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# An appraisal of genetic variability and diversity among traditional red rice landraces

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## Abstract

The current investigation was carried out during kharif 2019 at Zonal Agricultural and Horticultural Research Station, Shivamogga using Randomised Complete Block Design with an objective of evaluating 30 red rice genotypes comprised of 26 landraces and four varietal checks. Genetic variability parameters like phenotypic and genotypic coefficients of variation were high for number of tillers per plant, number of productive tillers per plant and grain yield per plant. The traits *viz*., plant height, days to 50 per cent flowering, number of tillers per plant, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, test weight, grain length and breadth ratio and grain yield per plant recorded high broad sense heritability along with high genetic advance as per cent of mean. Using Mahalanobis' $D^2$ analysis genotypes were grouped into four divergent clusters. Cluster Ⅲ and cluster Ⅳ possessed maximum inter cluster distance between them suggesting that the genotypes falling under these clusters are genetically more diverse.

**Keywords:** genetic diversity, genetic variability, $D^2$ analysis, traditional landraces, red rice

## Introduction

Rice is central to the lives of billions of people all over the world. Nowadays, compared to commonly used white rice, red rice is gaining more importance because of its high nutritional profile. As rightly said by the great sage Parashara in the Sanskrit text Krishi-Parashara "Rice is vitality, rice is vigor too and rice indeed is the means of fulfillment of all ends in life. All, Gods, demons and human beings subsist on rice" (Majumdar and Banerji, 1960) [13], rice is the most vital foodstuff for majority of people. Hence, enhancement of its productivity and quality improvement becomes a never ending mission. Therefore broadening the genetic base of breeding stocks becomes crucial for constant enhancement in rice productivity and quality through crop improvement programs (Vanaja and Babu, 2004) [22]. All the available traditional red rice landraces are foundation for the breeding efforts needed to impart desirable quality traits and to sustain productivity in rice production. Traditional landraces are the valuable sources of variation that should be carefully conserved for the future crop improvement program Though high yielding varieties are paving the way to feed the increasing world population, but are causing the erosion of valuable landraces. Importance of landraces can never be ignored in agriculture system because improvement in any existing variety depends upon desirable genes that are possibly present in traditional landraces and wild varieties only. The fundamental requirement for any crop improvement program is the presence of genetic variation in a population. A wider range of genetic variability helps in selecting the desired genotypes of a population. A breeder must have a good understanding of genetic variability along with heritability and expected genetic advance to employ a suitable breeding strategy. Exploitation of this variation in plant breeding program requires initial determination of degree of genetic divergence. To exploit maximum heterosis, selection of divergent parents is the most important step in hybridization program. So enumeration of the genetic diversity existing between and within the genotypes is very much helpful in proper choice of the parents in exploiting maximum heterosis and obtaining useful recombinants. Mahalanobis' $D^2$ statistic is the most suitable method for estimating the degree of divergence existing among the genotypes.

## 2. Materials and methods

The present investigation was carried out at Zonal Agricultural and Horticultural Research Station (ZAHRS), Navile, Shivamogga, during Kharif 2019. The experimental material for the present study consisted of 30 red rice genotypes, which included 26 local red rice landraces of hill Zone of Karnataka and four improved red rice varieties (Table 1.). The experiment was laid out in Randomized Complete Block Design with two replications. The experimental material was sown to raise the nursery bed. 21 days old seedlings were transplanted manually into the main field with single seedling per hill. The distance between row to row and plant to plant was 20 cm and 25 cm, respectively. Gap filling was done within a week in order to maintain uniform plant population. Recommended dose of fertilizer was applied. The entire dose of phosphorus and potassium along with half dose of nitrogen was applied as basal dose at the time of field preparation and the remaining nitrogen dose was applied in two splits at 20 days interval in the standing crop. Five randomly selected plants from each genotype were labeled for recording the observations on the characters *viz*., days to 50 per cent flowering, days to maturity, plant height (cm), number of tillers per plant, number of productive tillers per plant, panicle length (cm), number of grains per panicle, number of filled grains per panicle, grain yield (g), test weight (g), grain length and breadth ratio. The average of observations recorded on these five plants was considered for statistical analysis. The data of mean value for all the characters were analyzed for their variance following Randomized Complete Block Design outlined by Cochran and Cox (1957) [6]. The genotypic and phenotypic variances were estimated using the formula given by Weber and Murthy (1952) [23].

