Biological Forum – An International Journal **13(3a): 170-179(2021)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Characterization and Diversity Analysis of Rice Germplasm

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(Received 30 June 2021, Accepted 08 September, 2021)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Plant genetic resources are very important for crop improvement. The higher the variability, higher will be the chances of developing a character since the breeding programme requires much genetic variation for crop improvement. In the present study, genetic diversity of 30 rice germplasm was studied for agro-morphological characters based on 14 qualitative and 11 quantitative traits. Shannon weaver diversity indices for qualitative characters ranged from 0.21 to 0.90. High diversity index value (0.90) was exhibited by lemma tip color followed by decorticated grain shape, leaf senescence and decorticated grain color indicating that these characters are highly variable among the germplasm. The low value diversity index value (0.21) was exhibited by panicle characters namely, presence or absence of awns and its distribution, type of panicle exertion. Cluster analysis of rice germplasm based on qualitative characters grouped rice germplasm into five clusters with the maximum inter-cluster distance between III and IV (14.83). Principal component analysis of qualitative characters revealed that the first four principal components showed eigen values >1 and accounted for 69.42% of the total variation. Based on the quantitative characters, cluster anlaysis grouped the genotypes into five clusters with maximum inter cluster distance between cluster IV and Cluster V (50.50), while the minimum distance was observed between the clusters I and II (16.30). Principal component analysis for qualitative characters revealed that the first four principal components showed eigen values >1 and accounted for 86.20 % of the total variation. Evaluation of rice germplasm based on agro morphological characters revealed presence of substantial variability within the germplasm.

Keywords: Shannon weaver diversity index, Principal component analysis, agro morphological characters, Cluster analysis.

INTRODUCTION

Rice is one of the world's most important food crop and a primary food source for more than one third of world's population. The genetic improvement of rice for its yield and yield components is an important criterion to meet the food demand of the growing population. Hence, in order to improve the yield or any important trait creation of genetic variation is a prerequisite for any crop improvement programme. Rice genetic resource is the primary material for rice breeding programme (Zhang *et al.*, 2011). It is a rich reservoir of valuable genes that plant breeders can harness for crop improvement (Yadav *et al*., 2013). Mining elite genes within rice landraces is very important for the improvement of cultivated rice (Zhang *et al*., 2014). The amount of genetic enrichment is reliant on the extent of genetic diversity inherent in a population (Kumbhar *et al*., 2015). A reduction in germplasm diversity is an obstacle to plant breeding and reduce the tendency of plants to resist unfavourable environments (Xiyong *et al*., 2012). The landraces of rice can contain some valuable alleles not common in modern germplasm (Pervaiz *et al*., 2010). Genetic variation in plant material is the base for crop improvement (Iqbal *et al*., 2014). Any crop improvement programme depends on the variability and its utilization in the breeding programme. Evaluation and characterization of existing landraces of rice are very important in order to achieve the varietal improvement. Before utilizing a particular landrace or a germplasm line in a breeding programme for improvement of a trait, it is necessary to understand the magnitude of variability and diversity in that population which is a pre requisite for genetic improvement.

The concept of distinctness, uniformity and stability are fundamental to the characterization of a variety as a unique creation. The uniqueness of a particular variety is to be established by DUS test. The first step to implement PPV&FR Act provisions is formulation of

national test guidelines for conducting DUS tests. Morphological characterization is the first step in the classification and evaluation of the germplasm (Smith and Smith, 1989). Several morphological traits are the major determining factors of rice grain yield (Hien *et al.*, 2007). Characterization of rice germplasm increases its utility in any breeding program. The use of agro-morphological traits is the most common approach utilized to estimate relationships between genotypes. The conservation and characterization of these genetic resources is a necessity not only for posterity, but also for utilization in different improvement programs such as breeding for improved yield and tolerance to various stresses. It is important to assess the diversity of these germplasm to provide insights in the diversity of these germplasm (Rabara *et al.*, 2014). Characterization of both qualitative and quantitative characters have been commonly and traditionally used to estimate relationships between genotypes for further utilization in the breeding programme. In this context, an attempt was made to characterize a set of 30 genotypes of rice including traditional and land races for different agro morphological traits to identify the variability present within the germplasm.

MATERIALS AND METHODS

The 30 genotypes used in the present study were collected from farmers of different districts of Telangana and grown in *Kharif* 2018 in a Randomized Complete block Design (RBD) with three replications at Agricultural College farm, Bapatla (Table 1). All the 30 genotypes were sown separately in the raised nursery beds. Thirty days old seedlings of each genotype was transplanted separately in 5 rows of 3m length by adopting a spacing of 20cm between rows and 15cm between plants with in a row. All the necessary precautions were taken to maintain uniform plant population of each genotype per replication. The intercultural operations were done at regular intervals and necessary plant protection measures were adopted during the crop growth. Observations were recorded on five randomly chosen plants of each genotype per replication for 14 agro morphological traits and 11 quantitative traits *viz.*, basal leaf sheath color, anthocyanin coloration, flag leaf attitude of blade (early observation), anthocyanin coloration of keel, color of stigma, curvature of main axis (panicle), color of tip of lemma, awns, color of awns (late observation), distribution of awns, presence of secondary branching, panicle exertion, decorticated grain shape (in lateral view), decorticated grain color, length of leaf blade (cm), width of leaf blade (cm), time of heading, length of panicle, panicles/plant, time of maturity, test weight, grain length (mm), grain Width (mm), decorticated grain length, decorticated grain width. The observations of various characters were recorded at different stages of growth with appropriate procedures as per the DUS test guidelines of PPV & FR Act, 2001.

