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Assessment of genetic variability, heritability and genetic advance for yield contributing and quality traits in rice (*Oryza Sativa* L.) genotypes

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Abstract
The present investigation consisting of fourteen genotypes of rice was carried out with in order to obtain information on genetic variability, heritability and genetic advance for important yield attributing and nutritional traits. The analysis of variance revealed significant differences among all the genotypes for all the characters studied. High range of observed values was discerned for total number of tillers, days to 50 % flowering, number of productive tillers, plant height, days to maturity, panicle length, shoot dry weight and grain yield per plant. The phenotypic variance was in general greater than the genotypic variance for all the characters. High heritability was recorded for all the characters studied. Moderate PCV as well as GCV were observed in days to 50 % flowering and plant height. Low PCV and GCV was observed in days to maturity. Less difference between PCV and GCV with high heritability and high GAM was found for number of tillers, number of productive tillers, days for 50 % flowering, days to maturity, and grain yield per plant for yield associated characters suggesting that selection among the elite accessions for micronutrients should be done for only the above mentioned traits, thus reducing the effort, time and labour for future work.

Keywords: genetic variability, GCV, PCV, heritability, genetic advance, rice

Introduction
Being staple crop for more than 50 percent of population Rice (*Oryza sativa* L.) is a member of grass family Poaceae and subfamily Orezoidea has an exceptional place among cereals worldwide. There are two cultivated species viz., *Oryza sativa* and *O. glaberrima* whereas other twenty-two species are wild. The *O. sativa*; predominant Asian rice growing in countries contributing maximum production which originated from the Eastern region of the foot hills of Himalayas. The *O. glaberrima*: a cultivated annual species was originated from West Africa and growing across the central Delta of the Niger River to Senegal. About 20% of the total calorie supply worldwide comes from rice. More than 90% rice of world is produced and consumed in South and South Eastern Asia, where approximately 60% of the population of the world is living. In India, it is staple food for more than 65 percent of the people. It provides about 29.4 per cent of total calories/capita/day in Asian countries (FAO, 2006). In India it is grown on 43.4 million hectares of land and producing approximately 106.3 million tons rice grain having productivity of 2.42 tons per hectare on average (Anonymous, 2013-14). The burgeoning population correlates with the increasing demand of rice. This can be met by discovering more genes contributing towards improved genetic recombinants. By an estimate we will reach at 8 billion mark by 2030 and we will need 50 percent more rice production to feed these many peoples. It is important to evaluate the promising rice germplasm along with their hybrids for morphological characters and yield. As we have approaching self-sufficiency and moving towards the second largest rice exporting country in the world our breeding strategies should now focus on quality oriented traits rather than quantity centred approach. Grain quality traits like beta carotene enriched rice or biofortified rice with mineral nutrients without any adverse effect on plant yield is the need of hour in perspective to help all rice grower as well as consumers. Quality traits are not easily responsive for selection contributed by their complex genetics. Lack of distinct pathways governing component traits for good quality rice is prime causes for delayed advancement in quality rice breeding for varieties. A systematic and efficient breeding program involves the steps like creation of genetic variation, selection practices and utilization of selected genotypes to develop promising varieties and all of these steps involves biometrical and multivariate analyses (Chakravorty *et al.*, 2013). The genetic facts are inferred from the observations on phenotypes. Since phenotype is determined by the joint effect of genotype and environment, non-genetic part exerts large influence on genetic variability.

