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Assessment of the genetic variability, heritability and genetic advance percent mean in traditional rice (*Oryza sativa* L.) genotypes

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Abstract

Purpose: As per rice is a staple food over globe and its growing demand leads to identify elite variants to mitigate its need.
Research Methods: Twenty-three numbers of paddy genotypes (*Oryza sativa* L.) considered and were assessed through kharif 2021 and its character and the magnitude of variability; heritability (broad sense) and genetics advance for thirteen quantitative traits were tested.
Research Findings: High PCV, GCV, heritability and Genetic advance percent mean reported in flag leaf length (20.27, 22.39, 81 and 37.81), number of filled spiklets per panicle (32.37, 37.38, 75 and 57.76), 1000 grain weight (28.75, 29.96, 92 and 56.84) and yield per hill (23.04, 25.96, 78 and 42.14). From the ANOVA it reflected that the differences among twenty-three genotypes results showed that significant differences and amount of variation present between the genotypes for most of the characters under study.
Originality and value: High significant amount of variability was recorded for grain breadth, yield per hill and 1000 grain weight in both replication and genotypes. The traits plant height, days to 50% flowering, flag leaf length, flag leaf width, panicle length, culm length, number of panicles per hill, number of spiklets per panicle, number of filled spiklets per panicle, grain length, grain breadth, 1000 grain weight and yield per hill exhibited significant differences between genotypes. Which recommended that this trait would take action to selection owed their higher genetic variability and transmissibility. Genetic advance was recorded for number of filled spikelets per panicle (75%) with high value of heritability.
Limitations: Some other traits also have direct effect on yield that is not quality traits.

Keywords: GCV, heritability PCV and genetic advance

Introduction

Rice (*Oryza sativa* L.) is the prime crop providing food to over 75% of the Asian population and more than equal to three billion of world population that represents 50% - 80% of their daily calorie consumption and 55% of the protein intake in their average regular diet and aptly defines the slogan “Rice is life”. Rice is majorly grown in kharif and Rabi seasons and in some areas, it is also been grown in early kharif season. Early kharif rice crop is well known by various names in different regions of India. *viz.*, edagaru or mokkadugu in Nellore district of Andhra Pradesh, 'Aus'; West Bengal, 'Ahu' in Assam, 'Beali' in Orissa, 'Bhadai' in Bihar, 'Virippu' in Kerala and 'Kuruvai/Kar/ March- April Sornavari' in Tamil Nadu (www.rkmp.drr on 24 June, 2011).

In India, rice grown area during early kharif season (Autumn) of according to the statement, rice production in kharif season 2021-2022 is estimated to be 9.21 million tonnes higher than the earlier five years (2015-16 to 2019-20) average of 97.83 million tonnes correspondingly (Ministry of AFW, Govt. of India, 2021-2022). Popular Orissa rice cultivation in kharif season 41.24% and characterized by climatic factors like low (or) no rainfall and high temperatures ranging from 35 to 45 °C coupled with high velocity winds and these climatic factors had enormous effect on grain yield production. These climatic extremes reduce the activity of many physiological processes through physiological traits akin to SCMR, flag leaf length and its width along with flag leaf area and harvest index. Hence, the morphological traits like flag leaf size and shape, and the physiological traits of flag leaf for example chlorophyll content and capacity of photosynthesis have been considered to be the chief determinants of grain yield in cereals. However, harvest index reveals the division of the photosynthates between the seeds and the vegetative parts and improvement in harvest index accentuate the importance of carbon allocation in grain production.

So, effect on above mentioned characters leads to show a significant impact on yield and yield contributing characters. Global warming impart pressure on rice production. Over the last 100 years, global normal temperature has increased by a 0.6 °C and is anticipated to continue to hike at a faster rate, with another 0.5-2.8 °C increase assumed by the end of 21st Century (Vuuren *et al*., 2008) [23].

The large spectrum of the quantity of genetic variety among genotypes determines the genetic variability in segregating populations, which provides more selection opportunities. The amount of heritable distinction in the variables evaluated is extremely important in determining the genotype's breeding potential. The status of Many researchers have emphasised the importance of understanding the range and degree of genetic divergence in rice and how to use it to pick desirable parents/donors for hybrid vigour or desirable recombinants. Genetic divergence, according to Arunachalam (1981) [1], is the most important factor in obtaining heterotic hybrids and increasing variation in the segregating population of varietal improvement programmes. Every breeding project requires germplasm. During a crossing programme, the diversity and new traits found in the germplasm can be used to generate need-based varieties and hybrids. To employ efficiently in the crossover programme, the germplasm must first be described and the genetic diversity must be studied.

