reported that days to heading and maturity, tillering ability and grain size were the principal discriminatory characters in 434 accessions of rice. Nachimuthu *et al.*[33] also reported that days to 50% flowering, panicle length, number of filled grains per panicle, spikelet fertility and number of panicles per plant and some other characters were the principal discriminatory characters in a population panel of 192 rice genotypes, traditional landraces and exotic genotypes. Thus, the results of the principal component analysis have revealed the presence of a higher magnitude of genetic variation in the population panel and traits such as days to 50% flowering, stem thickness, number of panicles per plant, panicle length, number of filled grains per panicle and spikelet fertility contributed mostly to different principal components. As a result, the findings will be extremely useful in identifying parents for improving various quantitative traits analysed in this study.

Cluster analysis

Cluster analysis facilitated an overall picture of the variability and diversity existing among the 569 *asra* rice germplasm. It might be helpful in the plant breeding programme for genetic improvement. Cluster analysis provides genetic diversity information that can be used to evaluate promising heterotic products prior to cross-breeding, thereby speeding up breeding practices by saving resources and time in designing an appropriate breeding approach[34]. The magnitude of genetic diversity and cluster mean for different characters' performance played a crucial role in the hybridization programme in selecting the parents[35]. Genetically diverse parents belonging to different clusters used in hybridization programmes would offer a chance to bring together gene assemblages of diverse nature and reliable hybrid products due to the complementation of divergent genes in parents[36]. It was expected to generate highly variable transgressive segregants with higher heterotic effects[37,38]. Genetic diversity plays an important role in plant breeding, not only resulting in genetic variation but also creating novel recombinations of genes in the gene pool. The idea and knowledge of the genetic variability in the rice genotypes are produced from the comprehensive

study of patterns and levels of genetic divergence[39]. The genetic gains in yield or attributing traits can be exploited by recombining the diverse germplasm and subsequent selection[40].

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Through multivariate analysis using R software, nine quantitative traits were grouped into three clusters. The clustering pattern of germplasm into three clusters was presented in (Fig. 1 and Supplementary Table 5). The genetic diversity that arises among germplasm might be due to factors like history of selection, selection under diverse environments, heterogeneity, and genetic drift. Cluster I had 190 germplasm, whereas Cluster II had a maximum of 254 germplasm and Cluster III had a minimum of 130 germplasm. Cluster analyses of eighteen qualitative traits were also grouped into three clusters as listed in (Fig. 2 and Supplementary Table 6). Cluster I had the maximum number of 421 germplasm and Cluster II had 112 germplasm, whereas Cluster III had the minimum number of 41 germplasm. Compared with both the quantitative and qualitative trait clusters, some common germplasm

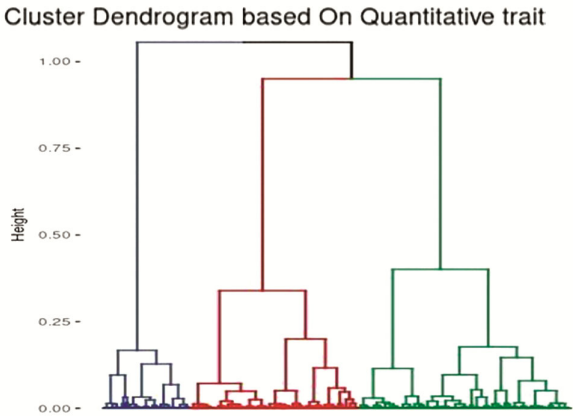

Fig. 1 — Dendogram of quantitative characters in 569 *asra* rice germplasm

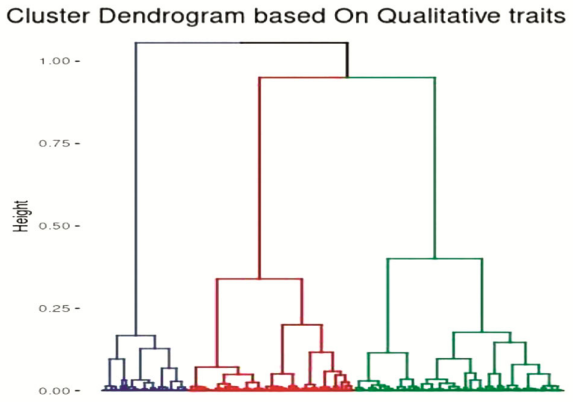

Fig. 2 — Dendogram of qualitative characters in 569 *asra* rice germplas

for both the clusters is listed in Supplementary Table 7. Cluster I had the maximum number of 139 common germplasm and Cluster II had 33 germplasm, whereas Cluster III had the minimum number of 12 common germplasm. These germplasm accessions belong to the same cluster and share more similarity in terms of qualitative and quantitative traits, whereas those belonging to different clusters have more diversity. As a result, this germplasm can be used in hybridization programmes for either qualitative or quantitative traits.