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The utilisable variability is consequently, compulsory to be judged through various genetic parameters like genetic advance, heritability and few others. Information about such genetic parameters its genetic variation alongwith heritability and genetic advance will helpful in predicting the genetic improvement that could be attained in subsequent progenies. Estimation of heritability measures the flow of information for traits from parents to offspring. Great heritability values specify that traits and their expression under these studies are less biased against environmental influence. The genetic advance is a expedient indicator of the improvement that can be anticipated as result of selection on the appropriate population. Heritability in combination with genetic advance would give a more dependable index for better selection values (Akinwale *et al.*, 2011) [1]. Estimates of heritability and genetic advance will help in knowing the nature of gene action affecting concerned trait. It also specifies the possibility of genetic improvement for these traits through selection. High heritability with high genetic advance exhibited by these traits, controlled by additive gene action, (Panse *et al.*, 1957; Singh *et al.*, 2013) and further improvement will be achieved merely applying simple or progeny selection methods. Thus, selection for the traits with high heritability associated with high genetic advance leads to gather more additive genes. It can enhance the opportunities for further improvements of their performance. On the other hand, estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) also play vital role in selection practice for an effective rice breeding program. Yield owing to complex nature of its control by multiple genes regarded as complex character. Therefore identification of yield attributing components as well as nutritional components related to it will be of utmost importance for evolving effectual breeding approach to breed for high yielding varieties. Thus, breeding for components derived from theses analyses will be supportive and effective for increment in grain yield. Breeding rice cultivars with consumers choice grain quality as well as enriched micronutrients features has become second most significant aim next only to yield. As yield determinants quality traits also controlled through polygenic group of traits that are influenced by environmental factors, crop management and their interactions among themselves. As unattractive grain characters and unsatisfactory cooking quality hampers the acceptance and spread of the modern high yielding varieties, quality improvement needs special emphasis since last decades. With increase in yield, there is also a need to look into the quality aspects to have a better consumer acceptance, which determine the profit margin of rice growers which in turn ultimately affects export quality and foreign exchange in India. Grain quality characteristics are very important in rice breeding as it is predominantly consumed as a whole grain. Thus, knowledge on the nature and scale of the genetic variation prevailing the inheritance of quantitative character like yield, its components and quality traits is vital for effecting genetic improvement. A critical investigation of the genetic variability is a criterion for beginning any crop development programme and for implementing of suitable selection practices.

Materials & Methods

The present experiment was conducted at the field allotted to aerobic rice/biotechnology rice research laboratory, Department of Plant Biotechnology, University of Agricultural Sciences, GKVK campus, Bangalore, India during *Kharif*-2014 in order to study the amount of genetic variability present among the forteen selected genotypes of rice. A series of quality tests were also conducted at ICRISAT, Hyderabad, Andhra Pradesh. The Experimental material for the present investigation comprising of 14 genotypes was planted in Randomized Complete Block Design with three replications with the spacing of 30 cm between rows and 15 cm between plants. The recommended dose of fertilizer *i.e.* nitrogen 100 Kg, phosphorus 50 Kg and potassium 50 Kg along with 5 tone of FYM per hectare was applied. N was applied in the form of urea at basal, 30 and 60 DAS @ 50 %, 25 % and 25 % respectively. P was provided through single super phosphate (16 % P_2O_5) and K as Murite of potash (60 % K_2O). The recommended package of agronomic practice was followed to raise a healthy crop. The observations were recorded on five randomly selected competitive plants from each plot in all replications for plant height, total number of tillers, number of productive tillers, panicle length, percentage spikelet fertility, days to first flowering, hundred grain weight, days to 50 % flowering, days to maturity and shoot dry weight. The mean data after computing for each character was subjected to standard method of analysis of variance following genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Heritability in board sense (h2), genetic advance as percent of mean were estimated by the formula as suggested.

The phenotypic and genotypic coefficient of variation was computed as per Burton and Dewane (1953) for low moisture stress.

$$PCV = \frac{P}{\overline{X}} \times 100$$

$$GCV = \frac{G}{\overline{X}} \times 100$$

Wherein,
P = Phenotypic standard deviation
G = Genotypic standard deviation
X = Grand mean of character
PCV = Phenotypic coefficient of variation
GCV = Genotypic coefficient of variation

Heritability (h^2)

Broad Sense Heritability was calculated using the formula (Hanson *et al.,* 1956).

$$h^2 \% = \frac{Vg}{Vp} \times 100$$

Wherein,
h^2 % = Heritability percentage
Vg= Genotypic variance
Vp= Phenotypic variance
Heritability percentage was categorized as follows (Robinson *et al.,* 1949).
0-30 % was considered as low,
30-60 % was considered as moderate
60 % and above as high

Genetic advance (GA)

Genetic advance was calculated by using formula given by Johnson *et al.,* (1955).

$$GA = h^2 \times \sigma_p \times K$$

Wherein,

h^2 = Heritability (Broad sense)

σ_p = Phenotypic standard deviation

K = Selection differential which is 2.06 at 5 % intensity of selection (Lush, 1949).

