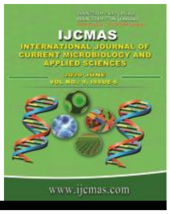
Int.J.Curr.Microbiol.App.Sci (2020) *9*(6): 1167-1174

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 9 Number 6 (2020)**
Journal homepage: http://www.ijcmas.com



Original Research Article https://doi.org/10.20546/ijcmas.2020.906.145

Evaluation of Variability, Heritability and Genetic Diversity in Rainfed Rice Genotypes

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ABSTRACT

The experiment was conducted under rainfed rice ecosystem to investigate genetic variation, heritability and diversity of yield and related attributes of 34 advanced rice cultures. The analysis of variance revealed that all the treatments are significant for various characters under studied. The higher magnitude of PCV and GCV were recorded for number of filled grains per panicle, number of panicles per square metre plot area and plant height. High heritability coupled with high genetic advance was recorded for plant height and number of filled grains per panicle indicated the major role of additive gene action in the inheritance of this trait. Maximum number of genotypes (15 genotypes) was grouped in cluster I. Maximum inter cluster distance was observed between cluster IV and VI (36.32) indicating wider genetic diversity between genotypes. The intra cluster distance was higher in cluster VI (4.07) indicates hybridization involving genotypes within the same clusters may result in good cross combinations. Among the ten traits studied, plant height contributed maximum divergence (35.29%) followed by days to fifty per cent flowering (22.82%), grain yield (14.80) and filled grains per panicle (9.09) and these characters may be given importance during hybridization programme in rainfed rice ecosystem.

Keywords

Variability, heritability, genetic advance, diversity, rainfed rice

Article Info

Accepted:
18 May 2020
Available Online:
10 June 2020

Introduction

Rice (*Oryza sativa* L.) is the most important cereal food crop of the world and about 90 per cent of the people of South-East Asia consume rice as staple food. Rainfed rice has been gaining popularity, because current high-yielding varieties have led to an increase in genetic vulnerability, a scarcity of water for irrigation, and a breakdown of resistance genes against emerging races of pathogen due to intensive cultivation. It is important in cropping systems, because of the lack of irrigation facilities and lower cost of production (Fageria *et al.*, 2014). Further, a majority of area under rainfed rice cultivation suffer from poor productivity due to lack of promising rice cultivars under such eco-climatic condition. Thus, in order to improve the productivity level, a breakthrough would be desirable by way of increasing biological efficiency through hybridization and the productivity of new varieties suited to rainfed condition. The success of developing new varieties would depend on the exploitation of existing variability and therefore it is desirable to collect, evaluate and utilize the available diversity to suit specific need with regards to specific ecosystem. Study of variability parameters and D^2-statistics are expected to provide reliable basis for selecting out desirable elite and diverse parents for hybridization and exploitation of variability. Grouping of genotypes on the basis of genetic distance finally provides a clear picture about the inter-relationship of the genotypes and helps to pick up appropriate genotype. This study was therefore conducted to select potential genotypes and to identify the most important characters for breeding programmes by exploiting the genetic variation, heritability, and diversity analysis of yield and related attributes of 34 rainfed rice genotypes.

Materials and Methods

Details on experimental site and traits

The experimental material comprised with thirty four advanced rice cultures collected from various research institutes which were evaluated in a randomized block design with three replications at Agricultural Research Station, Tamil Nadu Agricultural University, Paramakudi, India during Rabi 2016-17. The experimental site is located at 9” 21’ N latitude, 78” 22’ E longitudes and an altitude of 242 m above mean sea level with average annual rainfall of 840 mm. This site has clay loam soil texture with pH of 8.0. Each genotype was raised in 5x2 m plot keeping 15 x 10 cm spacing. The recommended agronomic practices followed to raise good crop stand. The data were recorded on ten randomly selected plants from each replication for various quantitative traits studied were *viz,* days to 50% flowering, plant height (cm), number of productive tillers per plant, number of panicles per square metre plot area, panicle length, number of filled grains per panicle, spikelet fertility (%), grain yield (kg), straw yield (kg) and harvest index.

