Impact of Agromorphological Quantitative Traits Towards Divergence of Rice (*Oryza sativa* L.) Landraces

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Abstract
Background
Rice Landraces has a never deniable Importance in agriculture because existing variety improvement and future breeding program depends on the desirable genes present in the landraces only. Landraces can be selected on the basis of various morphological parameters. So, assessment, analysis and documentation are very much essential.
Methods
In this review, authors searched various different databases to study the morphological diversity and relationship within the landraces. Observational and Interventional studies of Rice landraces and morphological markers are included in this review studies.
Results
In an efficient breeding technique, selecting important characters on the basis of detailed information and association patterns between the yield and yield related components is very significant for crop up-gradation. To understand the genetic variability between enviable landraces, presence of genetic divergence in the landraces is essential and it guides to successful exploitation of landraces in breeding program. In this study it is revealed that there are significant interrelationships among yield and yield

related characters where the yield related traits applied their direct and indirect effect through other traits for improving grain yield/hectare.

Conclusions

An extensive amount of variation was recorded for maximum characters within the genotypes studied which indicate that the selection on the basis of these characters is imagined to be effectives. Characterization of rice landraces expressed distinctiveness among the rice landraces. It is very much important for utilizing the proper characteristic in breeding programmes and also important in the present time for protecting the landraces of rice.

Keywords: Landrace, Morphological Diversity, Morphological markers.

1. Introduction

Rice (*Oryza sativa* L.) is the most important widely grown ancient cereal crop and staple food for over half of the world population (Garris et al. 2005; Ramkumar et al. 2010) and the second most consumed cereal crop after wheat. An about 250 million farms of the 112 Countries grown rice. Rice is being cultivated for more than 10,000 years and estimated that 3.5 billions of people worldwide depends on it and nearly more than 90% of the rice is cultivated in developing countries There are lots of species of rice in the world including twenty three wild rice and two cultivated rice species. It is evidenced and reported that rice has originated from the single domestication (Molina et al. 2011) near about 8200-13,500 years before present(ybp) in a Chinese valley named Yangtze Valley (Huang et al., 2012). Though Protein percentage in rice are in very small amount, but its nutritional value is very high. Rice protein is near about 88% highly digestible (Ma et al., 2007). A notable success has been gained in the field of rice production during last 25 years. This enhancement in the global rice production is due to the adoption of high yielding varieties, modern technology and better crop management strategies (Byerlee, 1996). Every year available land for cultivation are decreasing for the improper use of land and for the urbanization (Khush, 1997; Fischer et al., 2000). India have to maintain the increase rice productivity in the rate of 3 percent per year (Thiyagarajan and Selvaraju, 2001). Asian rice (Oryza sativa L.) is very important and frequent staple foods for nearly more than 3.5 billion population worldwide and gives approximately 20% of their daily calory intake where wheat gives 19% and maize gives 5% of that. Nearly 90% of the world's rice are cultivated in the Asian continent (Salim et al., 2003; Paranthaman et al., 2009). Though landraces are less productive, also posses high genetic variance for many biotic stresses (Hanamaratti et al., 2008).Landraces are genetically dynamic and shows equilibrium for the both pathogens and the environment (Harlan,1975). Traditional landraces are vital for maintaining crop diversity, conservation, characterization and collection of rice. In plant breeding, markers which are related to shape, size, color and surface of different plant parts, photoperiod sensitivity, disease response and many other traits that are visually scorable are called morphological markers. In morphological marker, morphological characters are used to distinguish the varieties or cultivars, to assess systematic position and to detect the taxa etc. That type of classical markers refers to available gene loci which have obvious impact on the morphology of plant. The different morphological characters of rice varieties or landraces in India give relatively broad phenotypic variance indicating great possibility for genetic improvement as well as for increasing the yield of the crop through varietal improvement (Deb 2000; Chakravorty et al., 2011; Chakravorty et al., 2013; Tiwari 2015; Sinha et al., 2013; Dikshit et al., 2014;

Lahkar et al., 2017. According to Deb (2005), Indica landraces can be selected on the basis of various morphological parameters like plant height, leaf length and leaf width, grain weight, grain size and presence/absence of aroma etc. Information based on genetic diversity helps in parental selection from the enormous number of landraces or germplasm. Multivariate analysis is used to summarize and describe the inherent variations among landraces. Many researchers have already described morphological characterization, the level and pattern of relationship among yield and its component traits and extent of genetic divergence in different crops like rice (Pandey et al., 2009; Latif et al., 2011; Chakma et al., 2012; Idris et al., 2012; Basavaraja et al., 2013a; Tripathi et al., 2017; Adhikari et al., 2018; Roy et al., 2020), wheat (Arya et al., 2017; Lakra et al., 2020; Hai et al., 2006), maize (Pandit et al., 2016; Kumari et al., 2017), Barley (Dido et al., 2020), chilli (Krishnamurthy et al., 2013). In this study, valuable information provided would help for further analysis of diversity at pheno-typical level in cereal crops.

