

Original Research Article

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Studies on Genetic Variability, Heritability and Genetic Advance for Yield and Yield Components in Drought Tolerant Rice (*Oryza sativa* L.) Landraces

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ABSTRACT

Information regarding genetic variation for drought attributes, their heritability and genetic advance coupled with association of different component traits among themselves and with grain yield are of immense help to breeder for selection of parents in hybridization programme. Phenotypic variation does not directly indicate its usefulness for selection in order to obtain genetic improvement unless the genetic fraction of variation is known. Therefore, it is important to partition out the genotypic component of total variation to arrive at reliable conclusion about the exploitable (genetic) variability in a set of genotypes. The present investigation was carried out at the Agriculture Research Farm, Institute of Agricultural Sciences, BHU, Varanasi during the *kharif*-2016 using 20 diverse rice genotypes with the objectives to assess direct selection parameters (variability, heritability and genetic advance). The results of the investigation revealed the high estimates of genotypic coefficient of variation and phenotypic coefficient of variation were observed for traits viz. sterile spikelets per panicle followed by grains yield per plot and grain yield per plant. Low magnitude of GCV and PCV was exhibited by canopy temperature depression followed by chlorophyll content and amylose content, rest other traits exhibited medium values of PCV. Further, high heritability coupled with high expected genetic advance as percent of mean was also observed for the traits viz. panicle weight, grain yield per plant, kernel breadth, kernel L/B ratio, proline content(99%) followed by days to 50% flowering, days to first flowering, panicle length (98%) and 1000grain weight, kernel length (97%). Lowest heritability was observed in canopy temperature depression (24%) followed by chlorophyll content (36%) and stomatal conductance (53%). Other traits showed intermediate heritability.

Keywords

Drought, Genetic advance, GCV, Heritability, PCV and Variability

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Introduction

Rice is a cereal crop, belongs to genus *Oryza* of Poaceae family. It is cultivated in 114 countries across the globe, but 90 percent of world's rice is grown in Asia (FAO, 2016). It is the staple food across Asia where around

half of the world's poorest people live and is becoming increasingly important in Africa and Latin America (ricepedia.org/rice-as-a-crop). In April 2017, United State department of Agriculture (USDA) estimated that the world rice production 2016/2017 will be 481.14 million tons, around 0.8 million tons more

than previous year's projection. Similarly, the Indian rice production is expected to be around 109 mt during the year 2016-17 which is the highest ever production of rice till date (AICRIP annual meeting report 2017). About 25% of the world's rice area is under rainfed lowlands. Water is the critical and most important factor in rice production. Drought reduces yield by 15–50 per cent depending on the stress intensity and crop growth period at which the stress occurs in rice (Srividhya *et al.*, 2011). Genetic variability for agronomic traits is the key component of breeding programs for broadening the gene pool of rice and would require reliable estimates of heritability in order to plan an efficient breeding program. Yield component breeding to increase grain yield would be most effective, if the components involved are highly heritable and genetically independent or positively correlated with grain yield. However, it is very difficult to judge whether observed variability is highly heritable or not. Moreover, knowledge of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a character into future generations (Sabesan *et al.*, 2009). So by considering the above points the present investigation was conducted with an objective to assess direct selection parameters (variability, heritability and genetic advance).

Materials and Methods

The field experiment was conducted at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The present research work confined with 20 rice landraces (drought donors including checks) which were received from the project of Stress Tolerant Rice for Africa and South Asia (STRASA), IRRI, Philippines (Table 1). The experiment was laid out in randomized block design (RBD) with three replications. The nursery was raised

on uniform raised beds applied with recommended fertilizer dose. Twenty one days old seedlings were transplanted in main research plot with one seedling per hill. The recommended agronomic practices were followed to raise a good and healthy crop. A bund was made all around the field and water was removed from the field regularly to create drought environment. Data was recorded on five competitive normal looking plants from each treatment in each replication randomly to record the following observations for twenty seven quantitative *Viz.*, Days to 50 per cent flowering, Days to maturity, Plant height (cm), Number of tillers per plant, Number of effective tillers per plant, Panicle length (cm), Number of Spikelets per panicle, Number of grains per panicle, Number of Sterile spikelets per panicle, Grain weight per panicle (g), 1000- grain weight (g), Grain yield per plant (g), Grain yield per plot (g), Biomass (kg/ha), Harvest Index, Grain quality characters, Hulling recovery, Milling recovery, Kernel length (mm), Kernel breadth (mm), Kernel L/B ratio, Amylose content, Canopy temperature depression (CTD), Stomatal conductance ($\text{mmol/m}^2/\text{s}$), Chlorophyll content (SPAD value), Proline content ($\mu\text{mol/g}$ fresh weight). Phenotypic and genotypic coefficient of variation was calculated by the method suggested by Burton and Devane (1953). Heritability was calculated by the formula given by Allard (1960) and genetic advance i.e. expected genetic gain resulting from selecting five per cent superior plants was estimated by the following formula suggested by Allard (1960). The data was analyzed by windostat *version* 9.2 with indostat services.

