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# Estimation of Variability for Grain Yield and Quality Traits in Rice (*Oryza sativa* L.)

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## ABSTRACT

*Analysis of variance revealed highly significant differences among 27 genotypes for all the yield components and most of the kernel quality traits except hulling percent, volume expansion ratio and water uptake indicating that enough variability is present in the studied material. The magnitude of difference between PCV and GCV was less for the traits indicating little influence of environment. The higher estimates of PCV and GCV were observed for yield per plant (42.42;42.04) and filled seeds per panicle (34.67;33.19) indicates possibility of genetic improvement through direct selection for these traits, while hulling percent, milling percent, kernel elongation ratio, day to 50% flowering, panicle length, kernel length and kernel width showed low PCV and GCV values indicating the need for creation of variability by hybridization or mutation followed by selection.*

*High heritability in broad sense and high genetic advance as percent of mean exhibited by the traits, effective tillers (88.8; 30.2), plant height (96.0; 35.3), flag leaf length (84.0 ; 32.8), filled seeds per panicle (96.0;68.7) test weight ( 96.0; 39.1), yield per plant (98.0;68.7) ,head rice recovery (94.0; 27.7) and length/breadth ratio (93.0 ; 20.4) indicating preponderance of additive gene action, which provide good scope for further improvement by selection.*

***Key words**: Genetic Variability, Heritability, Grain Yield, Quality Traits, Rice*

## INTRODUCTION

Rice is one of the most important cereal crop of the world meeting the dietary requirements of the people living in the tropics and sub tropics. Traditionally rice plant breeders concentrated on breeding for high yield. In recent decades as living conditions are being steadily improved, human demand for high quality rice is continuously on increase, which entailed in incorporation of preferred grain quality features as the most important objective next to enhancement in yield. Like grain yield, quality is not easily amenable to selection due to its complex nature and depends on its several components. These components were further depend for their expression on several morphological traits which interrelated with each other showing a complex chain of relationship and also highly influenced by the environmental conditions.

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Lack of clear cut perception regarding the component traits of good quality rice is one of the important reasons for the tardy progress in breeding for quality rice varieties. With increase in yield, there is also a need to look into the quality aspects to have a better consumer acceptance, which determines the profit margin of rice growers which intern dictates the export quality and foreign exchange in India. Therefore the parents selected for the breeding programme aimed at increased grain yield should possesses wide range of genetic variability for the character. Besides it could be of important to know the magnitude of variation due to heritable component which intern would be a guide for selection for the improvement of a population. Keeping in view above perspectives, the present investigation is carried out with the objective of estimating the genetic variability for yield, yield contributing character and quality traits and their heritability and genetic advance which would help in selection and further improvement of rice genotypes For the development of high yielding varieties with good quality the information on variability and genetic parameter of grain quality attributes and their association with each other including grain yield is necessary to formulate suitable breeding strategies for grain quality improvement.

## MATERIALS AND METHODS

The experimental material used in the study consists of 27 genotypes of rice grown in a completely randomized block design with three replications at Regional Agricultural Research Station, Warangal during kharif 2014. Twenty five days old seedling of each genotypes were transplanted in three rows of 2.0 m length by adopting a spacing of 20 cm between rows and 15 cm between plants, with in the rows at the rate of 20 plants per row. The crop was grown with the application of fertilizers, N, P and K at the rate of 120:60:40 kg/ha respectively. Standard agronomic practices were followed to raise a good crop. A composite sample of 10 plants from the middle row was used to record observation on these plants for plant height, effective tillers per $m^2$ ,plant height, panicle length, flag leaf length, flag leaf width, filled seeds per panicle,test weight, yield per plant, except days to 50% flowering which was computed on plot basis. Data was recorded on physical, chemical quality characters viz hulling percent, milling percent, head rice recovery kernel length, kernel width, length/breadth ratio, kernel length after cooking, kernel breadth after cooking, elongation ratio, alkali spreading value, volume expansion ratio and water uptake.

