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Genetic divergence study in traditional local landraces of rice (*Oryza sativa* L.) predominant in Bastar Plateau Zone of Chhattisgarh

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ABSTRACT : 100 local landraces of rice from Bastar plateau of Chhattisgarh state along with five check varieties were studied for genetic diversity on the basis of nineteen quantitative characters using Euclidian distance between genotypes. This analysis allowed the 105 genotypes of rice to be identified into ten distinct clusters. Among the different clusters, cluster III contained maximum of 46 genotypes and cluster I, II and X contained a minimum of 1 genotype each. Cluster I was characterized by highest mean value for number of effective tillers per hill, spikelet fertility and grain length breadth ratio. Cluster VII had highest mean value for harvest index. The cluster VIII was characterized by highest mean value for flag leaf length, panicle length, number of fertile spikelets per panicle and total number of grains per panicle. The cluster IX was characterized by highest mean value for grain yield per plant, days to 50 per cent flowering, days to maturity, plant height, test weight and grain breadth. The highest inter cluster distance was observed between cluster II and VIII while the lowest between III and IX. The lowest intra cluster distance was observed in cluster I, II and X while highest intra cluster distance was observed in cluster IX. There is good scope to bring about genetic improvement in rice through hybridization and selection by crossing accessions from different clusters.

KEY WORDS : Genetic divergence, Euclidian distance, Cluster analysis, Rice landraces

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Rice is one of the most important cereal crops in the world and provides more than 50 per cent of the calories consumed by humans in Asia (Khush, 1997). Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations. For the same, genetic distance plays a vital role, as the parental diversity in optimum magnitude is required to obtain superior

genotypes in segregating population (Varshney *et al.*, 2008). A successful breeding programme will depend on the genetic diversity of a crop for achieving the goals of improving the crop and producing high yielding varieties. Study of genetic diversity assists the plant breeders in selecting appropriate materials for further genetic improvement of cultivars and effective management of rice genetic resources. Morphological characterization

is the first step in classification and evaluation of the germplasm (Smith *et al.*, 1991). In order to develop high yielding varieties it is essential to select parental lines which have high yielding traits. The available diversity in the germplasm serves as an insurance against unknown future needs. The more the diversity is conserved and made available for future use the better the chance of fulfilling the future demand. The breeders are interested to evaluate genetic diversity based on morphological traits because they are inexpensive, rapid, and simple to score. Hence, the present investigation was attempted to assess the nature and magnitude of genetic diversity among the genotypes on the basis of different quantitative traits for further utilization in breeding programmes.

RESEARCH PROCEDURE

The experimental materials comprised of hundred local landraces of rice collected from Bastar plateau zone of Chhattisgarh and five popular standard check varieties namely CR 40, Danteshwai, Maheshwari, MTU 1010 and MTU 1001. Twenty one days old seedlings were subsequently transplanted into the field in Augmented Block Design (ABD) wherein test entries were sown only once and checks were replicated. This experiment was conducted during *Kharif*, 2015-16. The experimental material was planted in four blocks and each block comprised of 25 genotypes and five checks. Each entry was transplanted in single row. Spacing of 20 cm between

rows and 15 cm between plants were maintained. The check varieties were randomized within block. Observations were recorded on five randomly selected plants from each row for 19 morphological characters *viz.*, harvest index, days to 50 per cent flowering, days to maturity, flag leaf length, flag leaf width, plant height, panicle length, number of effective tillers per plant, number of filled spikelets per panicle, spikelet sterility percentage, test weight, grain length, grain breadth, grain length:breadth ratio, kernel length, kernel breadth, kernel length:breadth ratio, total number of grains per panicle and grain yield per plant. In the present study, the analysis of genetic divergence was done using Euclidian distance between genotypes which was calculated from the standardized data matrix by unweighted pair group method using arithmetic averages (UPGMA) method and clustering was done by Agglomerative Hierarchical method using XLSTAT, 2014 software and the material was grouped into different clusters.