Materials and Methods

The experiment was conducted at Bhaguasala Farm, M. S. Swaminathan School of Agriculture, Centurion University of Technology and Management (CUTM), Paralakhemundi, Odisha. The farm is located at 23.39 ^{0} N latitude and 87. 42 ^{0} E longitude at an elevation of 182.9 m above the mean sea level (ASL). Twenty-three genotypes of rice were sown and transplanted in Randomized Block design (RBD) with three replications. Each plot size was 1 m × 2 m with 20 × 15 cm spacing between plant to plant and row to row. The crop was cultivated as per recommended package of practices. For Uniformity five representative plant hills for each genotype in each case of replication were randomly selected that were subjected to record the observations for eleven quantitative traits *viz*., flag leaf length (cm), flag leaf width (cm), days to 50% flowering, plant height (cm), culm length (cm), panicle length (cm), number of panicles per hill, number of spiklets per panicle, number of filled spiklets per panicle, grain length (mm), grain breadth (mm), 1000 grain weight and yield per hill. Following Panse and Sukhatme (1967) [15], the mean data was subjected to the average method of analysis of variance, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability in the broad sense (h2), and genetic advance as percent of mean were estimated that use the formula suggested by Burton (1952) and Johanson *et al* (1955) [3, 6].

Results and Discussion

The mean sum of square for yield per plot and their constituent characters in 23 genotypes are computed. The results showed that significant differences and amount of variation present between the genotypes for most of the characters under the study. High significant amount of variability was recorded for grain breadth, 1000 grain weight and the yield per hill in case of both replication and genotypes. The traits plant height, days to 50% flowering, flag leaf length, flag leaf width, length of panicle, culm length, number of panicles per hill, number of spiklets per panicle, number of filled spiklets per panicle, grain length and its breadth, 1000 grain weight and yield per hill showed significant differences between genotypes. In the current study of research, 23 genotypes were tested for 13 characters including yield, attributing traits. The results specified that significant number of differences and variation present in-between the genotypes for the majority of the characters studied may be due to differences in breeding procedures, duration and also geo-ecological status of genotypes from which they created. The considerable amount of variation exhibited by genotypes for yield and other characters indicates that there is plenty scope for the selection of capable genotypes from the current study for further enhancement in breeding programmes. Phenotypic variance (PCV) was higher than the genotypic variances (GCV) for all the characters that reflect the influence of environmental factor on these particular traits.

Phenotypic coefficient of variation (PCV) was observed to be slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters (Table 1). The improvement in any crop breeding program vastly depends on the nature and magnitude of variability present in genotypes. From the perusal, it was observed that the phenotypic variances of all characters were elevated than the genotypic variances representing the result of environment on genotypes.

The PCV and GCV were exhibited high in flag leaf length (20.27 and 22.39), number of filled spiklets per panicle (32.37 and 37.38), 1000 grain weight (28.75 and 29.96) and yield per hill (23.04 and 25.96), so environmental influence for this character is low. Same result reported in Kumar *et al* (2008) [12] followed by Sadeghi *et al* (2011) [18], Krishna *et al*., (2008) [8], Krishna Veni *et al*., (2013) [10] and Sharma *et al*., (2013) [19]. Moderate GCV and PCV found in, plant height (17.16 and 17.46), panicle length (15.60 and 15.90), culm length (17 and 17.42), number of panicles per hill (13.75 and 18.84), grain length (10.33 and 10.92) and grain breadth (17.95 and 18.97). Same results reported in Singh *et al*., (2011) [22] followed by Chakraborty *et al*., (2010) [4], Singh *et al*., (2014) [20], Krishna veni *et al*., (2013) [10] and low GCV and PCV found in Days to 50% flowering (8.33 and 9.10) and number of spiklets per panicle (6.26 and 9.87), here environmental influence is high. Same results reported in Singh *et al*., (2007) [21].