2. Morphological marker and diversity analysis

In plant breeding, markers which are related to shape, size, color and surface of different plant parts, photoperiod sensitivity, disease response and many other traits that are visually scorable are called morphological markers. In morphological marker, morphological characters are used to distinguish the varieties or cultivars, to assess systematic position and to detect the taxa etc. That type of classical markers refer to available gene loci which have obvious impact on the morphology of plant and are well known as "naked eye polymorphism" and generally detectable by eye, by simple visual inspection. The utilization of morphological or phenotypical traits as descriptors is the conventional method for the assessment of genetic diversity and morphological traits still play a vital role in the analysis of variation in crop species because their use does not require any sophisticated technology, are readily available and they form the most direct measure of phenotype. The utilization of qualitative and quantitative phenotypic traits is extremely valuable for the breeding purpose and also for improvement though there are various Limitations of morphological markers. According to the guidelines of IRRI there are 60 rice descriptors. Here we considered only about 20 quantative traits.

3. Agro-morphological Characters

The observations on different Agro-morphological quantitative characters of rice landraces were recorded.

3.1. Quantitative characters

3.1.1 Twelve days plant height (inches):

The height of the plant was measured in inches from the ground level to the tip of the tallest leaf at the twelve days age.

3.1.2 Panicle weight (gm):

Actual measurement in grams of a whole panicle were done.

3.1.3 Panicle length (cm):

The measurement in centimeters were taken from the base of the panicle to the tip of the panicle at the physiologically mature stage.

3.1.4 Number of primary branches / panicle:

There are different types of panicles based on the mode of branching like open, compact and intermediate. Number of primary branches of the panicles were counted and average values were taken for the statistical analysis.

3.1.5 Number of total grains / panicle:

Number of spikelets including filled and unfilled were counted and then averaged.

3.1.6 Number of chaffy grains / panicle:

Number of chaffy grains were counted on the panicle of the plants and then averaged.

3.1.7 Number of filled grains / panicle:

After removing the chaffy grains, remaining filled grains were counted on the panicle of the plants and then averaged.

3.1.8 100 grains weight (gm):

100 well developed whole grains weight were measured which were dried at 13% moisture content.

3.1.9 Grain length (mm):

For characterization of cultivars grain length is very much important criteria. Ten grains including husk were taken arbitrarily and then arranged linearly and then measured the length. Averaged length was recorded.

3.1.10 Grain Breadth (mm):

For characterization of cultivars grain breadth is also very much needed .Ten grains including husk were taken arbitrarily and then arranged horizontally and then measured the length. Averaged length was recorded.

3.1.11 Boiled or cooked kernel length (mm):

Ten boiled or cooked kernel taken arbitrarily and then arranged linearly and then measured the length. Averaged length was recorded.

3.1.12 Boiled or cooked kernel breadth (mm):

Ten boiled or cooked kernel taken arbitrarily and then arranged horizontally and then measured the length. Averaged length was recorded.

3.1.13 ligule length(cm):

Ligule length is one of the most important parameter for characterization of cultivars. Ligule lengths were measured and average length was measured.

3.1.14 Leaf length (cm):

The leaf length was measured in centimeters from the base of the leaf to the apex of the leaf. The data were recorded on ten arbitrary plants and average length was measured.

3.1.15 Leaf breadth (cm):

The leaf breadth was measured in centimeters from the one margin to the next margin.

The data were recorded on ten arbitrary plants and average breadth was measured.

3.1.16 Kernel length before boiling (mm):

Ten milled grains were taken arbitrarily and then measured the length in millimeter. The data was recorded and average length was measured.

3.1.17 Kernel breadth before boiling (mm):

Ten milled grains were taken arbitrarily and then measured the breadth in millimeter. The data was recorded and average breadth was measured.

3.1.18 Number of days required for flowering:

Number of days required for the flowering in the primary panicle from the date of sowing was recorded.

3.1.19 Number of days required for maturation:

Total number of days required for the maturation of the rice were counted and the data were recorded. The days required for sowing to the ripening of the spikelets are counted.

3.1.20 Grain yield (tons/hectare):

Total yield of filled grains of each of the ten plants was measured in grams after the drying in sun for 5-8 days after harvesting and the average weight was recorded. Then the data were converted in to the tons/hectare unit.