RESEARCH ANALYSIS AND REASONING

The analysis of variance for 19 quantitative characters showed that there were considerable inherent genetic differences among check varieties for different characters studied. Analysis performed by unweighted variable pair group method of the average linkage cluster analysis (UPGMA) using Euclidean distance as dissimilarity measure divided the 105 accessions of rice

Table 1: Distribution of 105 rice accessions among ten clusters

| Cluster number | Number of genotypes | Genotypes name |
|----------------|---------------------|---|
| I | 1 | MTU 1010 |
| II | 1 | Danteshwari |
| III | 46 | CR 40, MTU 1001, Maheshwari, SofaKaan, Vishnubhog, Gurmatiya, Kurludhaan, Gangabaaru, Machripoti, Madiadhaan, Photkidhaan, Jatiya, Pandrilochai, Kaalaumari, Mankidhaan, Mokdo, Aasanchudi, Kusumjhopa, Kukdimundi, Gechidhaan, RaniKaajar, Baadilochai, Kantabargi, Laal Bansa, Rangadakhuta, Dogarkaabri, Kaatamehar, Pilkosnai, Lochai, Milkoor Mail, Begnidhaan, Guthiya, Badekhuji, Motilur, Haldigodi, Dhadhardhaan, Sargiphool, Laalbargi, Karigrass, Khujidhaan, Gada Khuta, Kaalamaali, Pandrisatka, Sela, Ram-Laxman, Pakhiyadhaan. |
| IV | 16 | Turejagadakhuta, Ghotiyadhaan, Sorchubaadi, Naani Chudi, Hansa Dubraj, Chiradhaan, KursoBhog, Basomati, Teenkormail, Kumda Phool, Bagdi Chudi, Gongel, Goydi, Dhaagan, Keraphool, Dubraj. |
| V | 7 | Kaakad Kado, Jhumra, Baadichudi, Kolyara, Bhokvadhaan, Shivdharohar, Khudbudi. |
| VI | 11 | Rangchudi, Aanjan, Adgadhaan, Pharadhaan, Pakhiyadhaan, Jondranakti, Rakhidhaan, Meharaldhan, Bhatamokdo, Haldijeera, Sendursenga. |
| VII | 11 | Safurlochai, Masuridesi, Kukdi, Sonasaari, Olesar, Muthiya, Dengichud, Madras Chudi, Baudi, Bahiyakhuta, Bhayar. |
| VIII | 8 | Baanskantiya, Mayurdhaan, Jeeradhaan, Baadshah Bhog, Idiraghotiya, Baadigoydi, Umarichudi, Mundrichudi. |
| IX | 3 | Baasta Bhog, Sonpuri, Haldigaathi. |
| X | 1 | Kabrodhan |