Heritability estimates is important as it indicates the extent of possibility of genetic relationships in successive generations and also improvement through selection. It measures the degree of expression of a particular character in successive generations. Heritability along with genetic advance are more significant than the only heredity could predict the outcome of selecting the best individuals. (Johnson *et al*., 1955) [6], hence the knowledge of both heritability and genetic advance was important for the selection indices for improvement in programs.

Heritability and Genetic advance percent mean were exhibited high in flag leaf length (81 and 37.81), plant height (96 and 34.74), panicle length (96 and 31.52), culm length (94 and 34.03), number of filled spiklets per panicle (75 and 57.6), grain length (89 and 20.15), grain breadth (89 and 35.01), 1000 grain weight (92 and 56.84) and yield per hill (78 and 42.14). Same result found in Kumar *et al*., (2011) [11] followed by Babu *et al*., (2012) [2], Prasad *et al*., (2011) [16], Sharma *et al*., (2013) [19], Kiani *et al*., (2013) [7], Gokul Krishna *et al*., (2014) [5], Singh *et al*., (2014) [20]. High and moderate results reported in days to 50% flowering (83 and 15.70) Reddy *et al*., (2013) [17], medium and high result reported in flag leaf width (53 and 22.59), number of panicles per hill (53 and 20.67) same results reported in Kumar *et al*. (2013), Paikhamba *et al*., (2014) [13, 14].

Low heritability and low genetic advance percent mean found in number of spiklets per panicle (40 and 8.19).

Table 1: Genetic parameters for the grain yield and its component characters in rice

S. No	Characters	GCV%	PCV%	h^2 heritability	Genetic advance percent mean
1	Days to 50% flowering	8.33	9.10	83	15.70
2	Flag leaf length (cm)	20.27	22.39	81	37.81
3	Flag leaf width (cm)	14.00	20.41	53	22.59
4	Plant height (cm)	17.16	17.46	96	34.75
5	Panicle length (cm)	15.60	15.90	96	31.52
6	Culm length (cm)	17.00	17.42	94	34.03
7	Number panicles per hill	13.75	18.84	53	20.67
8	Number of spiklets per panicle	6.26	9.87	40	8.19
9	Number of filled spiklets per panicle	32.37	37.38	75	57.76
10	Grain length (mm)	10.33	10.92	89	20.15
11	Grain breath (mm)	17.95	18.97	89	35.01
12	1000 grain weight (gm)	28.75	29.96	92	56.84
13	Yield per hill (gm)	23.04	25.96	78	42.14