Observations on hulling and milling were taken with the help of SATAKE company make laboratory huller and polisher. The milling characterizers were computed. Data on head rice recovery was recorded. Kernel length and kernel width of 20 whole milled rice were measured by means of dial caliper and length/breadth ratio was computed as per Murthy *et al.*[13]. Kernel elongation was determined by soaking 5 g of whole milled rice in 12 ml distilled water for 10 minutes and later cooked for 15 minutes in water bath. Observations on length and breadth of cooked kernels and elongation ratio were recorded with the help of graph sheet to quantify cooking traits. Water uptake, volume expansion ratio, alkali spreading value were estimated by following the standard procedures.

The treatment means for all the characters were subjected to analysis of variance techniques on the basis of model proposed by Panse and Sukhatne[16]. The genotypic and phenotype variances were calculated as per the formulae proposed by Burton[3]. Heritability in broad sense ($h_b^2$ ) was calculated by the formula given by Lush[11] as suggested by Johnson *et al.*[8]. From the heritability estimates, the genetic advance (GA) was calculated by the following formula given by Johnson *et al.*[8].

## RESULTS AND DISCUSSION

Genetic variability in any crop is pre requisite for selection of superior genotypes over the existing cultivars. The analysis of variance indicated the existence of significant differences among all genotypes for all the characters except hulling percent, volume expansion rate and water up take indicating the existence of sufficient amount of variability (Table-1). The results were in confirmity with the earlier findings of Dhanwani *et al.*[5] and Dhurai *et al.*[6] for all the traits, Abdus salam *et al.*[1] for volume expansion ratio.

The range of mean variation observed among yield components and kernel quality characters revealed that highest range of mean variation was noticed for number of filled grains per panicle (245) and effective tillers (202) whereas the range was found to be least for elongation ratio (0.29) and volume expansion ratio (0.6) (Table-2). The results were in consonance with the finding of Venkata *et al.*[20]. Similarly the highest magnitude of phenotypic and genotypic variance was registered for filled grain per panicle (5425.1), effective tillers (2547.8), water uptake (1353.0) and head rice recovery (76.6), while least estimates were recorded for kernel width (0.031), flag leaf width (0.06) kernel breath after cooking (0.07).

The magnitude of phenotypic coefficient of variation (PCV) in general was found to be higher than genotypic coefficient of variation (GCV) for all the characters studied indicated the influence of environment on the manifestation of these characters. However the difference between PCV and GCV was less for the traits day to 50% flowering plant height, test weight, yield per plant, head rice recovery, kernel length, kernel width, length/breadth ratio and kernel length after cooking. Similar results were observed by Dhurai *et al* .[6]. Large difference between PCV and GCV values reflects high environmental influence on the expression of traits. Among the characters the higher estimates of PCV and GCV were observed for yield per plant (42.04) and filled seeds per panicle (33.9). This indicates the existence of wide genetic base among the genotypes taken for study and possibility of genetic improvement through direct selection for these traits. These results are also in conformity with the findings of Bhadru *et al* .[2] and Dhanwani *et al* .[5]. The PCV and GCV recorded moderate values for the traits test weight, flag leaf length, plant height, alkali spreading values, effective tillers and head rice recovery. Hence selection for these traits may be misleading if adopted for improvement. Similar kind of findings were also observed by Raju *et al.*[17] and Venkata *et al.*[20] for effective tiller and test weight, Kumar *et al* .[10] and Dhurai *et al* .[6] for plant height.

The estimates of PCV and GCV were low (<10%) for the characters hulling percent milling percent, kernel elongation ration, day to 50% flowering, kernel length, kernel width, panicle length and L/B ratio. The selection for these traits would offer very little scope for genetic improvement of the genotypes under study. Similar results were also obtained by Singh *et al* .[18] for kernel length, kernel width, kernel length/breadth ratio, Mamata *et al* .[12] for day to 50% flowering and Nirmala *et al* .[14] for hulling percent. High coefficient of variability indicated that these in a scope of selection and improvement of these traits. Low values indicated the need for creation of variability by hybridization or mutation followed by selection.