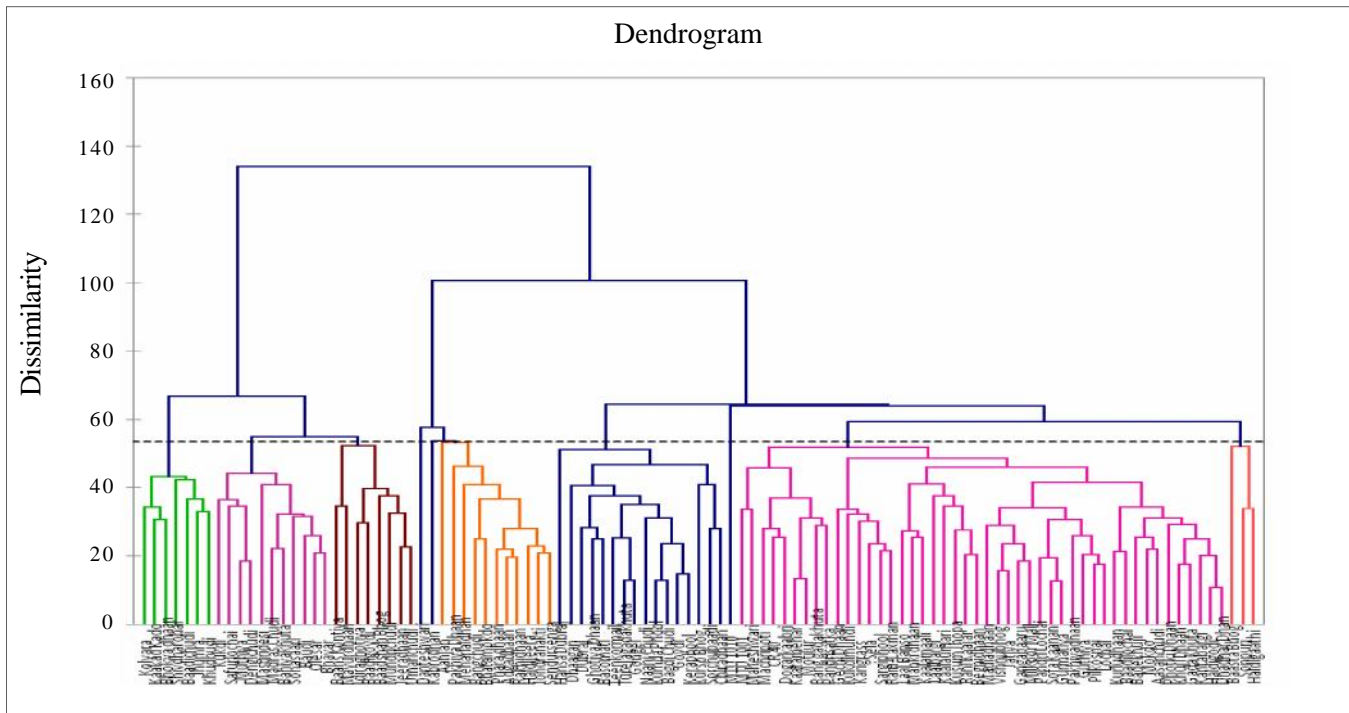


Fig. 1 : Dendrogram depicting distribution of genotypes

into ten clusters. The accessions were not evenly distributed among the clusters (Table 1 and Fig. 1). The cluster III constituted of 46 accessions, forming the largest cluster followed by cluster IV (16 accessions), cluster VI and VII (11 accessions each), cluster VIII (8 accessions), cluster V (7 accessions), cluster IX (3 accessions) and cluster I, II and X (only one accessions each). The pattern of group constellation proved the existence of significant amount of variability. The clustering pattern of genotypes revealed that, most of the genotypes released/ recommended for state were clubbed together in one group (clusters I, II and III). The other genotypes clubbed together with cluster III might be the valuable sources for further improvement of well adapted local landraces of zone. The clusters I, II, and X were represented by single genotype indicating high degree of heterogeneity among the genotypes. The clustering distribution of some other clusters indicated that the genetic diversity found among the genotypes belonging to same geographic origin (Bastar region) might be due to differences in adaptation, selection criteria, selection pressure and environmental condition (Vivekanandan and Subramanian, 1993 and Nayak *et al.*, 2004).

The cluster mean values showed a wide range of

variations for all the characters undertaken in the study (Table 2). Cluster I exhibited highest mean value for number of effective tillers per plant (10), spikelet fertility (87.30) and grain length breadth ratio (3.76) while cluster II contained genotypes with highest mean value for grain length (9.85), kernel length (7.42) and kernel length breadth ratio (3.73) while highest mean value for harvest index (52.74) was recorded by cluster VII. Cluster VIII had highest value for flag leaf length (35.83), panicle length (25.13), number of fertile spikelets per panicle (230.48) and total number of grains per panicle (293.96) whereas, cluster IX had highest value for grain yield per plant (24.71), days to 50 per cent flowering (109.94), days to maturity (145.28), plant height (159.11), test weight (27.22) and grain breadth (3.35). Cluster X had highest value for flag leaf width (2.06) and kernel breadth (2.98). These results are in confirmation with the findings of Chanbeni *et al.* (2012); Shiva *et al.* (2013) and Apsath and Venkatesan (2015).