4. Statistical methods for analysis of diversity in Rice

4.1 Analysis of variance (ANOVA)

At first, mean values for every traits of each genotypes were calculated. Then these mean data were used for calculating different variability parameters i.e, coefficient of variation, range, standard deviation. Methodology of Cochran and Cox (1957) was adapted for statistically analyzing the data.

Table 1. Structure of ANOVA

Variation source	Degree of freedom	Sum of square	Mean sum of square	F calculated
Replication	(r-1)	SSR	MSR	MSR/ MSE
Genotypes	(g-1)	SSG	MSG	MSG/ MSE
Error	(r-1)(g-1)	SSE	MSE	
Total	(rg-1)	SS		

4.2 Variability Assessment

4.2.1 Range:

The difference between the highest and smallest value of a data set of a character are defines by the range and is expressed as,

Range = Highest value – smallest value

4.2.2 Mean:

Mean is the mathematical average of the set of two or more numbers and is calculated by subtracting the total observations ($\sum$xi) with their number (N) and defined as x.

$X = \sum Xi / N$

Where, $\sum Xi$ = Summation of total observation N = Total observation number

4.2.3 Standard deviation (SD):

Standard deviation measures the dispersion of a dataset relative to its mean and is calculated as the root of sum of squares of deviation subtracted with their number and is expressed as,

$SD = \sqrt{\sum d2} / \sqrt{n}$

4.2.4 Standard error (SE):

SE or standard error is related with the variability of the treatment means and is expressed as,

$SD = S / \sqrt{n}$

4.2.5 Estimation of coefficients of variation:

Estimation of coefficient of variation of various characters were done by the method of Burton and De Vane (1953). Where,

GCV (%) = ($\sqrt{\sigma g2}$ /X) 100 and

PCV (%) = ($\sqrt{\sigma p2}$ / X) 100

Where,

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

X = Mean of character

$\sigma g2$ = Genotypic variance

$\sigma p2$ = Phenotypic variance

The extent of coefficient of variation was classified as high (> 20%), medium (20% -10%) and low (< 10%).

4.2.6 Heritability

Heritability in broad sense is the ratio of genotypic variance with the phenotypic variance. The method of Hanson et al., (1956) was followed for calculation in present study. It is expressed as

$h^2 = \sigma g^2 / \sigma p^2$

where,

h^2 = Heritability (broad sense)

σg^2 = Genotypic variance

σp^2 = Phenotypic variance

According to Johnson et al. (1955) values of heritability was classified as high (> 20%), medium (20% - 10%) and low (< 10%).

4.2.7 Genetic advance

Genetic advance is the measure of gain or improvement in the value of genotypic mean of the selected plants upon the parental population. It depends mainly on the intensity of selection , heritability (broad sense) of character and on the values of phenotypic variability. Genetic advance was measured with the method of Johnson et al., (1955) and is expressed as,

G A= K.h^2.σp

Where,

GA represents Genetic advance, K denotes Constant (Standardized selection differential) which have the value of 2.06 at 5 per cent level of selection intensity, h^2 represents the Heritability of the character and σp represents the Phenotypic standard deviation.

4.2.8 Genetic advance as percentage of mean (GAM)

Genetic advance as percentage of mean or GAM was measured by that method,

GAM = $\dfrac{\text{Genetic Advance}}{\text{General Mean}}$ x 100

According to Johnson et al. (1955) values of Genetic advance as percentage of mean was classified as high (> 20%), medium (20% -10%) and low (< 10%) .

4.3 Association analysis

4.3.1 Correlation coefficient analysis

Measurement of mutual relationship between different characters at phenotypic (p), genotypic (g), and environmental levels are done by the Correlation coefficients analysis. Miller et al. (1958) suggested a method for that purpose.

For calculating genotypic correlation coefficient between characters x and y,

r xy (g) = Cov xy (g) √(Var x (g) x Var y (g))

For calculating Phenotypic correlation coefficient between characters x and y

r xy (p) = Cov xy (p) √(Var x (p) x Var y (p))

Here, r xy (g) represents the Genotypic correlation coefficient between x and y,

r xy (p) represents the Phenotypic correlation coefficient between x and y,

Cov xy (g) represents the Genotypic covariance between x and y,

Cov xy (p) represents the Phenotypic covariance between x and y,

Var x (g) represents the Genotypic variance of x,

Var x (p) represents the Phenotypic variance of x,

Var y (g) represents the Genotypic variance of y,

Var y (p) represents the Phenotypic variance of y,

4.3.2 Path analysis

Measurement of the independent variable's direct and indirect contribution over dependent variable are done by the path analysis. This analysis was developed by Wright (1921) and Dewey and Lu (1959) at first used this method for selection of plants.

