Environment & Ecology 35 (1B) : 458—462, January—March 2017
Website: environmentandecology.com ISSN 0970-0420

Genetic Variability Studies on Yield and Yield Related Traits of Rice (*Oryza sativa* L.) under Aerobic Condition

Ratnakar Manjunath Shet, M. P. Rajanna, S. Ramesh, M. S. Sheshshayee

Received 20 April 2016; Accepted 25 May 2016; Published online 28 June 2016

Abstract Two hundred *indica* rice accessions were evaluated under areobic condition for thirteen quantitative traits to examine the nature and magnitude of variability and genetic divergence. Among all traits, grain yield per plant exhibited highest estimate of PCV and GCV followed by productive tillers/plant and filled grains/panicle. Broad sense heritability was highest for 50% flowering followed by 1000 seed weight and filled grains/panicle. Accessions with Contrasting expressions for yield and yield related traits were identified for developing suitable rice genotypes under aerobic cultivation.

Keywords Rice, Genetic Variability, Heritability, Aerobic condition.

Introduction

Rice (*Oryza sativa* L.) is the most important cereal food crop of the world and about 90% of the people of South-East Asia consume rice as staple food. Asia's food security depends largely on irrigated rice fields, which produce three quarters of all rice harvested. But rice is a profligate water user, consuming half of all developed fresh water resources. Aerobic rice is a one of the water saving rice production technology. Growing rice aerobically saves water by eliminating continuous seepage and percolation, reducing evaporation and eliminating wetland preparation [1]. Meeting ever increasing demand under water scarcity requires expanding the area od rice under aerobic condition. Exploitation of existing variability is an immediate option for increasing productivity of rice under aerobic condition. Under these considerations, a set of rice germplasm was evaluated for assessing the genetic variability and identifying lines with higher productivity under aerobic conditions.

Materials and Methods

The experimental material comprised of 200 upland

R. M. Shet[1]*, S. Ramesh[2]
College of Horticulture, Sirsi,
UHS Bagalkot, Karnataka, India
Department of Genetics & Plant Breeding.
UAS, GKVK, Bengaluru, Karnataka, India

M. P. Rajanna
Rice Breeding Section, ZARS, V.C. Farm,
Mandya, Karnataka, India

M. S. Sheshshayee
Department of Crop Physiology, USA,
GKVK, Bengaluru, Karnataka, India
e-mail : ratnakarms@gmail.com
*Correspondence

Table 1. Pooled analysis of variance (mean square values) of rice germplasm accessions for productive traits. **Significant @ 0.01.

Source of variation	df	Days to 50% flowering	Plant height (cm)	Total tillers	Productive tillers	Panicle length (cm)	Filled grain per panicle	1000 grain weight (g)	Straw yield per plant (g)	Grain yield per plant (g)
Genotype	199	179.5**	541.6**	9.98**	7.09**	10.7**	2518.9**	23.65**	81.8**	79.8**
Years	1	60.6	16349.9	139.51	329.56	331.15	15313	0.143	222.0	1123
Genotype×year	199	41.48**	56.8**	5.2**	4.4**	1.98	354.3**	0.034	15.49**	27.7**
Pooled error	398	0.32	2.53	0.57	0.40	0.39	19.48	0.13	2.31	2.12

rice genotypes obtained from Central Rice Research Institute, Cuttack. These genotypes were evaluated in randomized complete block design with two replications during 2010 and 2011 rainy seasons at Zonal Agricultural Research Station (ZARS), VC Farm Mandya, Karnataka, India. Each line was grown in a single row of three meters length by maintaining a row spacing of 25 cm and 25 cm between plants within a row in 10 blocks with two replications. Each block consisted of 20 accessions. The crop was directly seeded under the aerobic condition at appropriate moisture condition. Fertilizer dose was applied @ 100:50:50 N:P_2O_5:K_2O kg ha^{-1}. Nitrogen was applied in three split doses, 50% at sowing, 25% at 30 days after sowing and remaining 25% at 45 days after sowing. 100% phosphorus was applied at sowing while potassium was applied in two split doses; 50% at sowing and 50% at 45 days after sowing along with 3rd split of nitrogen. Inter-cultivation with hoe at an interval of 15 days was practiced to control weeds effectively and good crop establishment. Irrigation was given at an interval of 3–5 days during vegetative stage and once in three days during grain filling stage depending on soil moisture condition. Five plants from the each entry in each replication were randomly taken for recording observations on grain yield $plant^{-1}$ and eight yield attributing traits namely, days to 50% flowering, total tillers $plant^{1}$, and 1000-seed weight.