Results and Discussion

The experimental results obtained from the present study are as follows. The analysis of 27 traits was carried out to partition the total variation into genotypic variation and

variation due to other sources. Analysis of variance was based on the mean values of eleven quantitative traits in 20 rice genotypes. The results pertaining to phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance expressed as percent of mean for all the characters under study are presented in Table 2.

The results of ANOVA revealed considerable variation over the traits under study exhibiting a wide range of phenotypic as well as genotypic coefficient of variation. In general, the values of phenotypic coefficient of variance were higher than those of genotypic coefficient of variance. The relative magnitudes of the phenotypic as well as genotypic variances between the traits were compared based on the phenotypic and genotypic coefficient of variation. PCV was recorded highest for sterile spikelets per panicle (67.48) followed by grains yield per plot (43.24) and grain yield per plant (38.31). Low magnitude of PCV was exhibited by canopy temperature depression (1.98) followed by chlorophyll content (5.32) and amylose content (5.37). The remaining traits exhibited medium values of PCV.

Similarly, GCV was also high for sterile spikelets per panicle (65.94) followed by grains yield per plot (42.22) and grain yield per plant (38.21). Whereas, low magnitude of GCV was exhibited by canopy temperature depression (0.96) followed by chlorophyll content (3.2) and days to maturity (7.03). The differences between the values of PCV and GCV were small for almost all the traits indicating less influence of environment in expression of these traits. However, the differences was comparatively greater in case of stomatal conductance (5.29) followed by effective tillers per plant (4.42) and tillers per plant (2.44).

In the present study, heritability (broad sense) ranged from 36% to 99%. The highest heritability was found in days to maturity, plant height, grain weight per panicle, grain yield per panicle, grain yield per plant, kernel breadth, kernel L/B ratio, proline content(99%) followed by days to 50% flowering, days to first flowering, panicle length (98%) and 1000grain weight, kernel length (97%). Lowest heritability was observed in canopy temperature depression (24%) followed by chlorophyll content (36%) and stomatal conductance (53%). Other traits showed intermediate heritability.

Genetic advance as percent of mean (5%) was realized highest for sterile spikelets per panicle (132.75) followed by grain yield per plot (84.92) and grain yield per plant (78.49). Lowest value was observed in canopy temperature depression (0.97) followed by chlorophyll content (3.97) and amylose content (10.11).

The magnitude of genetic variability decides the effectiveness of selection. It is an established fact that greater the variability among the genotypes better is the chance for further improvement in the crop. But this variability can be utilized better if it is heritable. The heritable portion of the overall observed variation can be ascertained by studying the components of variation such as GCV, PCV, heritability and predicted genetic advance. In this study, the estimates of PCV were higher than their corresponding GCV for all the traits studied. These findings were similar to the findings of Souroush *et al.*, (2004) and Singh *et al.*, (2013). The highest PCV and GCV were high recorded for sterile spikelets per panicle followed by grains yield per plot and grains yield per plant indicating that these traits were under the major influence of genetic control and less variable due to environmental factors. Therefore, such traits are important for further improvement.