Table 1: List of genotypes studied in the present investigation.

Sr. No.	Genotype	Sr. No.	Genotype	Sr. No.	Genotype
1.	Ambemohar	11.	Kalajira	21.	Pathariya
2.	Arakuloya	12.	Karuppukavuni	22.	Poongar
3.	Badshabhog	13.	Kulakar	23.	Ramsri
4.	Bahurupi	14.	Madumurangi	24.	Ramyagali
5	Burma black	15.	Mappillai samba	25.	Ranikanda
6.	Chintalurisannalu	16.	Mysore malliga	26.	Ratnachudi
7.	Doddiga	17.	Narayanakamini	27.	Sammelbhog
8.	Ghani	18.	Navara	28.	Sannajajulu
9.	Illapaipu samba	19.	Pancharatna	29.	Selamsanna
10.	Kalabhatt	20.	Parimalasanna	30.	Tulasibaso

Shannon Diversity Index: Shannon diversity indices (H^1) were calculated to study the phenotypic diversity for each character in the entire germplasm as described by Perry and Mcntosh (1991) is given as:

$$H^1 = 1 - \sum_{i=1}^{n} p_i \log_e p_i$$

where p_i is the proportion of accessions in the i^{th} class of an n-class character and n is the number of phenotypic classes for a character. The indices are standardized by dividing each value of H' by $\log_n e$ to keep the value in a range of 0 to 1 in order to estimate the importance of phenotypic diversity. Analysis was done by using MSEXCEL. An arbitrary scale of diversity indices adapted from Rabara *et al.*, (2014) to categorize the computed indices into maximum (H' = 1.00), high (H' = 0.76–0.99), moderate (H' = 0.46–0.75) and low diversity (0.01–0.45). Cluster analysis by UPGMA and Principal component analysis was done using XLSTAT 2020 software.

RESULTS AND DISCUSSION

Phenotypic frequencies and traits distribution: Phenotyping is an important activity to evaluate and utilization of the germplasm collection in a gene bank. In this study 30 rice germplasm were scored using 14 qualitative and 11 quantitative characters. Frequencies of phenotypic classes expressed in percentage for each trait are shown in Table 2. The results revealed that most of the accessions showed green basal leaf sheath color, lack of anthocyanin leaf color, semi erect attitude of flag leaf blade, very weak anthocyanin color of lemma, white colored stigma, drooping panicle, yellowish color of tip off lemma, awnless spikelets, absence of distribution of awns in the entire panicle, well exerted panicle, late leaf senescence, short bold decorticated grain shape and white colored decorticated grain. Variation observed for leaf, panicle and grain related characters were represented in Fig. 1 and 2.

Table 2: Classification of rice germplasm based on 14 qualitative characters.