According to Lenka and Mishra (1973) values of path coefficient analysis was classified as 0.00 to 0.09 Negligible, 0.10 to 0.19 Low, 0.20 to 0.29 Medium, 0.30 to 0.99 High and ˃ 1.00 Very high.

4.3.3 Principal component analysis

In 1901 PCA or Principal Component Analysis was first invented by Karl Pearson. Principal Component Analysis, or PCA, is the method of dimensionality reduction. This method is applied for reducing the variable numbers of a set of data in to the data set with smaller number of variables though it contains the most of the information of the previous data set. This method also used for making data more accurate, simple and easy to explore. This method is also used for the exploratory analysis of data and for making the predictive models

The basic equation of PCA is, Y =W ′X

where W, is a matrix of coefficients which is determined by PCA.

X= data matrix which consists set of all data vectors

4.4 Genetic divergence analysis

In 1928 P.C. Mahalanobis at first developed D² statistic and Rao (1952) suggested this technique for assessing the genetic divergence between the populations. It measures the relative contribution of every component trait in to the total divergence and determines the differentiation forces at intra and inter-cluster levels .These clusters grouped the varieties by   following the method described by Spark (1973).

Various distinguished researchers have already highlighted morphological characterization. The data was assessed by multivariate analysis of variance, coefficient of variation, heritability (Broad sense), genetic advance also with Genetic divergence analysis, Principal component analysis, Association analysis and Path analysis for each quantitative traits. Ogunbayo et al. (2005) assessed forty accessions

of rice by the use of fourteen agro-morphological traits. Total tiller numbers and effective tiller numbers also with the date of maturity and heading were identified to influence grain yield. Block effects were observed significantly for the date of flowering, day of maturity, height of the plant and beside that non-significant block effects means that non-importance of the blocking for the other eleven traits. Bisne and Sarawgi (2008) assessed 32 accessions of aromatic rice of Badshah bhog group by the use of 22 morphological, eight quality characters and six agronomical characters. They detected few genotypes for good quality and agronomic characters for the use of hybridization programme for achieving desired segregants with higher yield and quality. Sedeek et al. (2009) assessed the twenty four varieties at the Rice Research and Training Center, Sakha, Kafr EL-Sheikh, Egypt, during 2007 and 2008 seasons to study the genetic variability of some physiological traits and grain yield and its components. The cluster analysis were carried out using three parameters i.e, vegetative period, days to heading and reproductive period. Heritability estimates were high (ranged between 86 to 99.4%)for all studied traits. The expected genetic advance from selection appeared to be effective and ranged between 3.56 % to 44.88 % over the two seasons. Since reproductive phase was almost constant and had a very low range, the cluster was mainly influenced with days to heading and vegetative stage period. Florence et al. (2010) characterized thirty two cultivars of upland rice in citu by using some important morphological traits from the farmer's fields and was limited from the reproductive phase prior to the harvest. Ten quantitative morphological traits were selectd for that purpose like plant length, plant height, culm number, culm diameter, culm length, leaf length, leaf width, leaf angle, flag leaf angle, leaf width etc.Nascimento et al.(2010) characterize 146 accessions of upland rice by using qualitative and quantitative agro-morphological descriptors. Total of 14 qualitative and 14 quantitative descriptors were used. Polymorphism was observed among 12 of 14 qualitative characters which evaluated significant differences (p < 0.05) and were observed for 11 of the 14 analysed quantitative traits. Genetic variance was higher than environmental variance. Jaccard similarity coefficient was used for qualitative traits, while Euclidean distances were estimated for the quantitative traits. Cluster analysis for the quantitative traits using the Euclidean distance formed three major groups with few sub-groups. cluster analysis for qualitative traits clustered the landraces in to two groups with a total of 18 duplicates. High variability among the rice Landraces from the germplasm collection studied will help the rice breeding and improvement programme in future. Mathure et al. (2011) assessed sixty nine rice genotypes. Characterization was done by the use of agronomic traits and between sixty nine genotypes , thirty six exquisite genotypes possessed few superior traits like strong aroma, long panicles, early flowering, dwarf stature, productive tiller numbers per plant, filled grains number per panicle etc. Ashim Chakravorty and P. D.Ghosh (2012) assessed fifty one landraces of rice during kharif season of 2008 2009 and 2010 from the Zonal Adaptive Research Station,Krishnagar, Nadia, West Bengal and forty Six agro-morphological traits were used for the establishment of the distinctness. Distinctiveness, Uniformity and Stability test (DUS) was done .Out of fifty one varieties studied, twenty seven were found to be distinctive on the basis of twenty two essential and twenty four additional characters. This study will be useful for breeders, researchers and farmers to identify and choose the restoration and conservation of beneficial genes for crop improvement. Bajpai et al. (2012) characterized forty lines of rice named Kalanamak from different areas of uttar Pradesh regarding the quality of grains. In this study, aroma varied from very low to strong. Out of total varieties three variety expressed very low aroma, eleven varieties shows low aroma, twelve varieties expressed moderate aroma, rest fourteen varieties