Table.1 List of 20 landraces and their sources

S. No.	Name of Genotype	Source
1	B 6149 F-MR-7	I.R.R.I., Philippines (S.A. Hub)
2	DZ 78	I.R.R.I., Philippines (S.A. Hub)
3	E KHAKEHA	I.R.R.I., Philippines (S.A. Hub)
4	E ZI 124	I.R.R.I., Philippines (S.A. Hub)
5	GOPAL	I.R.R.I., Philippines (S.A. Hub)
6	KAUKHMWE	I.R.R.I., Philippines (S.A. Hub)
7	NP 125	I.R.R.I., Philippines (S.A. Hub)
8	NS 252	I.R.R.I., Philippines (S.A. Hub)
9	RTS 4	I.R.R.I., Philippines (S.A. Hub)
10	SOLOI	I.R.R.I., Philippines (S.A. Hub)
11	TCHAMPA	I.R.R.I., Philippines (S.A. Hub)
12	VELLAISEENETTI	I.R.R.I., Philippines (S.A. Hub)
13	WANNIDAHANALA	I.R.R.I., Philippines (S.A. Hub)
14	WAR 72-2-1-1	I.R.R.I., Philippines (S.A. Hub)
15	XI NUOZAO	I.R.R.I., Philippines (S.A. Hub)
16	IR -74371-54-1-1	I.R.R.I., Philippines (S.A. Hub)
17	IR -119	I.R.R.I., Philippines (S.A. Hub)
18	IR-64	I.R.R.I., Philippines (S.A. Hub)
19	SWARNA	ANGRAU, Hyderabad
20	Local check (NDR 359)	NDUAT, Faizabad

IRRI - International Rice Research Institute, Philippines, S.A. Hub – South Ashia Hub, ANGRAU - Acharya N. G. Ranga Agricultural University, NDUAT - Narendra Deva University of Agriculture and Technology

Table.2 ANOVA of 20 rice genotypes for twenty seven yield and yield attributing trait

	Days to First Flowering	Days to 50% Flowering	Days to Maturity	Plant Height cm	Tillers/ Plant	Effective Tillers/ Plant	Panicle Length (cm)	Spikelets/ Panicle	Grains/ Panicle	Sterile Spikelets/ Panicle	Spikelet Fertility %	Grain Weight/ Panicle (g)	1000- Grain Weight (g)	Grain Yield/ Plant (g)	Hulling Recovery %	Milling Recovery%	Kernel Length (mm)	Kernel Breadth (mm)	Kernel L/B Ratio	Amylose Content	Canopy Temperature Depression	Stomatal Conductance (mmol/M ² /S)	Chlorophyll Content (spad Value)	Proline Content (µmol/g Fresh Weight)	Grain Yield/ Plot (kg)	Biomass (kg/ha)	Harvest Index
GCV	9.08	8.46	7.03	18.11	26.60	25.67	7.86	15.03	16.26	65.94	10.79	21.26	10.91	38.21	9.25	12.55	9.41	12.75	19.88	5.13	0.96	14.03	3.20	22.92	42.22	13.49	34.32
PCV	9.19	8.53	7.08	18.23	29.03	30.09	7.95	15.42	16.56	67.48	11.01	21.38	11.06	38.31	9.51	13.04	9.55	12.81	20.00	5.37	1.98	19.33	5.32	23.02	43.24	14.52	34.95
h² (Broad Sense)	0.98	0.98	0.99	0.99	0.84	0.73	0.98	0.95	0.96	0.96	0.96	0.99	0.97	0.99	0.95	0.93	0.97	0.99	0.99	0.91	0.24	0.53	0.36	0.99	0.95	0.86	0.96
Gen.Adv as % of Mean 5%	18.48	17.28	14.39	37.05	50.19	45.12	16.02	30.16	32.90	132.75	21.80	43.56	22.16	78.49	18.53	24.88	19.08	26.15	40.69	10.11	0.97	20.99	3.97	47.01	84.92	25.81	69.42
General Mean	89.63	94.55	117.37	157.19	6.35	4.95	27.01	141.53	116.95	24.55	84.80	2.70	23.63	9.39	81.49	71.51	6.37	2.31	2.86	23.95	29.27	751.41	42.71	17.34	0.46	1.56	28.53
Exp Mean next Generation	106.20	110.89	134.26	215.43	9.54	7.18	31.34	184.22	155.42	57.14	103.28	3.88	28.87	16.76	96.59	89.30	7.59	2.91	4.02	26.37	29.55	909.14	44.41	25.49	0.84	1.97	48.33
Range Lowest	79.33	84.00	106.67	93.13	4.33	3.33	23.30	105.67	84.33	11.33	52.93	1.74	18.04	4.57	62.20	50.89	5.29	1.89	2.04	21.16	28.70	527.17	38.60	9.06	0.21	1.15	16.77
Range Highest	108.33	112.33	141.33	206.31	11.67	8.33	30.07	186.00	158.33	84.67	93.38	3.69	30.26	16.17	92.51	89.01	7.89	2.84	4.15	24.88	30.24	988.40	46.77	25.61	0.82	1.90	45.03