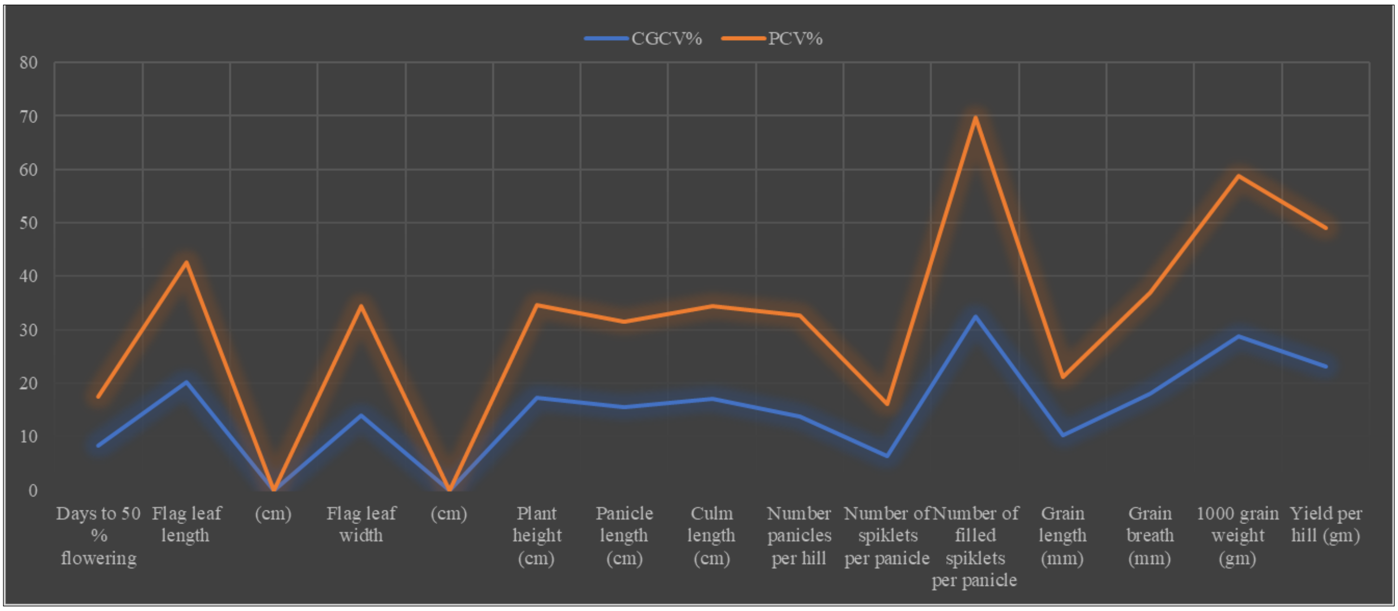

Fig 1: Genotypic coefficient of variation (GCV %) and Phenotypic coefficient of variation (PCV %)

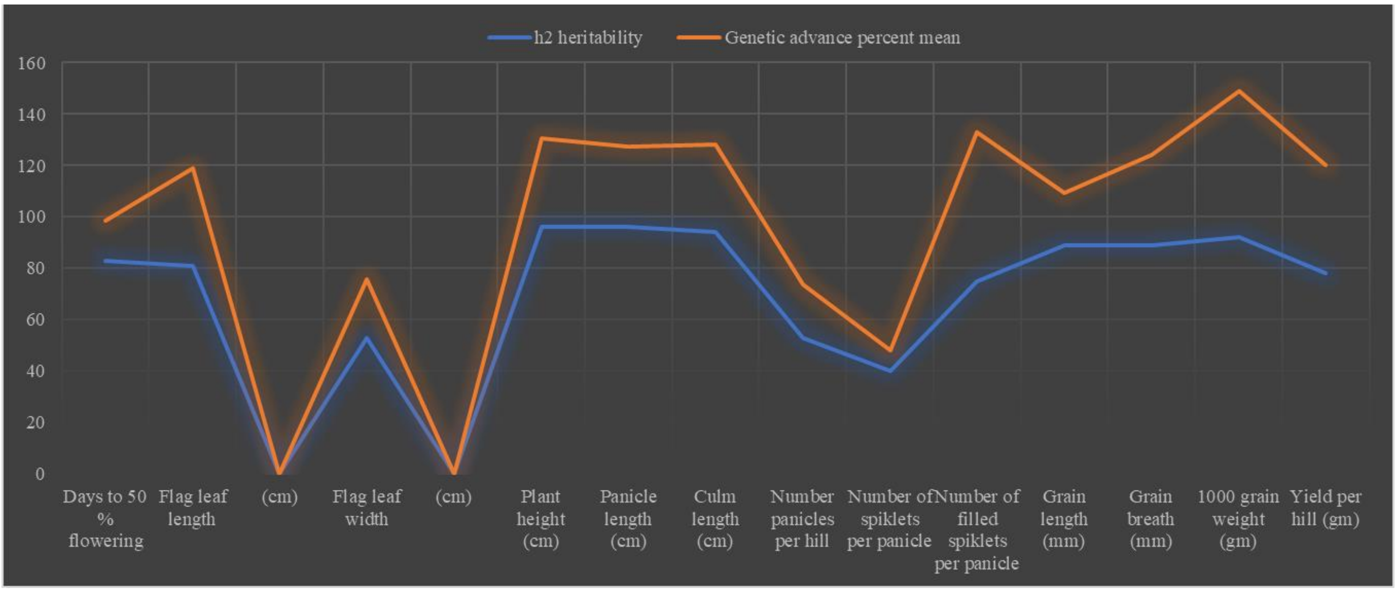

Fig 2: Heritability percentage and Genetic advance percent mean

The considered characters like flag leaf length, numbers of filled spiklets per panicle, weight of 1000 grain and yield are showed high PCV, GCV, Heritability and Genetic advance percent mean indicates a minimal environmental influence. The traits like plant height, panicle length, culm length, grain length and grain breadth are highly heritable and high genetic advance percent mean indicate presence of additive gene action. Hence these characters can be used in future in improvement in plant breeding program.

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