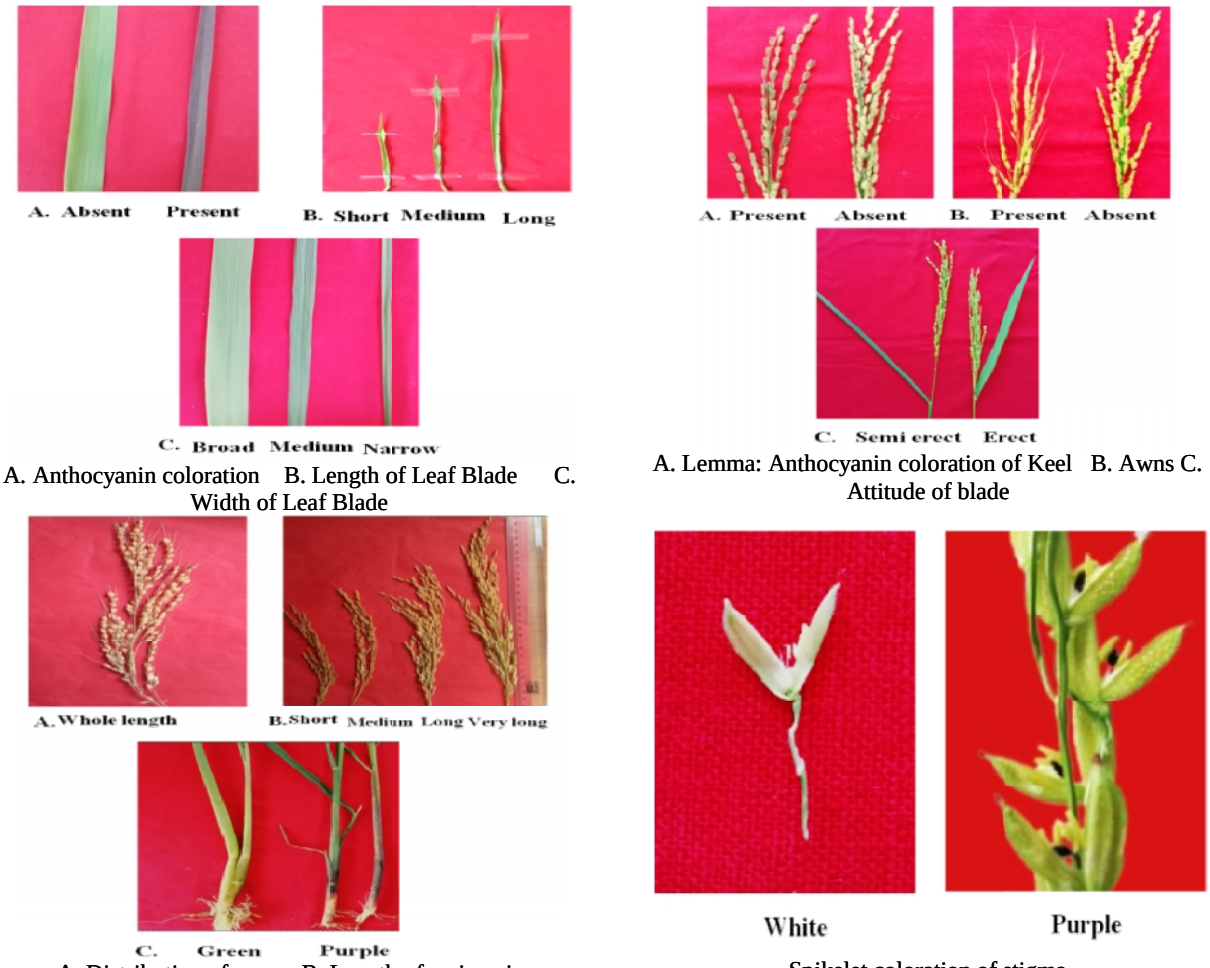
Sr. No.	Characteristics	Phenotypic classes	Relative frequency	Absolute frequency %)	Names of the Genotypes (Serial numbers in Table 1)
1.	Basal leaf: Sheath color	Green	24	80.0	17, 25, 27, 6, 29, 2, 1, 11, 3 22, 8, 20, 30, 23, 7, 28, 9, 24, 4, 26,14, 18, 16, 21
		Purple lines	2	6.7	5, 13
		Purple	4	13.3	19, 10, 12, 15
2.	Leaf: Anthocyanin coloration	Absent	27	90.0	17, 25, 27, 6, 29, 2, 1, 3, 22, 8, 20,30, 23, 7, 28, 9, 24, 4, 26,14, 18,16,21,5,13,15,12
		Present	3	10.0	19, 11, 10
3.	Flag leaf: Attitude of blade (early observation)	Erect	6	20.0	17, 27, 28, 14, 3, 22
		Semi-erect	24	80.0	25, 6, 29, 2, 1, 8, 20, 30, 23, 7, 9, 24, 4, 26, 18, 16, 21, 5, 13, 15, 12, 19, 11, 10
4.	Lemma: Anthocyanin coloration of keel	Absent/ Very weak	20	66.7	17, 25, 27, 6, 2, 10, 3, 8, 20, 30, 23, 7, 28, 9, 13, 4, 26, 18, 16, 21
		Weak	1	3.3	29
		Medium	5	16.7	1, 19, 22, 24, 14
		Strong	3	10.0	15, 5, 12
		Very strong	1	3.3	2
5.	Spikelet: color of stigma	White	25	83.3	17, 25, 27, 6, 29, 2, 1, 3, 8, 20, 30, 23, 7, 28, 9, 4, 26, 14, 18, 16, 21, 13, 12, 11, 10
		Purple	5	16.7	19, 22, 15, 5, 24
6.	Panicle: Curvature of main axis	Semi-straight	1	3.3	3
		Deflexed	7	23.3	29, 1, 19, 23, 28, 24, 4
		Dropping	22	73.3	17, 25, 27, 6, 2, 8, 20, 30, 7, 9, 4, 26, 14, 18, 16, 21, 13, 12, 11, 10, 22, 15, 5
7.	Spikelet: Color of tip of lemma	Yellowish	11	36.7	17, 25, 6, 2, 22, 8, 20, 7, 28, 14, 16
		Brown	7	23.3	19, 3, 15, 24, 13, 4, 26
		Red	2	6.7	23, 29
		Black	10	33.3	27, 1, 11, 10, 30, 9, 5, 12, 18, 21
8.	Panicle: Awns	Absent	28	93.3	17, 25, 27, 6, 29, 2, 1, 3, 22, 8, 20, 30, 23, 28, 9, 24, 4, 26, 18, 16, 21, 5, 13, 15, 12, 19, 11, 10
		Present	2	6.7	14, 7
9.	Panicle: Color of awns (late observation)	Absent	28	93.3	17, 25, 27, 6, 29, 2, 1, 3, 22, 8, 20, 30, 23, 28, 9, 24, 4, 26, 18, 16, 21, 5, 13, 15, 12, 19, 11, 10
		Yellowish White	2	6.7	7, 14
10.	Panicle: Distribution of awns	Absent	28	93.3	17, 25, 27, 6, 29, 2, 1, 3, 22, 8, 20, 30, 23, 28, 9, 24, 4, 26, 18, 16, 21, 5, 13, 15, 12, 19, 11, 10
		Whole length	2	6.7	7, 14
11.	Panicle: Exertion	Mostly exerted	1	3.3	7
		Well exerted	29	96.7	17, 25, 27, 6, 29, 2, 1, 3, 22, 8, 20, 30, 23, 28, 9, 24, 4, 26, 18, 16, 21, 5, 13, 15, 12, 19, 10, 11, 14
12.	Leaf: Senescence	Early	4	13.3	18, 7, 22, 23
		Medium	6	20.0	27, 2, 30, 15, 23, 21
		Late	20	66.7	17, 25, 6, 29, 1, 3, 8, 20, 28, 9, 4, 26, 16, 5, 13, 12, 19, 11, 10, 14
13.	Decorticated grain: Shape (in lateral view)	Short slender	3	10.0	6, 29, 16
		Short bold	13	43.3	27, 1, 3, 22, 8, 20, 30, 7, 15, 13, 4, 18, 21
		Medium slender	3	10.0	26, 9, 23
		Long bold	7	23.3	2, 19, 10, 5, 14, 24, 12
		Long slender	4	13.3	17, 25, 11, 28
14.	Decorticated grain: Color	White	18	60.0	17, 27, 6, 2, 1, 11, 3, 8, 20, 30, 23, 7, 28, 24, 4, 26, 16
		Light brown	3	10.0	25, 29, 9
		Light red	2	6.7	15, 14
		Red	4	13.3	19, 22, 13, 18, 21
		Dark purple	3	10.0	10, 5, 12