The amount of genetic variation considered alone will not be of much use to the breeder unless supplemented with the information on heritability estimates, which given a measure of the heritable portion of the total variation. It has been suggested by Burton *et al* .[4] that the GCV along with heritability estimates would provide a better picture of the amount of advance to be expected by phenotypic selection. Since genetic advance is dependent on phenotypic variability and heritability in addition to selection intensity, the heritability estimates in conjunction with genetic advance will be more effective and reliable in predicting the response to selection[8]. Heritability in bread sense includes both additive and non additive gene effects[7]. In the present study, the heritability estimates ranged from 16.0% (volume expansion ratio) to 98.0% (yield per plant). High estimates of heritability were obtained by most of the character except hulling percent, volume expansion ratio and water uptake which showed low values, indicating the major role of additive gene action in inheritance of these traits. According to Panse[15] if a character in governed by non additive gene action, it may give heritability but low genetic advance. Whereas of it is governed by additive gene action, high heritability (above 60%) along with high genetic advance (above 20%) provide good scope for further improvement. The traits effective tillers per m$^2$, plant height, flag leaf length, filled seeds per panicle, test weight, yield per plant, head rice recovery and length/breadth ratio expressed high heritability values with high genetic advance as percent of mean.

The additive gene effects were responsible for those and selection for there traits could be beneficial. These results were in accorded with the findings of Singh *et al* .[18] for effective tillers, Dhurai *et al* .[6] for test weight, effective tillers, plant height, filled grain per panicle and yield per plant, Krishan *et al* .[9] for grain yield per plant and effective tillers.

High estimates of heritability associated with moderate genetic advance as percentage of mean were recorded for days to 50% flowering, kernel length, kernel width and kernel length after cooking indicating both additive and non additive gene effects governed these characters. Hence simple direct selection may be effective to improve these traits. These traits could also be improved by adapting recurrent selection method. These results were in consonance with the findings of Mamata *et al* .[12] for day to 50% flowering, [6] for day to 50% flowering and kernel breadth. Raju *et al* .[17] recorded high heritability coupled with low genetic advance for kernel length which is in conformity with present experiment suggesting greater role of non additive gene action in their inheritance of these character. Therefore heterosis breeding could be used to improve these traits.

The overall results indicated that these is adequate genetic variability present in the material studied. The GCV, PCV, broad sense heritability and genetic advance as percent of mean suggested number of filled seeds per panicle yield per plant, test weight, effective tillers, plant height, L/B ratio, head rice recovery, kernel length, kernel width, kernel length after cooking were important contributing traits and selection based in there traits would be more effective.

**Table: 1. Components of genetic parameters for yield and quality traits in rice (*Oriza sativa* L.)**

| Character | Mean | Range | PV | GV | PCV | GCV | Heritability in broad sense (%) | Genetic advance over mean (%) |
|---|---|---|---|---|---|---|---|---|
| **Days to 50% flowering** | 100 | 89 - 119 | 60.93 | 55.59 | 7.799 | 7.45 | 91.25 | 14.7 |
| **Effective tillers** | 327 | 231 - 433 | 2863.22 | 2547.78 | 6.38 | 15.45 | 88.98 | 30.2 |
| **Plant height(cm)** | 117 | 83 - 152 | 429.95 | 414.68 | 17.75 | 17.44 | 96.0 | 35.3 |
| **Panicle length (cm)** | 24.7 | 20.9 - 29.6 | 7.168 | 5.455 | 10.82 | 9.44 | 76.0 | 16.9 |
| **Flag leaf length(cm)** | 34.8 | 23.0 - 48.9 | 43.42 | 36.42 | 18.96 | 17.36 | 84.0 | 32.8 |
| **Flag leaf width(cm)** | 1.8 | 1.6 - 2.3 | 0.06 | 0.03 | 13.63 | 9.66 | 50.0 | 14.11 |
| **Filled seeds /Panicle)** | 217 | 107 - 352 | 5642.89 | 5425.12 | 34.67 | 33.99 | 96.0 | 68.7 |
| **Test weight(g)** | 19.0 | 13.7 - 26.2 | 14.22 | 13.63 | 19.81 | 19.39 | 96.0 | 39.1 |
| **Yield/Plant (g)** | 32.9 | 13.8 - 58.9 | 194.28 | 190.86 | 42.42 | 42.04 | 98.0 | 85.8 |
| **Hulling recovery(%)** | 81.1 | 76.9 - 83.2 | 2.80 | 0.26 | 2.06 | 0.63 | 9.00 | 0.39 |
| **Milling recovery(%)** | 68.7 | 47.1 - 75.9 | 37.31 | 28.06 | 8.89 | 7.71 | 75.0 | 13.8 |
| **Head rice recovery** | 61.3 | 36.9 - 71.5 | 76.55 | 72.11 | 14.27 | 13.85 | 94.0 | 27.7 |
| **Kernel length(mm)** | 5.2 | 4.5 - 6.2 | 0.24 | 0.21 | 9.45 | 8.77 | 86.0 | 16.8 |
| **Kernel width (mm)** | 1.8 | 1.5 - 2.3 | 0.031 | 0.027 | 9.75 | 9.07 | 87.0 | 17.4 |
| **L/B ratio** | 2.9 | 2.3 - 3.6 | 0.09 | 0.08 | 10.64 | 10.27 | 93.0 | 20.4 |
| **Kernel length after cooking(mm)** | 6.5 | 5.6 - 7.7 | 0.43 | 0.38 | 10.19 | 9.59 | 89.0 | 18.6 |
| **Kernel breadth after cooking (mm)** | 2.2 | 1.9 - 2.7 | 0.07 | 0.049 | 12.06 | 9.99 | 69.0 | 17.0 |
| **Kernel elongation ratio** | **1.3** | **1.1 - 1.39** | **0.0061** | **0.0036** | **6.24** | **4.78** | 59.0 | 7.5 |
| **Alkali spreading value** | 4.7 | 2.0 - 6.0 | 0.97 | 0.55 | 20.75 | 15.60 | 57.0 | 24.2 |
| **Volume expansion ratio** | 1.8 | 1.6 - 2.2 | 0.09 | 0.0153 | 17.58 | 7.05 | 16.0 | 5.8 |
| **Water uptake** | 161.8 | 122 - 242 | 1353.01 | 296.30 | 22.73 | 10.64 | 22.0 | 10.3 |