Statistical analysis

Mean values were subjected to analysis of variance to test the significance for each character as per methodology advocated by Panse and Sukhatme (1967). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated by the formula given by Burton (1952). PCV and GCV were classified as suggested by Sivasubramanian and Menon (1973). Heritability in broad sense (h^2[b]) was estimated as per the formulae suggested by Allard (1960). The heritability (h2[b]) was categorized as suggested by Johnson *et al.*, (1955). Genetic advance (GA) was estimated as per formula given by Allard (1960) Genetic advance over mean (GAM) was calculated using the following formula and was expressed in percentage. The genetic advance as per cent over mean was categorized as suggested by Johnson *et al.,* (1955). The genetic distance between the genotypes was worked out using D^2 analysis explained by Mahalanobis (1936) and grouping of varieties into clusters was done following the Tochers method as detailed by Rao (1952).

Results and Discussion

Variability

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating existence of variability among the genotypes (Table 1.). The genotypic coefficient of variation measures the range of variability available in the crop and also enables a breeder to compare the amount of variability present among different characters. The perusal of coefficient of variability indicated that wide range of variability was present at both phenotypic and genotypic levels for all the characters under studied. The magnitude of phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits which may be due to higher degree of interaction of genotypes with the environment (Kavitha and Reddy, 2002). The differences in the magnitude of PCV and GCV for number of productive tillers per plant, number of panicles per square metre plot area, number of filled grains per panicle, grain yield, straw yield and harvest index were of high order. The higher magnitude of PCV and GCV were recorded for number of filled grains per panicle, number of panicles per square metre plot area and plant height (Table 2.).

Heritability and genetic advance

Burton (1952) pointed out that the heritability in combination with intensity of selection and amount of variability present in the population influences gains to be obtained from selection. Thus, genetic advance is yet another important selection parameter which although independent, represents the expected genetic advance under selection. According to Panse (1957) if a character is governed by non-additive gene action, it may give high heritability but low genetic advance, whereas, if it is governed by additive gene action, high heritability along with high genetic advance provided good scope for further improvement.

High heritability coupled with high genetic advance was recorded for plant height and number of filled grains per panicle (Table 2.). It indicates that most likely the heritability is due to additive gene effects and selection may be effective. This finding is in close agreement with the findings of Babu *et al.*, (2012) and Allam *et al.*, (2015).

Genetic diversity

Based on the relative magnitude of D^2 values, thirty four genotypes were grouped into seven clusters (Table 3). Maximum number of genotypes (15 genotypes) was grouped in cluster I. Cluster II consists of 12 genotypes, Cluster III and Cluster VI includes two genotypes others were represented by a single genotype each. The overall composition of the clustering pattern showed that genotypes collected from the same geographic origin were distributed in different clusters. Similar findings of non- correspondence of geographic origin with genetic diversity were also reported by Shanmugasundaram *et al.*, (2000) and Nayak *et al.*, (2004). The intra and inter cluster distance are presented in Table 4. The maximum inter cluster distance was observed between cluster IV and VI (36.32) followed by between cluster III and VI (28.82) indicating wider genetic diversity among the genotypes between these groups. The hybrids developed from the selected members of these clusters would produce highly variable population in the segregating generations. Surprisingly the clusters identified with maximum inter cluster distance were possessed one or two genotypes in each cluster. Hence selection of parents for hybridization is already over. The minimum inter cluster distance was found between cluster I and VII (5.63) followed by between cluster IV and VII (5.76). These genotypes in these clusters are genetically very close and hence, hybridization among the varieties will not give fruitful result.

The maximum intra cluster distance was observed in cluster VI (4.07) followed by cluster II (3.14). Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which would be made use of an improvement through inter-varietal hybridization (Joshi *et al.*, 2008).