Basal leaf sheath color: Variations were observed for basal leaf sheath color. Most of the available germplasm were green (80%), some were purple (13.3%) and few were with purple lines on basal leaf sheath (6.7%). Similarly, Hein *et al.,* (2007) reported green and purple colors in their investigation. Roy *et al.,* (2016) identified green, light purple, purple lines and purple color phenotypic classes under basal leaf sheath color in the germplasm studied. Prakriti *et al.,* (2017); Islam *et al.,* (2018); Rawte and Saxena, 2018 reported green color basal leaf sheath in majority of the accessions.

Leaf anthocyanin coloration: Rice germplasm were characterized for leaf anthocyanin coloration revealed that 90% of germplasm exhibited absence of leaf anthocyanin coloration, while 10% showed anthocyanin leaf color. On the contrary, Prakriti *et al.* (2017); Rawte and Saxena (2018) reported 95% of the accessions exhibited absence of anthocyanin coloration in leaf.

Flag leaf- attitude of blade: On the basis of attitude of blade, 24 germplasm (80%) had semi erect attitude and 6 germplasm (20%) had erect attitude. Hein *et al.,* reported intermediate angle of flag leaf as a dominant trait in their studies whereas, Shamim and Sharma

(2014), reported semi erect flag leaf attitude as a dominant trait in their studies. Further, Roy *et al.*, (2016) observed erect, semi erect, horizontal and deflexed type attitude of blade in 126 aromatic short grain rice genotypes. Orientation of flag leaf sheath is important in relation to the photosynthetic efficiency because erect flag leaves have higher photosynthetic ratio.



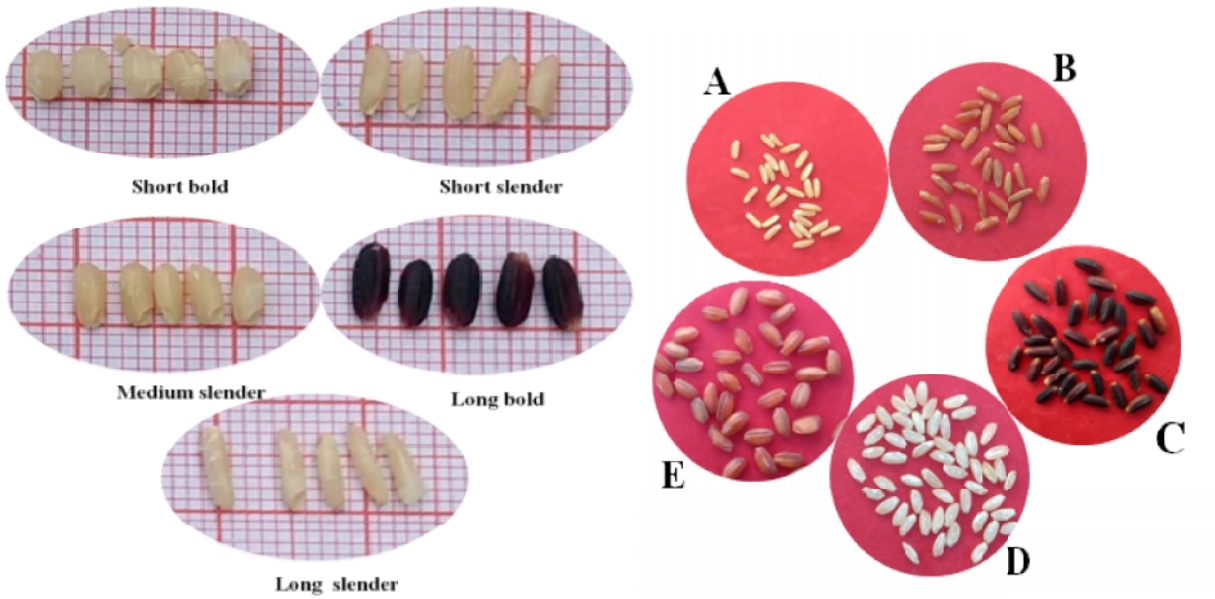
A. Anthocyanin coloration B. Length of Leaf Blade C. Width of Leaf Blade