expressed strong aroma characteristics. Gelatinizing temperature also varied in the varieties, where thirty three varieties expressed low gelatinizing temperature, six varieties expressed intermediate and one varieties expressed high gelatinizing temperature. Elongation ratio of the different kalanamak rice varieties varied between 1.60 to 2.33. This study indicated about the aromatic non Basmati rice varieties which should be maintained properly for the future rice improvement program and for economical reason.Chakrabarty et al. (2012) characterized ninety one farmers variety of southern west Bengal by the use of fifty two plant morphological traits and grain characters which were recorded for two years. It was revealed that there are many varieties which possess distinct characteristics for better genetic and economic values and will be used in future rice improvement and breeding program. Parikh et al. (2012) assessed 36 rice genotypes by using cooking quality and physico-chemical characters. It was revealed that like Kalimuchh, Munibhog and Rajim-12 which are the fine grain genotypes were good for Length:Breadth ratio and for moderate kernel length. Jhulari, Baghmuchha and Rajabhog for after cooking kernel length. Kalajira for Length:Breadth ratio of cooked rice. Genotype Bikoni for elongation ratio and for head rice recovery %; Barang, Bantaphool, Gangabalu genotypes were also good for elongation ratio. For elongation index, genotype Rajabhog, Barang, Bikoni, Gangabalu, and Chirainikhi and for intermediate alkali values Rajim-12, Jhulari, Sonth, Jhilli, Bikoni, Gangabalu and Safri were good. These genotypes will be useful in the improvement of quality traits in future rice breeding program. Tehrim et al.(2012) assessed Genetic polymorphism and relationships among 35 commercial varieties and primitive cultivars of Rice (*Oryza sativa* L.) by using random amplified polymorphic DNAs (RAPDs) primers. 14 primers produced a total of 126 different marker bands, of which 82.5% were polymorphic. The size range of the amplified DNAs was mostly between 0.2 and 3.63 kbp. Genetic distances obtained from RAPD data were used to create a cluster diagram. Three clusters formed from the cluster analysis. First cluster contains 15 genotypes, second cluster contains 16 and third cluster contains 4 genotypes. Cluster analysis placed most of the aromatic cultivars close to each other showing a high level of genetic relatedness. Lower levels of polymorphism in aromatic cultivars of rice indicated that there is a basic similarity among cultivars. A. K. Sinha AND P.K Mishra (2013) analysed 34 landraces of rice from Bankura District of west Bengal to identify the phenotypic diversity by using Morphology based multivariate analysis. 12 quantitative agro-morphological characters were taken. Five cluster groups were obtained by using (UPGMA), principal component analysis (PCA). PCA displayed the contribution of each characters to the classification of the rice landraces into different cluster groups. First three PCA explained about 86.9% of the total variation among the 12 characters. This analysis helps to identify the major traits and pattern of variation of the germplasm of landraces of rice. Results of PCA suggested that such phenotypic characters like leaf length, width, panicle length and grain size were the principal discriminatory characteristics of landraces of rice. Anjan Kumar Sinha and Mishra, P. K. (2013) investigated the agro-morphic characterization and relationship between 20 landraces of rice cultivars of Bankura District of West Bengal. Characterization was carried out for 20 qualitative and 13 quantitative morphological characters with 82 agro-morphic descriptors. In Cluster analysis of qualitative traits the cultivars were grouped into five clusters based on similarity coefficient of Jaccard. Pearson correlation matrix . Principal Component Analysis (Pearson –n type) and the unweighted variable pair group method of the average linkage cluster analysis (UPGMA-Person) were used to analyzed quantitative data. Using UPGMA four cluster groups were obtained from 13 quantitative agro-morphological characters. The present study indicated that morphological traits were useful for