The average inter and intra cluster distances among ten clusters were computed and have been given in Table 3. The intra cluster distance ranged from 0.00 to 33.58. Highest intra cluster distance was found in cluster IX (33.58) followed by cluster III (33.14) and cluster VIII (31.57) while, lowest intra cluster distance was found in

cluster I, II and X (0.00) each. High intra cluster distance indicates wide genetic divergence among the constituent genotypes. The inter cluster distance was maximum between cluster II and VIII (15.35) followed by cluster VI and VIII (15.11) and cluster II and VII (14.50) suggesting that these groups of genotypes were highly divergent from each other. The genotypes in above clusters revealed substantial differences in the means for

important yield contributing characters, suggesting that the genotypes belonging to these clusters form ideal parents for initiating hybridization. The minimum inter cluster distance was observed between cluster III and cluster IX (6.05) indicating that the genotypes of these clusters were genetically very close to each other. To realize much variability and high heterotic effect, parents should be selected from two clusters having wider inter

Table 2: Cluster mean values of ten clusters for different characters in varying genotypes of rice

| Characters | Clusters | | | | | | | | | |
|------------|----------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| | I | II | III | IV | V | VI | VII | VIII | IX | X |
| HI | 47.81 | 44.76 | 42.77 | 52.12 | 39.86 | 32.27 | 52.74 | 41.2 | 51.8 | 11.96 |
| GYP | 24.27 | 5 | 16.61 | 21.28 | 16.64 | 10.84 | 24.01 | 19.52 | 24.71 | 0.78 |
| DTF | 87.35 | 75.65 | 100.09 | 106.88 | 94.76 | 90.91 | 104.19 | 98.64 | 109.94 | 89.83 |
| DTM | 115.3 | 109.85 | 124.82 | 138.17 | 109.44 | 115.82 | 130.11 | 128.71 | 145.28 | 115.87 |
| FLL | 27.8 | 23.55 | 33.61 | 32.68 | 35.11 | 35.47 | 33.89 | 35.83 | 33.63 | 30.96 |
| FLW | 1.45 | 1.3 | 1.64 | 1.63 | 1.75 | 1.56 | 1.7 | 1.58 | 1.65 | 2.06 |
| PH | 87.85 | 78.45 | 131.24 | 134.89 | 127.07 | 123.74 | 133.73 | 136.29 | 159.11 | 101.86 |
| PL | 21.95 | 21.45 | 24.4 | 24.86 | 24.42 | 23.34 | 24.88 | 25.13 | 25.06 | 19.81 |
| NETH | 10 | 6.2 | 5.86 | 5.9 | 5.68 | 6.12 | 5.16 | 5.88 | 6.27 | 5.02 |
| NFSP | 159.33 | 88.58 | 137.44 | 165.72 | 192.3 | 90.62 | 218.47 | 230.48 | 129 | 111.2 |
| SF | 87.3 | 80.07 | 81.08 | 80.74 | 81.28 | 86.14 | 84.08 | 78.63 | 85.27 | 83.65 |
| TW | 25.15 | 22.83 | 25.65 | 25.92 | 19.06 | 26.24 | 23.68 | 16.73 | 27.22 | 22.25 |
| GL | 9.28 | 9.85 | 8.25 | 8.22 | 7.93 | 8.37 | 7.84 | 7.29 | 8.59 | 6.1 |
| GB | 2.49 | 2.77 | 2.96 | 3.11 | 2.5 | 3.08 | 2.98 | 2.74 | 3.35 | 3.21 |
| G L:B | 3.76 | 3.57 | 2.91 | 2.63 | 3.26 | 2.8 | 2.72 | 2.72 | 2.59 | 2.2 |
| KL | 6.96 | 7.42 | 6.04 | 5.98 | 5.62 | 6.14 | 5.65 | 5.35 | 6.13 | 4.87 |
| KB | 1.99 | 1.99 | 2.4 | 2.52 | 2.01 | 2.42 | 2.31 | 2.24 | 2.5 | 2.98 |
| k L:B | 3.51 | 3.73 | 2.58 | 2.57 | 2.92 | 2.55 | 2.58 | 2.47 | 2.58 | 1.67 |
| TNGP | 182.25 | 111 | 170.12 | 206.1 | 238.42 | 105.58 | 259.53 | 293.96 | 150.92 | 133.18 |