A. Lemma: Anthocyanin coloration of Keel B. Awns C. Attitude of blade

A. Distribution of awns B. Length of main axis C. Basal leaf: Sheath color

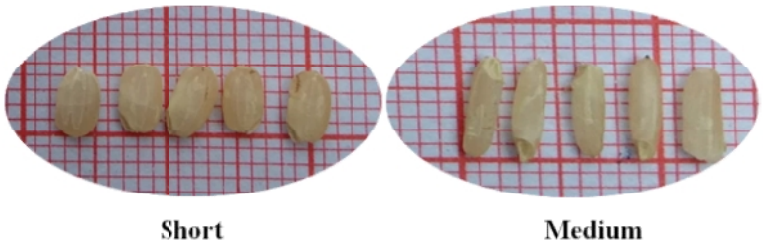
Spikelet coloration of stigma

Fig. 1. Variation in leaf and panicle related characters.



Decorticated grain: shape.

A. Light brown B. Light red C. Dark purple D. White E. Red. Variation in decorticated grain color.



Decorticated grain: length.

Fig. 2. Variation in grain characters.

Anthocyanin color of lemma: Variations were observed for anthocyanin coloration of lemma. A total of 66.7% of germplasm exhibited absence of anthocyanin color, 16.7% exhibited medium anthocyanin color of lemma while, 10% showed strong anthocyanin color of lemma. Further, 3.3 % showed very strong anthocyanin coloration of lemma.

Spikelet: Color of stigma: Of the 30 germplasm studied, around 25 germplasm showed white color of stigma and 5 showed purple color of stigma. Similar results of white stigma color as a dominant trait was reported by Shamim and Sharma (2014) whereas, Roy *et al.,* (2016) reported white, yellow, light purple and purple color of stigma in their investigation.

Panicle: curvature of main axis: Majority of germplasm (73.3%) had drooping habit while, 23.3 % of germplasm had deflexed habit and few (3.3%) had semi straight type. Similarly, Roy *et al.,* (2016) also reported straight and drooping habit in their germplasm studied.

Spikelet- color of tip of lemma: Variations were observed for tip of lemma color. A total of 36.7% of germplasm exhibited yellowish tip of lemma, 33.3% showed black color, 23.3% and 6.7% exhibited brown and red color respectively. Roy *et al.,* (2016) also observed wide variation in color of tip of lemma *viz.,* white, yellow, brown, red, purple and black color of tip of lemma in the germplasm.

Panicle – presence of awns, distribution and color: Out of 30 germplasm studied for awns presence, distribution and color, 28 germplasm (93.3%) exhibited absence of awns, distribution and color and only two germplasm (6.7%) possessed awns with yellowish white color and whole length distribution.

The awns in wild rice cultivars are considered to be advantageous because of protection of rice grains from the animal attack and play an important role in seed dispersal (Takahashi *et al*,. 1986). In this group of characters, the popularity of awnless trait maybe due to linkage with selective factors for yield and post-harvest production. The results suggested the presence of selection advantage to this trait in this collection. Hien *et al.,* (2007) and Prakriti *et al.,* (2017) reported awnless grain type as predominant in their studies. Rawte and Saxena (2018) and Islam *et al.,* (2018) reported 40% of accessions in their study had awns and 60% does not have awns. On the contrary, Roy *et al.,* (2016) observed wide variation in color of awns like yellowish white, light red, purple and black in 126 aromatic short grain rice genotypes whereas, Islam *et al.,* (2018) reported straw, brown and black color of awns. Further, Islam *et al.,* (2018) reported 69.23% of the accessions exhibited distribution of awns in tip only whereas, 30.76% of the accessions exhibited distribution of awns in upper half.

Panicle exertion: Out of 30 germplasm studied, 29 had well exerted panicles and only one had mostly exerted panicle. Similar results of well exerted panicles as a major phenotypic class was observed by Shamim and Sharma, (2014). On the contrary, Roy *et al.,* (2016); Islam *et al.,* (2018) observed partly exerted, exerted and well exerted panicle types in their germplasm studied.

Leaf senescence: The germplasm was characterized in to three groups based on leaf senescence. 66.7% of germplasm showed late senescence, 20% showed medium senescence and only 13.3% showed early leaf senescence.

Decorticated grain shape: Lot of variation was seen for the character decorticated grain shape. Majority of the accessions (43.3%) had short bold grains, 23.3% had long bold grains, 13.3% had long slender grains, remaining 20% had short slender and medium slender shapes. Hein *et al.,* (2007) reported slender and long grain shapes as dominant in their collections. Grain characters especially grain shape is an important character, depending on demand of customers, criterion of trading price changes (Hein *et al.,* 2007).

Decorticated grain color: Variations were observed for grain color. Majority of the accessions (60%) showed white color, 13.3% red color, 10% light brown, 10% dark purple and 6.7% exhibited light red colored grains. Adair *et al.* (1966) reported that grain size and grain shape are the first criteria for quality that a breeders consider in development of new varieties for commercial production.