preliminary evaluation for crop improvement program and can be used for assessing genetic diversity among morphologically distinguishable rice landraces.Ray et al.(2013) analyzed a suite of phenotypic characters from Indian landraces comprised of both aromatic and non-aromatic varieties. For that 414 varieties were selected. 29 phenotypic characters were selected. Principal co-ordinate analysis done with all 29 variables. Effective segregation of a majority of aromatic and non-aromatic landraces showed. In PCA, effective variance expressed. First, second and third component explained 29.11, 27.36 and 23.04 % respectively. Based on the loading and biplot, some morphological characters are the major determinants of phenotypic diversity like grain length, weight and width, leaf length,panicle density and plant height. Other characters seem to have a very minimal effects to variability. study indicated the effective segregation of aromatic and non-aromatic landraces, based on grain characters i.e, chosen from multivariate analyses. This has led to preservation, and enhancement of the allelic diversity in rice. Sarawgi et al. (2013) assessed seven hundred eighty-two germplasm of rice using eight agronomical and twenty-nine morphological traits. Most of the germplasm accessions possess green (72%) green leaf sheath colour, dark green intensity of leaf (60%), Absence of anthocyanin in leaf (90%), absence of anthocyanin in leaf sheath(82%),very weak anthocyanin intensity in leaf sheath (83%) , medium pubescence of Leaf blade surface (57%), presence of Leaf auricles (99.9%), light purple anthocyanin colouration of leaf auricles(59%), Absence of anthocyanin in Leaf collar (90%), white Leaf ligule colour(58%), semi erect Culm attitude (69%) etc With other different characteristics. Srivastava and Jaiswal (2013) characterized Twenty four aromatic indigenous Rice cultivars including aromatic short grain cultivars, basmati type and five high yielding rice varieties by using physico-chemical quality attributes and grain characteristics. Aromatic short grain varieties possessed intermediate position between basmati and non aromatic varieties on the basis of physical characteristics like grains length, breadth of kernel and related other traits. Subba Rao et al. (2013) characterized sixty five rice landraces by using forty three agromorphological traits. DUS test were done. Between total landraces thirty two landraces were detected as distinctive on regards of 24 additional characters and 22 essential characters. This study will help to identify, restoration and in conservation of rice landraces for future rice improvement program. Dinesh Prasad Semwal et al. (2014) studied Variability in seed morphology in 23 rice landraces using qualitative and quantitative characters collected from three districts (Dakshin Dinajpur, Uttar Dinajpur and Malda) of West Bengal, India during two exploration missions undertaken in summer and winter season (2012-2013). Cluster analysis classified 23 accessions into two major clusters (I and II) based on similarity in quantitative parameters (kernel size, kernel breadth, awn length and kernel weight). Traits such as kernel husk colour, seed coat colour, aroma, kernel size, 1000 kernel weight, presence of awn, awn length and Seven landraces viz., Dangibasful, Gauchi, Gogal sail, Gujanonia, Gujinina, Jeera sail and Lal cholis were collected for important traits such as drought and diseases tolerant. These data were also recorded. Information generated through seed morphology, cluster analysis and diversity study could be efficiently used in crop improvement programme harbouring different grain quality traits. Roy and Sharma (2014) assessed eighty four rice landraces from different agro-ecological regions areas of West Bengal regarding different quantitative and qualitative agro-morphological traits. The DUS test was done on the basis of 16 agro-morphological data such as vegetative(anthocyanin colouration, habit of plant) reproductive data (attitude of flag leaf, colour of stigma, panicle attitude) including eight grain quality traits (length of grains, width of grains, length of kernel, breadth of kernel ,weight of 1000 grains). Sarawgi et al. (2014) characterized some dwarf and