Note: HI=Harvest index, GYP=Grain yield/plant, DTF= Days to 50 per cent flowering, DTM = Days to maturity, FLL= Flag leaf length, FLW= Flag leaf width, PH= Plant height, PL= Panicle length, NETH= Number of effective tillers/plant, NFSP= Number of fertile spikelets/panicle, SF= Spikelet fertility, TW= Test weight, GL= Grain length, GB=Grain breadth, G L:B ratio=Grain length:breadth ratio, KL= Kernel length, KB=Kernel breadth, K L:B ratio= Kernel length:breadth ratio, TNGP= Total number of grains/panicle

Table 3: Estimates of intra (diagonal and bold) and inter cluster distances among ten clusters

| Class | I | II | III | IV | V | VI | VII | VIII | IX | X |
|-------|------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| I | 0.00 | 10.20 | 8.12 | 7.83 | 9.10 | 10.67 | 10.60 | 11.85 | 9.54 | 9.10 |
| II | | 0.00 | 10.13 | 11.91 | 13.19 | 7.30 | 14.50 | 15.35 | 10.71 | 7.39 |
| III | | | 33.14 | 7.39 | 9.82 | 9.17 | 11.29 | 12.34 | 6.05 | 8.46 |
| IV | | | | 29.71 | 8.12 | 11.63 | 8.90 | 10.45 | 8.42 | 10.67 |
| V | | | | | 29.02 | 12.86 | 7.44 | 8.28 | 11.06 | 11.69 |
| VI | | | | | | 28.64 | 14.34 | 15.11 | 9.65 | 6.70 |
| VII | | | | | | | 28.33 | 6.30 | 12.07 | 13.29 |
| VIII | | | | | | | | 31.57 | 13.12 | 14.16 |
| IX | | | | | | | | | 33.58 | 9.64 |
| X | | | | | | | | | | 0.00 |

cluster distance (Mishra *et al.*, 2004 and Chaturvedi and Maurya, 2005).

The selection and choice of parents mainly depends upon contribution of characters towards divergence (Table 4). It is well known that crosses between divergent parents usually produce greater heterotic effect than between closely related ones. Grain yield per plant (12.20) showed maximum contribution to the total divergence, followed by harvest index (8.33), total number of grains per panicle (7.90), number of fertile spikelets per panicle (7.84) and lowest contribution was found of spikelet fertility % (2.33).

| Sr.No. | Variables | Contribution (%) |
|--------|-----------------------------------|------------------|
| 1. | Harvest index (in %) | 8.33 |
| 2. | Gain yield/plant. (g) | 12.2 |
| 3. | Days to 50% flowering (in DAS) | 2.67 |
| 4. | Days to maturity (in DAS) | 3.03 |
| 5. | Flag leaf length (cm) | 4.2 |
| 6. | Flag leaf width (cm) | 3.53 |
| 7. | Plant height (cm) | 3.26 |
| 8. | Panicle length (cm) | 2.77 |
| 9. | No. of effective tillers/plant | 6.01 |
| 10. | No. of fertile spikelets /panicle | 7.84 |
| 11. | Spikelet fertility (in %) | 2.33 |
| 12. | Test weight (in g) | 6.08 |
| 13. | Grain length(in mm) | 3.9 |
| 14. | Grain breadth (in mm) | 3.74 |
| 15. | Grain L:B ratio | 6.76 |
| 16. | Kernel length (in mm) | 3.87 |
| 17. | Kernel breadth (in mm) | 4.5 |
| 18. | kernel L:B ratio | 7.08 |
| 19. | Total no. of grains /panicle | 7.9 |

Conclusion :

Considering the importance of genetic distance and relative contribution of characters towards total divergence, the present study indicated that parental lines selected from cluster II (Danteshwari) for grain quality characters like grain length, kernel length and kernel length:breadth ratio and from cluster VIII (Baanskontiya, Mayurdhaan, Jeeradhaan, Baadshah- bhog, Idiraghotiya, Baadigoydi, Umarichudi, Mundrichudi) for characters like number of fertile spikelets per panicle, total number of

grains per panicle, flag leaf length and panicle length could be used in crossing programmes to achieve desired recombinants.

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