Table.1 Analysis of variance for different traits in rainfed rice

Source of variation	Degrees of freedom	Days to 50% flowering	Plant Height	Productive tillers per plant	Panicles per square metre	Panicle length	Filled grains per panicle	Spikelet Fertility	Grain yield	Straw yield	Harvest index
Replication	2	13.18	26.6	0.77	2525	1.60	120.7	0.48	679225	1832059	0.003
Treatment	33	132.73**	410.9**	1.69*	5238**	8.04**	1198.1**	9.45**	668885**	4708307**	0.002**
Error	66	4.29	20.6	0.97	1001	1.13	196.5	3.15	264273	1266907	0.001

**significant at P=0.01 level *significant at P=0.05 level

Table.2 Estimates of mean, variability, heritability and genetic advance in rainfed rice

Traits	Mean	PV	GV	PCV	GCV	h^2	GAM
Days to 50% flowering	78.50	47.10	42.81	8.74	8.34	90.90	16.37
Plant height	95.86	150.70	130.10	12.81	11.90	86.33	22.77
Productive tillers per plant	5.99	1.21	0.24	18.34	8.18	19.90	7.52
Panicles per square metre	235.52	2413.08	1412.27	20.86	15.96	58.53	25.15
Panicle length	20.61	3.44	2.30	9.00	7.37	67.03	12.42
Filled grains per panicle	100.80	530.35	333.90	22.85	18.13	62.96	29.63
Spikelet Fertility	93.40	5.25	2.10	2.45	1.55	40.03	2.02
Grain yield	3733.24	399143	134870	16.92	9.84	33.79	11.78
Straw yield	11347.06	2414040	1147133	13.69	9.44	47.52	13.40
Harvest index	0.25	0.02	0.01	13.41	8.05	36.04	9.95

GV=Genotypic Variation; PV=Phenotypic Variation; GCV=Genotypic Co-efficient of Variation; PCV=Phenotypic Co-efficient of Variation; h^2=Heritability (Broad sense); GAM=Genetic Advance as % of Mean.

Table.3 Clustering pattern of 34 genotypes

Cluster	No. of genotypes	Name of genotypes
I	15	PM 18001 (G8), PM 18007 (G11), PM 18015 (G17), PM 13069 (G18), PM 17003 (G23), PM 16001 (G20), PM 13804 (G2), PM 17027 (G28), PM 18014 (G16), PM 18008 (G12), PM 18005 (G32), PM 17022 (G25), PM 18004 (G30), PM 18012 (G14) and PM 18005 (G9).
II	12	PM 15055 (G19), PM 17025 (G26), PM 17013 (G24), PM 17028 (G27), PM 18009 (G31), PM 15040 (G5), PM 15028 (G3), PM 15049 (G6), PM 15050 (G7) and PM 18006 (G10), PM 15033 (G4) and PM 18002 (G29).
III	2	PM 18013 (G15) and PM 18017 (G33)
IV	1	PM 12012 (G1)
V	1	PM 18010 (G13)
VI	2	PM 16004 (G21) and PM 16005 (G22)
VII	1	Anna(R)4 (G34)

Table.4 Intra (diagonal) and inter cluster average distance of yield traits in 34 genotypes

	I	**II**	**III**	**IV**	**V**	**VI**	**VII**
I	2.94	7.85	8.93	11.36	6.31	11.50	5.63
II		3.14	12.58	6.69	14.80	21.77	6.49
III			1.73	6.34	20.46	28.82	8.77
IV				0.00	24.49	36.32	5.76
V					0.00	7.53	13.95
VI						5.65	20.51
VII							0.00