medium duration germplasm accessions of rice regarding seven agronomical and eighteen morphological traits. Variable expressions were recorded for most of the traits without shape of the ligule, colour of coleoptiles and presence of auricle. Variability showed in colours of green basal leaf sheath (87.25%), pubescent leaf (48.03%), awnless (88.48%), pubescent leaf (48.03%) straw sterile lemma (97.05%). etc with some other traits. Semwal et al.(2014) Studied diversity in seed morphology in 23 rice landraces using qualitative and quantitative characters from three districts of West Bengal. Between 23 genotypes 18 landraces had greyed-orange and greyed-yellow husk and six landraces had brown - greyed brown husk colour. Beside that, between all the landraces aroma was present in 18 landraces and Seventeen landraces were awnless and six landraces were with awn. Cluster analysis done based on quantitative characters. Dendrogram constructed which clustered 23 landraces into two major clusters groups. Major cluster - I comprised 15 landraces while cluster - II comprises eight landraces. Cluster - I further grouped in two sub-clusters on the basis of similarity in quantitative characters. Present study will help breeders to utilize appropriate characters in rice improvement programme. Girish Chandra Tiwari (2015) crossed Ten diverse genotypes of rice (OryzasativaL.) to study variability, heritability and genetic advance for 12 quantitative characters. Variability (gcv) varied from 5.95 for no. of leaves per tiller to 17.40 for grain yield per plant and the estimates of pcv varied from 7.08 for days to 50% flowering to 17.49 for grain yield per plant. Heritability ranged from 0.721 for total biological yield per plant to 1.000 for plant height. The genetic advance varied from 0.71 for no. of leaves per tiller to 46.23 for no. of spikelets per panicle. High genetic advance was reported for plant height, days to maturity, days to 50% flowering and total biological yield per plant. High heritability was associated with high predicted genetic advance for plant height, days to maturity, days to 50% flowering and nos. of spikelets per panicle. The estimates of phenotypic coefficient of variation were higher than those of genotypic coefficient of variation for all the traits except plant height. Muhammad et al. (2015) assessed thirty germplasms of indigenous rice by using thirty two different agro-morphological traits including 17 quantitative and 15 qualitative traits. Germplasms showed genetic variation for most of the traits except the ligule shape and anther color. Flag leaf length, breadth of flag leaf, length of culm, day required for 50% flowering, length of panicle, primary branches length per panicle, length and width of grain, length of awn, secondary branches length and percent leaf lesion expressed Highly significant differences (p<0.01) and length of peduncle and primary branches per panicle showed significant differences (p<0.05). ShanshanLiang et al.(2015) tried to identify patterns of genotype, environment, and GEI for GY of irrigated lowland rice. 392 cultivars or advanced breeding lines mostly from the International Rice Research Institute (IRRI), Phil Rice (Philippines) and a few breeding programs of other countries were evaluated for GY and related traits in eight environments including Jiangxi (JX) and Sichuan (SC) in China, and six season (2) and nitrogen rate (3) combinations at IRRI headquarters (LosBa˜nos, Philippines). Wide ranges of variations across genotypes and environments were observed for all traits. Genotype, environment, and GEI all significantly affected GY and some of the yield associated traits. The 303 genotypes with GY data in all environments were clustered into ten groups based on GY using an agglomerative hierarchical clustering procedure. The eight environments were grouped into three groups based GY using the additive main effects and multiplicative interaction (AMMI) analysis. Wambua F Kioko et al.(2015) characterized 13 varieties of rice from Kenya and Tanzania to identify phenotyic diversity and segregation strength. For that, multivariate analyses were done. In PCA analysis Seven principal component were accounted, between that first three PCA showed 99.5% of the total

variation between all the varieties studied. Cluster analysis clustered the 13 varieties into two major distinct groups. Similarity index showed 1.25 which indicated about the presence of high diversity. Ahmed et.al(2016) characterized twenty seven Jesso-Balam rice accessions of Bangladesh by using agro-morphological qualitative characterization. 21 qualitative agro-morphological characters were studied. Between the 21 characters, presence and shape of penultimate leaf ligule showed no variations. Genotypes were grouped into three major clusters using UPGMA cluster analysis based on Dice coefficient. Cluster III was the major group with maximum genotypes (26), while clusters I had two and cluster II had three genotypes respectively. Genetic distance ranged from 0.000 to 9.969. The Jesso-Balam pure lines possessed exclusive variability and unique features. Identified variability and unique features can be selected for developing varieties. Bineeta Devi (2016) characterized 64 exotic rice germplasm during Kharif 2011 for investigating the nature and magnitude of genetic diversity. Based on the analysis, the genotypes were clustered into 9 groups. Maximum number of genotypes of 27 were grouped under cluster III, 17 genotypes were grouped under cluster I, 10 genotypes were grouped under cluster II and 5 were grouped under cluster IV respectively, while clusters V, VI, VII, VIII, and IX had only one genotypes each. Highest inter cluster distance was observed between cluster IV and IX (2091.48) followed by cluster VII and IX (1893.05) which indicates the wider genetic diversity between genotypes. Among the traits, number of spikelets per panicle had maximum contribution towards the genetic divergence followed by plant height, panicle length and harvest index whereas number of panicle per hill and panicle length had no contribution towards the genetic divergence. A. K. Pachauri et al.(2017) assessed one hundred twenty four germplasm of rice by using eleven agronomical and nineteen morphological traits. Variation observed in a significant amount for most of the traits. Principal Component Analysis was done for analyze quantitative data.Four PCs only expressed more than 1eigen value, PC-1 expressed 37.12% variability, PC2, PC3 and PC4 showed 13.56, 11.04 and 10.76% variability, and detected about 72.48% cumulative variability between the traits studied. PCA revealed the traits like100 grain weight and No. of effective tillers were the main discriminatory characteristics. H.R. Uday Kumar et.al (2017) assessed 64 landraces of rice to identify genetic variability using phenotypic marker. Ten yield and its components trait were used for that purpose. This genotypes were observed with two replications under control and stress condition i;e low moisture stress condition. Higher magnitude of phenotypic and genotypic coefficient of variation for yield and yield attributing characters and very less difference indicated about the environmental factor which showed a great influence on the expression of characters. A narrow gap between GCV and PCV in maximum characters supports that. Under control condition grain yield traits had positive association with 50 percent flowering days and with days to maturity though test weight ,number of total tiller and productive tiller per plant , spikelet number per panicle, percent of spikelet fertility both under stress and control conditions at phenotypic and genotypic level. This study will help in selection process in future breeding programme. Manjunatha et al.(2018) characterize the sixty rice landraces of Wayanad, Kerala by using the Agro-morphological marker. They characterized both qualitative and quantitative characters by abiding the guidelines of (UPOV) and (PPV&FRA). 24 discriptors studied and between them five monomorphic characteristics, thirteen dimorphic, four trimorphic, one character (Basal leaf sheath colour) is tetramorphic , stem length (excluding panicle) showed five states of expression.This detailed characterization is very important for rice breeding, selection and conservation of different landraces. M. S. Ahmed et al.(2018) Characterized Fifty-four landraces of T. Aman rice to identify Morphological