Statistical analysis

Computed average values over replications and years was used for statistical analysis. Rank correlation of performance of accessions in two years was performed for testing the stability of accessions over years for days to 50% flowering, plant height, productive tillers, 1000 seed weight, filled grains per plant and grain yield. Highly significant rank correlation indicated absence of significant G × E interactions and hence data pooled over two years was used for further statistical analysis.

Components of variability

The analysis of variance (ANOVA) was carried out to dissect total variability of the entries into sources attributable to genotype. Variability parameters such as phenotypic coefficient of variability (PCV) and Genotypic coefficient of variability (GCV) were estimated following Burton and De Vane [2]. Heritability in broad sense and genetic advance as per cent mean was estimated by using the formula of Johnson et al. [3].

Results and Discussion

Analysis of variance

The analysis of variance for nine traits including grain yield and its related traits in the present set of rice accessions revealed significant differences for all the traits (Table 1). The suggested that there is an inherent genetic difference among the genotypes. Similar finding for various traits in the rice genotypes were also reported by many rice workers [4, 5]. Considerable range of variation was observed for all the traits under study indicating enough scope for bringing

Table 2. Estimates of genetic variability parameters for nine traits in 200 accessions of rice. *Pooled mean value of two years 2010 and 2011.

Parameters		Days to 50% flowering	Plant height (cm)	Total tillers	Productive tillers	Panicle length (cm)	Filled grain per panicle	1000 grain weight (g)	Straw yield per plant (g)	Grain yield per plant (g)
Range	Min	70	51.80	6.30	4.30	12.26	31.30	11.95	7.10	3.70
	Max	130	144.2	19.10	23.30	26.7	250.55	33.1	50.39	39.54
Mean*		97.70	81.40	11.23	9.45	18.61	91.80	21.44	21.32	16.90
SEm(±)		3.98	0.93	0.11	0.10	0.13	1.82	0.17	0.33	0.33
PCV (%)		10.94	17.63	20.98	20.77	13.24	32.83	16.31	31.58	40.43
GCV (%)		10.87	17.34	19.39	19.29	10.97	32.33	16.15	29.58	38.61
Heritability (%)		98.96	96.81	88.69	87.19	68.61	96.96	97.98	91.48	91.22
Genetic advance % (% of mean)		22.29	35.14	35.36	32.95	19.4	68.57	32.93	58.13	75.99
Rank Correlation between two year performance										
Rank correlation coefficients		0.61	0.83	0.33	0.26	0.28	0.74	0.99	0.68	0.49

about improvement in the desirable direction.

Analysis of variance by itself is not enough and conclusive to explain all the inherent genotypic divergence in the collections. This is revealed by determining the total genetic variability inherent in the genotypes obtained after due partitioning of the phenotypic variance. The phenotypic variation of traits is attributable to genotype and environment assuming absence of interaction between them. The variation due to genotype can only be managed to suit to end-user needs. To compare variation of the accessions across eight productive traits at phenotypic and genotypic levels, the phenotypic and genotypic variations were standardized to make them unit-free and expressed as phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV). Days to 50% flowering was less variable while Grain yield plant^{-1} noticed high variability both at phenotypic and genotypic levels compared to other traits among the germplasm accessions as indicated by its PCV and GCV estimates in relation to other traits. Similar findings were reported by several rice workers [6—9]. However, substantial range in the expression of germplasm lines for all the traits offer ample scope for selection of desirable lines for further use in genetic enhancement. Comparatively limited influence of weather variables on the expression of germplasm lines for most of the traits including grain yield as suggested by narrow difference between PCV and GCV has clearly reflected in higher broad-sense heritability (Table 2). The co-efficient of variation at genotypic and phenotypic levels explain only the extent of variability in different traits, but this variation fails to explain the amount of heritable portion. In this situation, heritability in broad sense has an important role in the determining the heritable portion of variation. Knowledge of heritability of a trait is an essential measure to breeder in choosing suitable genotypes to employ in improving the trait under specified situation. The results in the experiment revealed higher heritability estimate for most of the characters except panicle length. High heritability indicates less influence of environment and is governed by additive gene effects. For the character with low heritability, selection may be considerably difficult or virtually impractical due to the masking effect of environment on genotypic effect [10]. In a comparable study, Vange [11] and Pandey and Anurag [12] also reported high heritability for grain yield per plant and filled

Table 3. Accessions with contrasting expressions for productive in rice germplasm (The mean values are of two years 2010 and 2011).