3.1.5.5 Genetic advance as per cent mean

$$GA \text{ as per cent mean} = \frac{GA}{\overline{X}} \times 100$$

Wherein,

GA = Genetic advance and

X = Treatment mean for the character.

Results & Discussion

Genetic variability exists among the elite accessions for micronutrient content and yield associated characters. The genotypic variation for micronutrient accumulation in grain have been reported in staple crops such as rice (Graham et al., 1999; Gregorio et al., 1999; Gregorio et al., 2000; Zhang et al., 2004) [10, 11, 16]. The heritability estimates aid in determining the relative amount of heritable portion of variation. However, heritability values itself provides no indication of the amount of genetic progress that would result from selecting the best individuals. Heritability in broad sense would be reliable when accompanied by high genetic advance (Burton and De Vane, 1953, Johnson et al., 1955). Therefore, the phenotypic and genotypic coefficient of variance, heritability, genetic advance and genetic advance as percentage of mean was calculated for all the fourteen characters as given in Table 1, 2 and 3.

The magnitude of phenotypic variability is reflected by range and deviation from the mean values. High range was noticed for days to 50 % flowering, total number of tillers, number of productive tillers, plant height, panicle length, days to maturity, shoot dryweight, grain yield per plant. Similar results were obtained by Hemareddy (1993) [12], Dhananjaya et al., (1998) [6], Venkataramana and Hittalmani (1999) [15], and Nagabhushana (2002) [13]. The range in the means of Zn and Fe content in brown rice, Zn content in brown rice, Zn and Fe content in white rice is higher except for Fe content in

brown rice, but there were no reports on these traits earlier. Tiwari et al. (2009) [14] reported that grain zinc content in wheat mapping population ranged from 19.9 to 64.2 mg/kg. Similarly, grain zinc content ranged from 0.4 to 104 mg/kg in rice germplasm accessions (Anuradha et al., 2012) [2].

Moderate PCV as well as GCV were observed in days to 50 % flowering and plant height. Low PCV and GCV was observed in days to maturity. These results were in accordance with Akinwale et al. (2011) [1] and Bekele (2012) [3]. Less difference between PCV and GCV with high heritability and high GAM was found for days for 50 % flowering, days to Maturity, number of tillers, number of productive tillers and grain yield per plant for yield associated characters suggesting that selection among the elite accessions for micronutrients should be done for only the above mentioned traits thus reduced the effort, time and labour for future work. Only percentage of spikelet fertility showed less GAM (5.70). These results were in accordance with Chauhan (1996) [5]; Elayaraja et al., (2005) [8]; Bisne et al., (2009) [4]; Akinwale et al., (2011) [1] and Bekele (2012) [3]. High heritability was recorded for all the characters studied. The reports of high heritability also given by El-Malky et al., (2008) for days to maturity, number of tillers per plant. Similar results were obtained by Akinwale et al., (2011) [1] for days to 50 % flowering, days to maturity, plant height and yield per plant. For micronutrient distribution across different parts of rice grain, mostly less difference existed between PCV and GCV proposing that environment does not forms an important factor for micronutrient loading in grain. Lowest difference was found for Zinc content in cooked rice (0.14), iron content in white rice (0.24). So, the traits with high heritability should be selected for Zinc and Iron content in brown and white rice. Lowest heritability was found for Zinc content in 10 % Bran and also having high GAM.

For cooking characters significant differences among genotypes were observed. The present investigation revealed high heritability coupled with high genetic advance as per cent of mean for most of the characters indicating the presence of considerable variation for yield associated characters and micronutrient distribution in elite accessions for Zn and Fe. Hence, improvement of these quality characters could be effective through phenotypic selection for yield associated characters with high GCV, PCV, GAM and heritability.