The cluster means for various quantitative traits indicated differences between the clusters for all the characters listed in (Table 7). The cluster I recorded the highest mean values significant for no. of panicles/ hill (15.91) and the lowest mean values for days to 50% flowering (137.49), plant height (160.48 cm), stem thickness (6.53 mm), panicle length (26.48 cm) and number of chaffs/ panicle (18.66). The cluster II recorded the highest mean values significant

Table 7 — Cluster means for nine quantitative traits in 569 *asra* rice germplasm

Characters Cluster	Days to 50% flowering	Plant height (cm)	Stem thickness (mm)	No. of panicles/ hill	Panicle length (cm)	No. of grains / panicle	No. of chaffs/ Panicle	Fertility (%)	Yield/plant (g)
Cluster-I	137.49	160.48	6.53	15.91	26.48	124.36	18.66	86.61	37.6
Cluster-II	139.01	182.77	7.74	13.38	29.51	175.16	27.86	86.67	49.05
Cluster-III	140.69	180.28	7.39	13.04	28.72	122.08	62.05	66.26	33.17

for plant height (182.77 cm), stem thickness (7.74 mm), number of grains /panicle (175.16), panicle length (29.51 cm), spikelet fertility (86.67%) and yield/ plant (49.05 g). The cluster III recorded the highest mean values significant for days to 50% flowering (140.69) and number of chaffs/ panicle (62.05) and the lowest mean value for number of panicles/ hill (13.04), number of grains/ panicle (122.08), spikelet fertility (66.26%) and yield/ plant (33.17 g). Cluster I with the lowest plant height and Cluster II with the highest plant height and stem thickness, could be considered in the hybridization programmes to develop dwarf and non-lodging rice cultivars.

Most of the yield traits exhibited the highest mean performances in cluster II and the lowest mean performances in cluster III. So, crossing between selected germplasm belonging to cluster II and cluster III in a hybridization programme is expected to yield the maximum number of transgressive segregants with a wide range of variability that can be further utilised in crop breeding programs. Similar results and conclusions were also reported by Chawdhury[41] and Nisar *et al.*[42]. Hybridization between the *asra* rice germplasm belonging to the same cluster like cluster I, cluster II or cluster III does not produce superior heterotic products or transgressive segregants. Similar kinds of results were reported by Sharma *et al.*[43]. The clustering pattern clearly displayed that neither of any clusters with the asra rice germplasm with all desirable characters could be selected and directly utilised as varieties. Hence, hybridization is needed between the germplasm of different clusters. A similar kind of interpretation was also reported by Bose and Pradhan[44].

Conclusion

In the present study, the 569 *asra* rice germplasm were characterised based on morphological characters and clustered into three groups. There was considerable variability among the germplasm for most of the morphological characters. Principal component analysis has identified few characters that play a key role in classifying the variation existing in the accessions. In future, the accessions may be screened and used as a potential genetic resource for submergence tolerance through the integration of traditional and molecular breeding approaches. This will also lead to area expansion with higher productivity of this crop in predominantly flood prone areas including Assam, NE India and Bangladesh.

Supplementry Data

Supplementry data associated with this article is available in the electronic form at http://nopr.niscpr.res.in/jinfo/ijtk/IJTK_22(01)(2023)7-16_SupplData.pdf

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Conflict of Interest

The authors declare that they have no conflict of interest on the manuscript's content and study undertaken.

Authors' Contributions

Conceptualization of research (SH, RNS); Designing of the experiments (SH, MRC); Contribution of experimental materials (SH, MRC); Execution of field experiments and data collection (SH, MRC); Analysis of data and interpretation (RNS, PPB, SH); Preparation of manuscript (SH, PPB, RNS).

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