Estimation of Shannon weaver diversity indices: The Shannon –Weaver diversity index values were calculated based on the frequency of 14 qualitative characters and the values ranged from 0.21 to 0.90. Estimates of phenotypic diversity for different characters are shown in Table 3. The indices for 14 qualitative characters were grouped into low, moderate and high diversity (Rabara *et al.,* 2014). The results revealed that most of the characters showed moderate to high diversity. High diversity indices were observed for four characters. Tip of lemma color had the highest diversity index of 0.90 followed by decorticated grain

shape (0.89), leaf senescence (0.78) and decorticated grain color (0.76).

Moderate diversity index was observed for 6 characters with indices ranging between 0.47-0.72. Flag leaf blade attitude had the moderate index value of 0.72, followed by anthocyanin coloration of keel (0.63), color of stigma (0.65), panicle curvature of main axis (0.62), basal leaf sheath color (0.57) and leaf anthocyanin coloration (0.47). The low diversity index value (0.21) was shown by panicle exertion. The characters like panicle exertion, distribution of awns in the panicle, color of awns and the presence of awns were dominated by one phenotypic class with a distribution ranging between 74%–96%. These four panicle related traits had low diversity indices ranging between 0.21–0.45.

Table 3: Shannon weaver diversity indices of 30 rice germplasm based on 14 qualitative characters.

Sr. No.	Character	Shannon Weaver diversity index ($H^{I)}$
High diversity (0.76-0.99)		
1.	Spikelet: Color of tip of lemma	0.90
2.	Decorticated grain: Shape (in lateral view)	0.89
3.	Leaf: Senescence	0.78
4.	Decorticated grain: Color	0.76
Moderate diversity (0.46- 0.75)		
5.	Flag leaf: Attitude of blade (early observation)	0.72
6.	Lemma: Anthocyanin coloration of keel	0.63
7.	Spikelet: Color of stigma	0.65
8.	Panicle: Curvature of main axis	0.62
9.	Basal leaf: Sheath color	0.57
10.	Leaf: Anthocyanin coloration	0.47
Low diversity (0.01-0.45)		
11.	Panicle: Awns	0.35
12.	Panicle: Color of awns (late observation)	0.35
13.	Panicle: Distribution of awns	0.35
14.	Panicle: Exertion	0.21

Hein *et al.*, (2007) reported that, the H^1 values ranged from 0 for apiculus color, lemma and palea color to 0.94 for grain size. In general, traits from group of grain characters displayed more variation than other groups by diversity index of total collection. Rawte and Saxena, 2018 analysed shannon wever diversity indices of the 20 agro morphological traits. The H^1 ranged from 0-1.223 with a mean of 0.548. The highest diversity index of 1.223 was observed for flag leaf attitude of blade.

Cluster analysis of qualitative characters: A dendrogram was constructed by using UPGMA clustering method based on dissimilarity coefficient across 30 rice genotypes. The cluster anlaysis grouped the genotypes into five clusters for 14 qualitative characters. Cluster I was the largest with maximum number of genotypes (23), while cluster III was the smallest with only one genotype (kalajira). Clusters II, IV & V had 2 genotypes each. Distribution of genotypes into five clusters was represented in Table 4.

Table 4: Distribution 30 rice genotypes into five clusters based on qualitative characters.

Sr. No.	No. of genotypes	Genotypes
1.	23	Narayana Kamini, Rani Kanda, Sammel Bhog, Chintaluri Sannalu, Selam Sanna, Arak, Loya, Ambemohar, Badshabhog, Poongar, Ghani, Parimala Sanna, Tulasi Baso, Ramsri, Mapillai Samba, Sannajajulu, Illapaipu Samba, Ramyagali, Kulakar, Bahurupi, Ratnachudi, Navara, Mysore Malliga, Pathariya
2.	2	Kalabhatt, Pancharatna
3.	1	Kalajira
4.	2	Madu Marangi, Doddiga
5.	2	Karuppu Kavani, BurmaBlack

Average intra and inter cluster dstances were presented in Table 5. The intra cluster distance was maximum in Cluster I (3.91) containing 23 genotypes followed by cluster IV (3.87) and zero intra cluster distance was observed in cluster III having one genotype. Regarding inter cluster distance, the maximum genetic distance was observed between the clusters III and IV (14.83), followed by II and IV (14.19), while the minimum was observed between the clusters II and V (9.26). The maximum inter cluster distance indicates that the genotypes belonging to cluster III were far diverged from cluster IV.

The minimum inter cluster distance indicates that the genotypes were genetically close. The inter cluster distances in all the clusters were higher than the intra cluster distances suggesting wider genetic variability among the genotypes of different groups. Similarly, Ahmed *et al.*, (2016) also grouped the germplasm into three major clusters according to the UPGMA clustering method based on Dice coefficient. Further, Hein *et al.*, (2007) grouped 36 cultivars into five clusters. The maximum number of gentoypes were placed in cluster III and the minimum of one genotype in cluster IV.