Table.5 Cluster mean of different yield characters in 34 rice genotypes

Cluster	Days to 50% flowering	Plant Height (cm)	Productive tillers per plant	No. of panicles per sq.metre	Panicle length (cm)	Filled grains / panicle	Spikelet Fertility (%)	Grain yield (kg/ha)	Straw yield (kg/ha)	Harvest Index
I	74.60	96.11	5.58	222.07	20.67	106.17	94.31	3612.51	4247.62	0.27
II	85.64	93.33	6.36	259.19	20.42	90.69	92.64	3878.00	4966.67	0.28
III	75.83	126.83	6.00	242.67	20.25	97.67	91.83	3347.67	3933.33	0.30
IV	87.00	117.33	6.00	192.67	22.57	120.33	94.33	4242.00	2333.33	0.22
V	73.33	78.33	5.33	191.67	18.23	136.67	95.33	3544.00	3600.00	0.41
VI	65.17	76.17	7.00	236.67	19.11	79.83	91.17	4097.50	6800.00	0.15
VII	80.00	96.00	6.33	223.33	25.83	134.33	93.67	3530.00	4733.33	0.24

Table.6 Percentage of contribution of each character towards total divergence

Character	No. of Times Ranked First	Contribution (%)
Plant Height (cm)	198	35.29
Days to 50% flowering	128	22.82
Productive tillers per plant	4	0.71
No. of panicles per sq.metre	22	3.92
Panicle length (cm)	39	6.95
Filled grains / panicle	51	9.09
Spikelet fertility (%)	6	1.07
Grain yield (kg/ha)	83	14.80
Straw yield (kg/ha)	14	2.50
Harvest Index	16	2.85
Total	**561**	**100**

A perusal of results of cluster means (Table 5) revealed that cluster I with fifteen genotypes exhibited highest or lowest mean value for none of the characters. Cluster II had genotypes with maximum number of panicles per square metre area (259.19) and the genotypes in Cluster III (PM 18013 and PM 18017) had tallest plants (126.83) and lowest grain yield (3347.67). Cluster IV had taken more days for fifty per cent flowering (87.00), given maximum grain yield (4242.00) and lowest straw yield (2333.33). The cluster V had maximum number of filled grains per panicle (136.67), spikelet fertility (95.33) and harvest index (0.41), while Cluster VI was characterized by lesser duration for fifty per cent flowering (87.00), shortest plants (76.17), highest productive tillers per plant (7.00) and straw yield (6800.00). The genotype Anna (R) 4 with lengthy panicles (25.83) was grouped in cluster VII. None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. However the cluster V and VI recorded desirable mean value for maximum number of productive traits. Similar results were also reported by Banumathy *et al.,* (2010) and Rai *et al.,* (2014), thereby underlining the fact that the hybridization between genotypes of different clusters is necessary for the development of desirable genotypes. Based on the *per se* performance of the best genotypes within the clusters, they may be directly selected or may be used as potential parents in hybridization programme.

The contribution of each trait to total divergence is presented in table 6. Among the traits studied, plant height contributed maximum divergence (35.29%) followed by days to fifty per cent flowering (22.82%), grain yield (14.80) and filled grains per panicle (9.09). The traits *viz.,* plant height, days to fifty per cent flowering, grain yield and filled grains per panicle contributed more than seventy five per cent towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population.

It is concluded from the variability studies that high heritability coupled with high genetic advance was recorded for plant height and number of filled grains per panicle and the major role of additive gene action involved in the inheritance of these traits. Thus, these traits may serve as effective selection parameters during breeding programme in the rainfed rice ecosystem. Divergence studies suggest that cluster V and VI recorded desirable mean value for maximum number of productive traits and best genotypes in these clusters may be directly selected or may be used as potential parents in hybridization programme by giving importance to the characters (plant height, days to fifty per cent flowering, grain yield and filled grains per panicle) which are contributing more to the total divergence.

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How to cite this article:

Muthuramu. S. and Ragavan. T. 2020. Evaluation of Variability, Heritability and Genetic Diversity in Rainfed Rice Genotypes. *Int.J.Curr.Microbiol.App.Sci*. 9(06): 1167-1174.
doi: https://doi.org/10.20546/ijcmas.2020.906.145