diversity. For that purpose eleven morphological and yield related characters were selected. Mahalonobis D² statistic grouped the total germplasms in to 15 clusters. in cluster II highest intra-cluster distance (1.0) was detected and in the clusters III and XIII lowest (0.0) were observed. Inter-cluster D² values varied between 19.2 to 0.6 which indicated the wide diversity range between the landraces. Pinto et al.(2018) characterized sixty landraces of dryland rice with three cultivars of improved rice varieties to identify phenotypic diversity. For that purpose thirty one descriptors were taken. Out of total landraces thirty five landraces expressed mixture characteristics of Indica and Japonica groups where 24 landraces showed only Indica Group characteristics and four landraces expressed Japonica group characteristics. Cluster analysis clustered the total varieties in to four groups based on quantitative and qualitative characteristics. Rawte and Saxena (2018) Characterized the 100 landraces of Rice from Chhattisgarh to identify the Phenotypic Diversity and Correlation for Agro-Morphological Traits by using morphological markers. 32 different agro-morphological traits (20 qualitative and 12 quantitative) were taken. DUS test were performed. The rice landraces under study showed a wide range of distinctiveness for almost all the morphological traits studied with a Shannon diversity Index ranging from 0 – 1.223 with a mean of 0.548. The highest diversity index of 1.223 was observed for flag leaf attitude of the blade. The coefficient of variation was more than 10 % for most of the characters; Correlation coefficients showed that all the traits were highly correlated with each other. Grain yield per plot showed a highly significant and positive correlation with biological yield per plot ($r= 0.512$) and days to 50% flowering ($r= 0.299$). The present study can be utilized when traditional rice cultivars are screened for future breeding programs. Soe et al. (2019) analysed genetic diversity of 87 rice accessions from six countries by using morphological traits. Seventeen quantitative traits were recorded based on the guidelines of IRRI. Highly significant ($P<0.001$) differences were observed in all accessions. Correlation analyses revealed that, out of the 14 morphological and agronomic characters only 100 grain weight, tiller number, days to 50% flowering, panicle number, days to 80% grain maturity, ligule length and panicle length showed significant positive association with grain yield. Principal component analysis grouped the 17 quantitative traits collected into 10 components. At 21% similarity coefficient, Cluster analysis clustered the 87 accessions into seven main clusters based on morphological traits. Study revealed that germplasm would therefore be a useful source of genes for development of improved rice varieties. Anup Dhakal et al.(2020) analysed Phenotypic Diversity in 30 rice landraces of rice from Tanahun and Lamjung district in Nepal. For that purpose thirteen quantitative characteristics were selected. Principal component analysis and Mahalanobis distance (D²) were done. PCA showed that out of thirteen principal components five were significant and occupied to 29.96%, 20.26%, 13.56%, 11.68%, and 9.22% of total variance. Cluster analysis grouped the total landraces in to six clusters. Sharma et al. (2020) characterized thirty landraces of rice from Tanahun and Lamjung district of Nepal to identify agro-morphological diversity. For that purpose 8 quantitative and 30 qualitative characters were selected. Minimum and maximum value, coefficient of variation and Pearson correlation were calculated. Coefficient of variation varied from 5.4% to 20% indicated about the higher variation which is expected for effectiveness. UPGMA cluster analysis clustered the genotypes in to four clusters.

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