Table 5: Avergae Intra and Inter Cluster Distance for 14 Qualitative Charaters.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	**3.91**	10.39	11.42	9.86	9.51
Cluster II		**3.67**	9.77	14.19	9.26
Cluster III			**0**	14.83	11.96
Cluster IV				**3.87**	13.23
Cluster V					**2.06**

*** Bold values indicate the intra cluster distance values**

The results of principal component analysis revealed that (Table 6) first four principal components showed eigen values more than 1 and accounted for about 69.4% of the total variation. The first principal component accounted for 28.31%, second principal component accounted for 20.37%, third and fourth accounted for 11.20% and 9.53% respectively. The characters presence of awn, color of awn and their distribution, basal leaf sheath color, anthocyanin coloration, color of stigma, decorticated grain color and stigma color contributed positively towards the variability. Similarly, Roy *et al.,* (2016) identified, three characters *viz.,* color of lemma, color of awn and color of stigma were the most important components while grouping of genotypes. The first three principal components together explained a cumulative 74% of the total variance.

Table 6: Eigen values, proportion of total variance represented by first four principal components, cumulative per cent variance and component loadings of different qualitative and quantitative characters in Rice genotypes.

Qualitative characters	**F1**	**F2**	**F3**	**F4**
Eigenvalue	3.964	2.853	1.568	1.334
Variability (%)	28.313	20.379	11.200	9.532
Cumulative %	28.313	48.693	59.892	69.424
Basal leaf: sheath color	-0.427	0.728	0.088	-0.027
Anthocyanin coloration	-0.325	0.514	-0.184	-0.367
Flag leaf: attitude of blade	-0.250	0.111	0.628	-0.260
Lemma: anthocyanin coloration of keel	-0.248	0.700	-0.188	0.232
Spikelet: color of stigma	-0.274	0.518	-0.093	0.717
Panicle: curvature of main axis	0.116	0.261	0.449	-0.314
Spikelet: color of tip of lemma	-0.417	0.241	0.421	-0.246
Panicle: awns	0.910	0.365	-0.072	-0.084
Panicle: color of awns	0.910	0.365	-0.072	-0.084
Panicle: distribution of awns	0.910	0.365	-0.072	-0.084
Panicle: exertion	-0.764	-0.212	-0.266	-0.008
Leaf senescence	-0.331	-0.034	-0.486	-0.558
Decorticated grain shape	-0.141	0.395	-0.584	-0.267
Decorticated grain color	-0.300	0.749	0.212	0.028
Quantitative characters	**F1**	**F2**	**F3**	**F4**
Eigenvalue	3.437	2.782	2.045	1.218
Variability (%)	31.249	25.293	18.587	11.077
Cumulative %	**31.249**	**56.543**	**75.130**	**86.207**
Length of leaf blade	-0.430	0.727	-0.291	0.000
Width of leaf blade	0.134	0.586	-0.122	-0.512
Time of heading	-0.726	0.577	0.185	0.161
Length of panicle	-0.601	0.458	-0.198	-0.214
Panicles/ plant	-0.299	-0.100	0.138	0.843
Time maturity	-0.721	0.581	0.184	0.152
Test wt	0.664	0.602	0.029	0.174
Grain length	0.334	0.292	0.885	-0.058
Grain width	0.739	0.493	-0.349	0.238
Decorticated grain length	0.342	0.294	0.876	-0.068
Decorticated grain width	0.722	0.492	-0.382	0.236

Quantitative trait characterization: Rice genotypes were evaluated for 11 quantitative traits *viz.,* length of leaf blade (cm), width of leaf blade (cm), time of heading (days), length of panicle (cm), panicles/ plant, time of maturity (days), test weight (g), grain length (mm), grain width (mm), decorticated grain length (mm) and decorticated grain width (mm). The descriptive statistics were employed to assess the magnitudes of genetic variation are presented in Table 7. Among all the genotypes Ramsri was an early flowering and maturing genotype, while Karuppukavuni was the long duration type. Madumurangi had long panicles (33.9 cm) and Kulakarhad small panicles (16 cm). The highest test weight was recorded by Mapillai samba (3.41g), while lowest was recorded by Parimalasanna (1.10g). Sannajajulu recorded longest (7.73mm) grain length and Badshabogh (4 mm) recorded short grain length. Doddiga recorded (2.9 mm) high grain width while, Chintalurisannalu recorded low (1.5mm) grain width. Maximum value for decorticated grain length was recorded by Sannajajulu (7.68) while, the minimum

(3.9) was recorded for Badhshabogh. For decorticated grain width, the highest value was recorded by Doddiga (2.81) and the lowest value was recorded by Chintalurisannalu (1.48). Prakriti *et al.,* (2017) conducted descriptive studies in rice germplasm for some quantitative characters and reported ranges for panicle length (21.7 – 29.6), test weight (1.63 – 3.08), grain length (5.83 -9.9) and grain width (2.03-3.3).

Table 7: Descriptive statistics for 11 quantitative traits of 30 rice genotypes.