Table 1: Estimates of genetic parameters for different quantitative traits among elite rice accessions for shoot morphological studies

Sl. No.	Characters	Mean ± SE	Min	Max	PCV (%)	GCV (%)	h² broad sense (%)	GAM (%)
1	PH	80.07±3.42	52.33	103.73	23.56	22.36	90.12	43.74
2	TNT	10.91±0.70	6.36	15.33	23.36	20.55	77.35	37.23
3	NPT	8.43±0.58	4.20	12.56	28.42	25.80	82.38	48.24
4	PL	18.78±0.82	16.07	21.9	11.25	8.31	54.57	12.64
5	PSF	64.60±1.21	61.12	69.71	4.92	3.69	56.25	5.70
6	DFF	94.95±3.76	72	122.33	17.99	16.62	85.41	31.65
7	DFPF	111±3.74	95	137	13.24	11.88	80.57	21.97
8	DM	132.02±2.31	121.67	148.67	6.83	6.12	80.25	11.30
9	SDW	32.03±2.24	24.49	39.24	16.98	11.92	49.24	17.23
10	HGW	1.95±0.15	1.20	2.58	22.41	17.87	63.63	29.37
11	GY/P	13.73±0.90	4.02	30.53	61.35	60.28	96.52	121.99

PCV = Phenotypic Coefficient of variation   GCV= Genotypic Coefficient of variation

h^2 % = Heritability percentage in broad sense   GAM= Genetic Advance as per Mean

Table 2(a): Estimation of genetic parameters for zinc content in rice grain

Sl. No.	Zinc content in	Mean ± SE	Min	Max	PCV (%)	GCV (%)	h² broad sense (%)	GAM (%)
1	Brown rice	29.27±1.51	23.35	43	23.37	21.58	85.27	41.04
2	White rice	26.23±0.48	18.7	37.45	21.56	21.32	97.86	43.46
3	Cooked rice	23.31±0.34	15.45	33.5	23.71	23.57	98.81	48.28

Table 2(b): Estimation of genetic parameters for iron content in rice grain

Sl. No.	Iron content in	Mean ± SE	Min	Max	PCV (%)	GCV (%)	h² broad sense (%)	GAM (%)
1	Brown rice	14.46±1.22	10.9	21.7	23.70	18.66	62.00	30.28
2	White rice	6.78±0.41	2.20	14.05	55.40	54.41	96.47	110.10
3	Cooked rice*	17.81±1.05	6.85	31.10	37.65	36.23	92.59	71.82

Table 3: Estimation of genetic parameters for cooking characters in rice grain

Sl. No.	Characters	Mean ± SE	Min	Max	PCV (%)	GCV (%)	h² broad sense (%)	GAM (%)
1	KLBC	0.24±0.00	0.16	0.64	50.13	49.72	98.38	101.59
2	KLAC	0.85±0.01	0.66	1.03	12.06	11.88	96.96	24.10
3	WUBC	3.70±0.13	2.46	5.33	22.38	21.47	92.03	42.43
4	WUAC	13.13±0.40	8.83	17	18.77	18.03	92.25	35.67
5	VEXP	3.63±0.16	2.28	4.49	19.17	17.65	84.80	33.49
6	ER	3.93±0.15	1.61	4.98	22.52	21.56	91.62	42.50

KLBC=kernel length before cooking KLAC= Kernel length after cooking
WUBC= water uptake before cooking WUAC=water uptake after cooking
VEXP=volume expansion ER= Elongation ratio

Conclusion
Any attempt to improve the yield and quality attributing traits coupled with high micronutrient distribution would be of no use without knowledge of heritability. Thus, information on phenotypic and genotypic co-efficient of variation and heritability was used to compare the variability observed among the studied characters required for the proper crop improvement program. Less difference between PCV and GCV with high heritability and high GAM was found for days for 50 % flowering, days to maturity, number of tillers, number of productive tillers and grain yield per plant for yield associated characters suggesting that selection among the elite accessions for micronutrients should be done for only the above mentioned traits thus reducing the effort, time and labour for future work. The present investigation revealed high heritability coupled with high genetic advance as per cent of mean for most of the characters indicating the presence of considerable variation for yield associated characters and micronutrient distribution in elite accessions for Zn and Fe. Hence, improvement of these quality characters could be effective through phenotypic selection for yield associated characters with high GCV, PCV, GAM and heritability.

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