$$\text{Genotypic variance } (\sigma^2{}_g) = \frac{\text{MSS (genotype)} - \text{MSS (error)}}{\text{Number of replications}}$$

$$\text{Phenotypic variance } (\sigma^2{}_p) = \sigma^2{}_g + \text{MSS (error)}$$

$$\text{PCV} = \frac{\sigma_p}{\overline{X}} \times 100$$

$$\text{GCV} = \frac{\sigma_g}{\overline{X}} \times 100$$

Where,
$\overline{X}$= grand mean of the character
$\sigma_p$= phenotypic standard deviation
$\sigma_g$= genotypic standard deviation

Mahalanobis' (1936) [12] $D^2$ statistic was used for assessing the genetic divergence between populations. The $D^2$ values were obtained as the corresponding uncorrelated (Ys) values of any two uncorrelated genotypes and all the (n-1)/2 $D^2$ values were clustered using Tocher method as described by Rao (1952)[17]. The intra and inter cluster distances were calculated by the formula given by Singh and Chaudhary (1977)[21]. All the statistical analyses were carried out using WINDOSTAT version 9.2 software.

## 3. Result and discussion

Highly significant difference was observed among all the 30 red rice genotypes with respect to all the evaluated traits from analysis of variance. Significant mean sum of squares for all the evaluated characters indicated that the studied genotypes were genetically diverse and exhibited a significant amount of variability in their mean performance for all the studied traits. The highest phenotypic and genotypic coefficients of variation was observed for the trait grain yield per plant (30.86 and 28.88 %) followed by number of productive tillers per plant (25.31 and 23.27 %) and the lowest PCV and GCV were observed for the trait days to maturity (7.57 and 7.55 %) followed by panicle length (9.67 and 9.23 %). In all the cases PCV was greater than GCV and a very narrow difference existed between PCV and GCV (Table 2.). High PCV and GCV values indicates that there is scope for the selection of these traits during yield improvement as they possess high genetic variability. High heritabilility coupled with high genetic advance was recorded for grain yield per plant and all the significant yield attributing traits except for days to maturity and panicle length which recorded moderate genetic advance as percent of mean. Similar results were observed by Sanghera *et al.* (2013) [19], Chuchert *et al*. (2016) [5], Anyaoha *et al.* (2018) [2], Patil (2014) [15], Singh *et al.* (2014) [20] and Battachraya and Chakraborty (2019) [3]. The Mahalanobis' $D^2$ statistic grouped 30 red rice genotypes into four clusters, where cluster II is the largest with 22 genotypes followed by cluster I with six genotypes and then by cluster III and IV each with only one genotype forming solitary clusters (Table 3.). The results were in harmony with the findings of Khalequzzaman *et al.* (2008) [8], Kumar (2015) [11], Khatun *et al.* (2015) [9] and Kodihalli and Dushyanthakumar (2014) [10]. Cluster II displayed maximum intra cluster distance followed by cluster I, indicating that the genotypes belonging to cluster II and cluster I were relatively more diverse than the genotypes within other clusters (Pandey *et al*., 2009)[14]. Hence, they could be utilized in hybridization program due to the existence of greater diversity within themselves. Inter cluster distance between cluster III and IV (5964.93) was found to be maximum followed by clusters I and III (4087.73). However, the least inter cluster distance was observed between cluster I and IV (765.19) followed by clusters II and III (872.99) (Table 4.). The results were in accordance with the reports of Pandey *et al*. (2009) [14]. Hence the genotypes belonging to cluster III and IV were considered to be most divergent followed by genotypes under cluster I and III The maximum inter cluster distance suggests the existence of wider genetic diversity among the genotypes belonging to these clusters and the genotypes under these clusters could be used as parents in hybridization programs to obtain transgressive segregants (Saini and Kaiker, 1987) [18]. While, the minimum inter cluster distance indicates that the genotypes falling into these clusters are genetically close (Akter *et al*., 2018) [1] and could exploit least heterosis upon hybridization. Yield improvement in any crop through indirect selection depends on selection of traits having direct positive effect on yield. These traits should be selected from the clusters, showing the highest mean values for these characters. Cluster II exhibited the highest mean values for the traits *viz*., panicle length, number of grains per panicle and number of filled grains per panicle. While, desired mean values for number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle and test weight were observed in cluster I and cluster III displayed high mean values for plant height, days to 50 per cent flowering, days to maturity and grain yield per plant (Table 5.). The genotypes are selected from these clusters showing desired mean values for yield attributing traits for hybridization program to obtain desired segregants with higher yield. Reports of Dushyanthakumar (2008) [7] and Kumar (2015) [11] are in conformity with the above results.

The maximum per cent contribution towards divergence was made by days to 50 per cent flowering followed by test weight, grain length and breadth ratio, grain yield per plant, plant height, number of filled grains per panicle, panicle length and number of tillers per plant. And the least contribution towards divergence was made by the trait days to maturity (Fig 1.).