These findings are in close agreement with the researchers Anjaneyulu *et al.*, (2010) and Singh *et al.*, (2013). In the present study traits such as canopy temperature depression followed by chlorophyll content, days of maturity had low estimates of PCV and GCV indicating that selection for these traits will be less effective in comparison to remaining traits. The GCV provides a measure of comparison of variability and sometimes give some indication regarding validity of traits for selection. However, it does not provide clean picture of the extent of genetic gain to be expected from selection of phenotypic traits, unless heritable fraction of variation (heritability) is known (Burton, 1952). The difference between the values of PCV and GCV were small for almost all the traits indicating less influence of environment in expression of these traits suggesting phenotypic differences may be considered as genetic difference among genotypes for selection. However, the difference was comparatively greater in case of stomatal conductance followed by effective tillers and tiller per plant. This cautions that *per-se* performance of these traits should not be taken directly as the basis of selection other variability parameter for these traits such as heritability may also be taken into consideration.

The relative magnitude of genotypic and phenotypic variances for the traits is the broad sense heritability and it is used as analytical role in selection procedures. In the present investigation, high heritability was recorded for most of the characters except spikelet fertility per cent and number of effective tillers. Days to 50% flowering and days to maturity exhibited highest heritability followed by panicle length and total grains per panicle. Similar results were obtained by Mahto *et al.*, (2003), Aktar *et al.*, (2004), Singh *et al.*, (2007), Chouhan *et al.*, (2014) and Lingaiah (2015) in rice genotype they

studied. This indicated that selection of these traits would be more effective as compared to others.

High heritability does not always indicate high genetic gain. Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. It is not necessary that a character showing high heritability will also exhibit high genetic advance. The breeder should be cautious in making selection based on heritability as it indicates both additive and non-additive gene action. Thus, heritability values coupled with genetic advance would be more reliable and useful in formulating selection procedure as it indicates that most likely the heritability is due to additive gene effects. In the present set of materials, high heritability coupled with high genetic advance as percent was recorded for panicle weight, total grains per panicle and filled grains per panicle indicating effectiveness of selection for the improvement of these traits while high heritability coupled with low genetic advance as percent of mean were observed for panicle length, days to maturity and days to 50% flowering which is indicative of non-additive gene action. High heritability coupled with high genetic advance may be attributed to additive gene action. The high heritability is being exhibited due to favorable influence of environment rather than genotype and selection for such traits may not be rewarding. These results are in conformity with the findings of Krishna *et al.*, (2010), Singh *et al.*, (2012) and Sawarkar and Senapati (2014).

In conclusion the Analysis of variance revealed the highly significant differences among the genotypes for all the characters under study. The genotypes exhibited a wide range of variability for most of the traits. This

indicated that there is ample scope for selection of promising genotypes from present set of genotypes for yield improvement. On the basis of *per se* performance, genotypes viz., RTS4, SWARNA, NS252, IR-74371-54-1-1 and IR 119 were found to be the best for yield and yield contributing traits. Therefore, these can be successfully utilized as parents in future breeding programme. Genotype MGD 1206 was earliest in flowering and maturity suggesting that this genotype can be used as a donor in hybridization programme for evolving early maturing rice variety.

The high estimates of genotypic coefficient of variation and phenotypic coefficient of variation were observed for traits viz. sterile spikelets per panicle followed by grains yield per plot and grain yield per plant. Low magnitude of GCV and PCV was exhibited by canopy temperature depression followed by chlorophyll content and amylose content, rest other traits exhibited medium values of PCV. Further, high heritability coupled with high expected genetic advance as percent of mean was also observed for the traits viz. panicle weight, grain yield per plant, kernel breadth, kernel L/B ratio, proline content(99%) followed by days to 50% flowering, days to first flowering, panicle length (98%) and 1000grain weight, kernel length (97%). Lowest heritability was observed in canopy temperature depression (24%) followed by chlorophyll content (36%) and stomatal conductance (53%). Other traits showed intermediate heritability.

Atlast, the present study has revealed valuable information on different yield traits in rice improvement. Genotypes SWARNA, RTS4 E KHA KEHA, IR 119 and IR 64 were found to be the promising genotypes for yield and yield contributing traits. Hence these genotypes can be utilized in future breeding programme to obtain potential transgressive segregants.

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