**Table: 2. Analysis of variance (mean squares) for grain yield and quality traits in rice (*Oryza sativa* L.)**

| S.No. | Characters | Replication (d.f=1) | Treatments (d.f=26) | Error (d.f=26) |
|---|---|---|---|---|
| **1** | **Days to 50% flowering** | 21.42 | 116.53** | 5.33 |
| 2 | **Effective tillers/m2** | 275.6 | 5411.0** | 315.4 |
| 3 | **Plant height(cm)** | 5.35 | 844.6** | 15.27 |
| 4 | **Panicle length (cm)** | 8.08 | 12.62** | 1.71 |
| 5 | **Flag leaf length(cm)** | 4.68 | 79.8** | 7.0 |
| 6 | **Flag leaf width(cm)** | 0.40 | 0.09** | 0.03 |
| 7 | **Filled seeds /Panicle)** | 93.35 | 11068.0** | 217.77 |
| 8 | **Test weight(g)** | 0.58 | 27.85** | 0.585 |
| 9 | **Yield/Plant (g)** | 64.4 | 385.1** | 3.42 |
| 10 | **Hulling recovery(%)** | 3.28 | 3.07 | 2.54 |
| 11 | **Milling recovery(%)** | 14.9 | 65.4** | 9.25 |
| 12 | **Head rice recovery** | 30.98 | 148.6** | 4.44 |
| 12 | **Kernel length(mm)** | 0.005 | 0.444** | 0.033 |
| 13 | **Kernel width (mm)** | 0.019 | 0.059** | 0.004 |
| 14 | **L/B ratio** | 0.035 | 0.178** | 0.006 |
| 16 | **Kernel length after cooking(mm)** | 0.520 | 0.817** | 0.049 |
| 17 | **Kernel breadth after cooking (mm)** | 0.66 | 0.122** | 0.022 |
| 18 | **Kernel elongation ratio** | 0.003 | 0.009** | 0.003 |
| 19 | **Alkali spreading value** | 0.074 | 1.514** | 0.420 |
| 20 | **Volume expansion ratio** | 0.015 | 0.11 | 0.08 |
| 21 | **Water uptake** | 4125.6 | 1649.3 | 1056.7 |