Days to 50 per cent flowering contributed 56 per cent towards total divergence indicating that the genotypes differed significantly with respect to flowering time. The findings of Patil *et al.* (2005) [16] are in conformation with the above results.

**Table 1:** List of 30 red rice genotypes used in the experiment

| Sl. No. | Genotypes | Sl. No. | Genotypes |
|---|---|---|---|
| 1 | Balesuli | 16 | Magadsugantha |
| 2 | Bilidaddi budda | 17 | Mahalaya |
| 3 | Budda | 18 | Mottaikar |
| 4 | Edikuni | 19 | Meesebatha |
| 5 | Kaisari | 20 | Sanna raja kaimae |
| 6 | Kangalli | 21 | Shankitha |
| 7 | Karana | 22 | Shivadappavalya |
| 8 | Karidaddi valya | 23 | Sidesale |
| 9 | Karimundige | 24 | Tulasimog |
| 10 | Kartha | 25 | Valtiga |
| 11 | Kempudadi | 26 | Sambamousam |
| 12 | Kempusanna | 27 | KHP-10 (Check) |
| 13 | Krishnaleela | 28 | Sahyadri Kempumukthi (Check) |
| 14 | Keervana | 29 | Sahyadri Megha (Check) |
| 15 | Madyadadodda | 30 | Jyothi (Check) |

**Table 2:** Genetic variability parameters for yield and yield related characters in 30 red rice genotypes

| Sl. No. | Character | Mean ±SEm | Range | | PCV (%) | GCV (%) | $h^2$ (bs) (%) | GAM (%) |
|---|---|---|---|---|---|---|---|---|
| | | | Min | Max | | | | |
| 1 | Plant height (cm) | 146.00 ± 1.91 | 83.53 | 194.79 | 16.44 | 16.33 | 98.68 | 33.43 |
| 2 | Days to 50 *per cent* flowering | 99.93 ± 0.43 | 75.50 | 115.50 | 10.11 | 10.09 | 99.62 | 20.75 |
| 3 | Days to maturity | 131.18 ± 0.55 | 107.00 | 146.50 | 7.57 | 7.55 | 99.36 | 15.49 |
| 4 | Number of tillers plant$^{-1}$ | 16.12 ± 1.10 | 8.00 | 23.00 | 23.61 | 21.45 | 82.59 | 40.16 |
| 5 | Number of productive tillers plant$^{-1}$ | 13.92 ± 0.96 | 7.00 | 19.00 | 25.31 | 23.27 | 84.53 | 44.08 |
| 6 | Panicle length (cm) | 24.81 ± 0.50 | 19.84 | 29.00 | 9.67 | 9.23 | 90.84 | 18.10 |
| 7 | Number of grains panicle$^{-1}$ | 143.29 ± 9.03 | 86.00 | 197.00 | 18.81 | 16.48 | 76.79 | 29.75 |
| 8 | Number of filled grains panicle$^{-1}$ | 118.08 ± 8.17 | 71.00 | 159.00 | 19.45 | 16.71 | 73.81 | 29.58 |
| 9 | Test weight (g) | 27.51 ± 0.38 | 15.62 | 34.76 | 17.36 | 17.24 | 98.68 | 35.28 |
| 10 | Grain length and breadth ratio | 2.97 ± 0.041 | 2.43 | 4.73 | 16.35 | 16.23 | 98.53 | 33.18 |
| 11 | Grain yield *per* plant (g) | 28.42 ± 2.15 | 14.90 | 49.55 | 30.86 | 28.88 | 87.57 | 55.66 |

Where, GCV- Genetic Coefficient of Variation PCV- Phenotypic Coefficient of Variation $h^2$(bs)- Broad sense heritability GAM- Genetic advance as *per cent* of mean

**Table 3:** Clustering pattern of 30 red rice genotypes based on $D^2$ values

| Clusters | No. of genotypes | Genotypes |
|---|---|---|
| **I** | 6 | Budda, Jyothi, Mottaikar, Sahyadri Kempumukthi, Sahyadri Megha, Shankitha |
| **II** | 22 | Balesuli, Bilidaddi budda, Edikuni, Kaisari, Kangalli, Karana, Karidaddivalya, Kartha, Kempudadi, Krishnaleela, Keervana, KHP-10, Madyadadodda, Magadsugantha, Mahalaya, Meesebatha, Sambamousam, Sanna raja kaime, Shivadappavalya, Sidesale, Tulasimog, Valtiga |
| **III** | 1 | Kempusanna |
| **IV** | 1 | Karimundige |