Sr. No.	Character	Mean	Min	Max	SD	SE
1.	Length of leaf blade (cm)	47.3	27.66	68.5	9.66	1.76
2.	Width of leaf blade (cm)	1	0.53	1.5	0.211	0.03
3.	Time of heading	88	76	105	7.42	1.35
4.	Length of panicle	24.5	16	33.9	4.32	0.78
5.	Panicles/ plant	11.6	7.73	17.2	2.16	0.39
6.	Time of maturity	118	106	136	7.38	1.34
7.	Test weight	19.6	1.10	3.41	6.15	1.12
8.	Grain length (mm)	5.7	4	7.73	0.89	0.16
9.	Grain Width (mm)	2.27	1.5	2.9	0.37	0.06
10.	Decorticated grain length	5.57	3.9	7.68	0.89	0.15
11.	Decorticated grain width	2.21	1.48	2.81	0.37	0.06

Cluster analysis of quantitative characters: A dendrogram was constructed using UPGMA clustering method based on dissimilarity coefficient among 30 rice genotypes. The cluster anlaysis grouped the genotypes into five clusters for 11 quantitative characters. Cluster I was the largest with maximum number of genotypes (14), while clusters III & V were smallest with only one genotype in each, where as cluster II had 11 genotypes and cluster IV had 3 genotypes. Distribution of genotypes into five clusters were shown in Table 8. Average intra and inter cluster dstances were presented in Table 9. Maximum intra cluster distance was showed by Cluster I (10.91) containing 14 genotypes. The intra cluster distance of zero was seen in clusters III & IV as the clusters contain only one gentoype. Regarding inter cluster distance, the maximum genetic distance was observed between the clusters IV and V (50.50), followed by III and IV (49.33), while the minimum was observed between the clusters I and II (16.30). The maximum inter cluster distance indicates that the genotypes belonging to cluster IV were far diverged from cluster V. The minimum inter cluster distance indicates that the genotypes were genetically close.

The inter cluster distances in all the clusters were higher than the intra cluster distances suggesting wider genetic variability among the genotypes of different groups. Akter *et al.,* (2018) reported that, 31 traditonal bangladeshi rice genotypes were grouped into five clusters with highest inter cluster distance between cluster II and V. The Principal component analysis (Table 6) revealed that, the first four principal components with eigen values >1, contributed 86.20 % of the total variations among the genotypes for 11 quantitative characters. The characters namely, test weight, grain width; decorticated grain width and number of panicles per plant were positively towards the variability. The first principal component accounted for 31.24% second principal component accounted for 25.29%, third and fourth accounted for 18.58% and 11.07% respectively. Similarly, Islam *et al.,* (2018) reported that the first five components with vector values > 1 contributed 76.51% of the total variations. On the other hand, Sohrabi *et al.* (2012) and Chakravorty *et al.*, (2013) reported contribution of 76.7 and 75.9% of the first six and four components, respectively to the total variation in their study.

Table 8: Distribution of 30 rice genotypes into five clusters based on 11 quantitative traits.

Sr. No.	No. of genotypes	Genotypes
1.	14	NarayanaKamini, Rani Kanda, SammelBhog, Kalabhatt, Badshabhog, Tulasi Baso, Doddiga, Mapillai Samba, Sannajajulu, Illapaipu Samba, Burma Black, Ratnachudi, Madu Murangi, Mysore Malliga
2.	11	Chintalurisannalu, Selamsanna, Arakuloya, Ambemohar, Pancha Ratna, Kalajira, Poongar, Ghani, Bahurupi, Navara, Pathariya
3.	1	Parimala Sanna
4.	3	Ramsri, Ramyagali, Kulakar
5.	1	Karuppu Kavuni

Table 9: Intra and Inter cluster distances based on 11 quantitative traits.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	**10.19**	16.30	19.91	31.88	22.71
Cluster II		**9.56**	33.52	16.53	37.21
Cluster III			**0.000**	49.33	24.54
Cluster IV				**5.885**	50.50
Cluster V					**0.00**

* Bold values indicate the intra cluster distance values

CONCLUSION

Morphological variation does not always reflect real genetic variation because of interaction between genotype and environement, and the large unknown genetic control of polygenic, morphological and agronomic traits. Morphological traits are useful for preliminary evaluation because it is fast, simple, and can be used as a general approach for assessing genetic diversity among morphologically distinguishable cultivars.The present study revealed wide variation among the germplasm with respect to the morphological characters studied.

FUTURE SCOPE

The traditional rice germplasms lines studied in the present study can offer a valuable gene pool which can be utilized in different varietal improvement/development program in future. The morphological characters used are very much useful for characterization, identification and grouping of genotypes for further utilization in the breeding programme. This study will also be useful for breeders, researchers and farmers to identify, restoration and conservation of beneficial genes for crop improvement. Further, comprehensive investigation including molecular markers and quantitative characters will probably provide a complete view about the genetic variation of rice cultivars.

Acknowledgment: This study was the part of the author's M.Sc. thesis work and he acknowledges the financial support and research facilities of Agricultural College, Bapatla, Acharya NG Ranga Agricultural University.
Conceptualization of research (VR, VSR); Designing of the experiments (VR); Contribution of experimental materials (NDR); Execution of field/lab experiments and data collection (NDR); Analysis of data and interpretation (VR, MT); Preparation of the manuscript (VR, MT).
Conflict of interest: All the authors have no conflicts of interest to declare. All co-authors have seen and agree with the contents of the manuscript

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How to cite this article: Rao, N.N.D., Roja, V., Tushara, M., Rao, V.S. and Rao, V.S. (2021). Characterization and Diversity Analysis of Rice Germplasm. *Biological Forum – An International Journal, 13*(3a): 170-179.