***Significant at 5% level** **** Significant at 1 % level**

## REFERENCES

1. Abdus salam khan, Muhammad Imran and Muhammad Ashafaq. Estimation of Genetic variability and correlation for grain yield components in rice *Oryza sativa* L. *American Eurasion J. Agric & Environ. Sci.,* **6(5):** 585-590 (2009).
2. Bhadru, D. Tirumala, R.V. Chandra, M. X and Bharathi, D. Genetic variability and diversity studies in yield and its component traits in rice *(Oryza sativa L) SAB RAO J of Breeding and Genetics.,* **44(1):** 129-137(2012).
3. Burton, G.W. Quantitative inheritance in grasses proceedings of 6th *Grassland congress J.,* **1:** 277-281(1952).
4. Burton, G.W. and Devane, Estimation of heritability in tall fescue *Festula arundnacea from replicated clonal material Agronomy. J.,* **45:** 478-481(1953).
5. Dhanwani, R.K. Sarawgi, A.K. Solanki, A and Tiwari, J.K. Genetic variability analysis for various yield attributing and quality traits in rice (*O.sativa L*) *The Bioscan.,* **8(4):** 1403-10407 (2013).
6. Dhurai, S.Y. Bhati, P.K. and Saroj, S.K. Studies on Genetic variability for yield and quality characters in rice (*oryza sativa L*) under irrigated fertilizer management. *The Bioscan* **9(2):** 745-478 (2014).
7. Hanson, C.H. Robinson, H.F. and Comstock, R.K. Biometrical studies on yield in segregating populations of Korean Lasphadezia. *Agron. J.,* **48:** 314-318 (1956).
8. Johnson, H.W. Robinsion, H.F. and Comstock, R.E. Estimation of genetic and environmental variability in soybean *Agro. J.,* **47:** 317-318(1955).
9. Krishan Veni, B. Vijaya lakshmi, B and Ramana, J.V. Variability and Association studies for yield components and quality parameters in rice genotypes. *Journal of rice research* **6 (2):**16-23(2013).

10. Kumar, A. Rangare, N.R. and Vidyakar, V. Study of genetic variability of Indian and exotic rice germplasms in Allahabad agro climate. *The Bioscan*., **8(4):** 1445-1451 (2013).
11. Lush, J. L. Intra sire correlation and regression of off spring in rams as a method of estimating heritability of characters proceeding of American society of Animal produce **33**:292-301(1940)
12. Mamata, S. Kumar, K. and Singh, R. Study of coefficient of variation, heritability and genetic advance in hybrid rice *oryza*., **44(2):** 160-162 (2007).
13. Murthy, P.S.N and Govinda swamy, Inheritance of grain size and its correlation with the hulling and cooling qualities *oryza* **4(1):** 12-21 (1967).
14. Nirmala Devi, G. Padmavathi, G. Suneetha Kota and Babu, V.R. Genetic variability, Heritability and correlation coefficients of grain quality characters in rice (*oryza sativa*) *SABRAO journal of breeding and genetics*: **47(1):** 424-433 (2015).
15. Panse, V.G. Genetics of quantitative characters in relation to *plant breeding India J. genet* **17:** 318-328 (1957).
16. Panse, V.G. and Sukhatne, P.V., Statistical methods for agricultural workers 2nd Edn ICAR New Delhi P: 361 (1961).
17. Raju, C.H.S, M.V.B and Sudarshanam, A., Genetic analysis and character association in F2 generation of rice *Madras Agri. J*. **91(1-3):** 66-69 (2004).
18. Singh, J. Dey, K. Sanjeev Singh and Shahi, J.P. Variability, heritability genetic advance and genetic divergence in induced mutants of irrigated basmathi rice (*oryza sativa* L) *oryza* **42(3):**210-213(2005).
19. Singh, S.P. Singhar, G.S. Parray, G.A. Bhat, G.N. Genetic variability and character association studies in rice (*Oryza sativa*) *Agri Sci. Digest*: **26(3):** 212-214 (2006).
20. Venkata Subbaiah, P. Reddi Shekhar, M. Reddy, K.H.P and Eswara Reddy, N.P. Variability and Genetic parameter for grain yield and its components and kernel quality attributes in CMS based rice hybrids (*Oryza sativa) International Journal of Applied Biology and pharmaceutical technology*: **2(3):** 603-609 (2011).