**Table 4:** Intra and Inter cluster distances for yield and its component characters in 30 red rice genotypes

| Clusters | I | II | III | IV |
|---|---|---|---|---|
| I | 395.51 | 1867.15 | 4087.73 | 765.19 |
| II | | 441.44 | 872.99 | 3258.28 |
| III | | | 0.00 | 5964.93 |
| IV | | | | 0.00 |

**Table 5:** Cluster means for yield and yield contributing characters in 30 red rice genotypes

| Cluster/ character | $X_1$ | $X_2$ | $X_3$ | $X_4$ | $X_5$ | $X_6$ | $X_7$ | $X_8$ | $X_9$ | $X_{10}$ | $X_{11}$ |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **I** | 114.69 | 85.75 | 117.50 | 18.16 | 15.81 | 24.39 | 141.78 | 117.33 | 31.43 | 2.79 | 27.22 |
| **II** | 154.21 | 104.20 | 135.32 | 15.82 | 13.59 | 24.98 | 146.12 | 119.84 | 27.04 | 2.99 | 27.99 |
| **III** | 182.62 | 115.50 | 146.50 | 8.00 | 6.64 | 24.05 | 112.00 | 97.50 | 23.60 | 3.78 | 33.65 |
| **IV** | 116.67 | 75.50 | 107.00 | 16.50 | 15.24 | 23.37 | 121.67 | 104.50 | 18.33 | 2.89 | 27.79 |

$X_1$ = Plant height (cm), $X_2$ = Days to 50 % flowering, $X_3$ = Days to maturity, $X_4$ = Number of tillers per plant, $X_5$ = Number of productive tillers per plant, $X_6$ = Panicle length (cm), $X_7$ = Number of grains/panicle, $X_8$ =Number of filled grains/panicle, $X_9$ = Test weight (g), $X_{10}$ = Grain length and breadth ratio, $X_{11}$ = Grain yield per pla

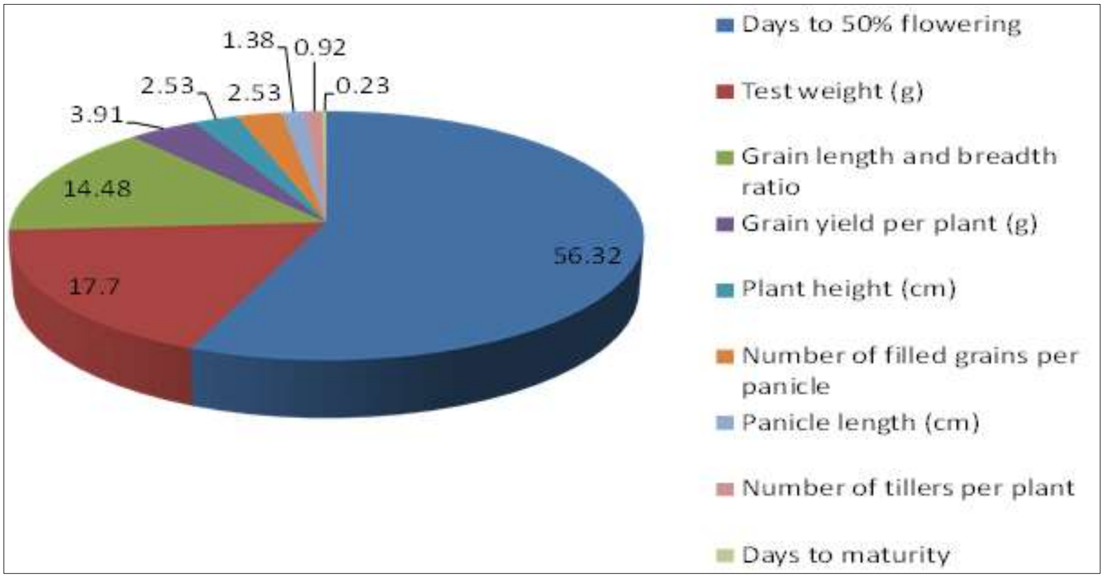

**Fig 1:** Percent contribution different traits towards total divergence

## 4. Conclusion

The analysis of variance revealed highly significant differences among the 30 red rice genotypes for grain yield and yield attributing traits indicated the presence of sufficient variability for all the traits under the study. From the genetic variability studies, it was confirmed that PCV was higher than GCV for all the evaluated traits, suggesting that environmental influence on the expression of all the traits is less. According to the results of $D^2$ analysis, maximum inter cluster distance was observed between clusters III and IV. Therefore, genotypes belonging to these clusters are more diverse and could exploit maximum heterosis in future crossing program. Thus the studied rice genotypes were genetically diverse and possess significant variation for all sthe evaluated yield and yield related traits. Hence, could be utilized in crop improvement program.

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