Sl. No.	Character	Accession with lowest performance	Mean value	Accessions with highest value	Mean value
1	Days to 50% flowering	APS-397	71	AC-35187	117
		AC-35375	72.75	AC-35382	117.5
		PS-397	74	BR-2655	118
		AC-39040	74.5	PS-207	121
		PS-402	75	JBT-38/109	130
2	Plant height	PS-290	54.3	AC-39020	120.5
		AC-35066	54.825	AC-35006	121.5
		PS-389	58.6	AC-39019	126.95
		MTU-1045	59.05	AC-39016	129.4
		SAMRAT	60	PS-267	134.85
3	Productive tillers	AC-39020	4.3	AC-35027	17.9
		JBT-37/126	5.15	RASI	17.95
		PS-224	5.35	AC-35516	18.2
		AC-35607	5.5	PS-225	18.55
		PS-402	5.75	JBT-36/76	23.3
4	Panicle length	JBT-37/85	12.625	AC-39016	25.1
		AC-39012	13.73	BR-2655	25.7
		JBT-36/114	14.54	AC-39021	25.75
		PS-367	14.87	AC-39020	26.7
		JBT-37/170	15.07	PS-267	27.4
5	1000-grain weight	JBT-37/24	11.97	AC-39016	31
		JBT-37/4	12.62	PS-302	31.66
		SAMRAT	13.66	PS-306	32.25
		IET-17616	14.46	DODDABATTA	33.1
		BPT-5204	14.68	PS-305	33.75
6	Filled grains per panicle	PS-367	31.3	SAMRAT	174.5
		JBT-38/109	41.05	AC-35135	180.4
		JBT-37/154	47	AC-39020	190.5
		JBT-36/119	47.5	PS-399	191.1
		JBT-37/29	47.5	PS-267	250.55
7	Straw yield	JBT--38/2	7.41	AC-39016	38.69
		JBT-27/110	9.47	JBT-38/61	39.91
		PS-253	9.52	AC-35027	41.85
		MTU-1045	10.52	RASI	41.98
		JBT-36/126	11/03	JBT-36/79	50.27
8	Grain yield	PS-250	3.7	JBT-36/79	35.24
		AC-35476	5.54	RASI	37.15
		JBT-36/126	5.858	AC-39000	37.18
		IET-17616	6.66	JBT-36/14	38.783
		JBT-38/109	7.095	JBT-38/88	39.32

grain per panicle. The broad-sense heritability does not indicate relative magnitude of additive (fixable) and non-additive (non-fixable) genetic variation [13]. Since rice is self pollinated crop, the germplasm represents a mixture of pure-lines. The genetic component of variability among rice germplasm accessions is therefore attributable to additive and additive-based epistatic interaction of genes controlling different traits. Hence, the broad-sense heritability estimates for different traits in the present study also represent narrow-sense heritability estimates. Fairly higher broad-sense heritability (also narrow-sense heritability for reasons explained) suggested effectiveness of selection for the traits under study as is also indicated by higher predicted genetic advance. Higher predicted genetic advance could be realized as the genetic variation among the germplasm accessions is solely attributable to genes acting additively, which cause greater resemblance between selected parents and their progeny. Maximum genetic gain per cycle could be realized even with simple pure-lines selection.

Productive trait-specific accessions

Enhanced utilization of germplasm resources requires identification of accessions possessing useful traits. In some of the crop improvement programs, especially those in international crop research organizations, where trait-based breeding is followed, identification of trait-specific accessions is a prerequisite. The accessions such as AC-35375 PS-397 AC-39040 PS-402 and APS-397 with least days to 50% flowering. AC-39020, AC-35006 AC-39019 AC-39016 and PS-267 with highest plant height and RASI, AC-39000, JBT-38/88, JBT-36/79 and JBT-36/14 with highest grain yield plant^{-1} (Table 3) are useful in breeding early duration (which help escape terminal drought, a common a biotic stress in acrobic rice growing areas) cultivars with higher grain and straw yields. The accessions contrasting for economic traits are useful in inheritance studies and developing trait-based mapping populations for chromosomal localization and molecular dissection of genes controlling the economic traits. For example, accessions such as RASI, AC-39000, JBT-36/14, JBT-38/88 and JBT-36/79 with highest expression for grain yield plant^{-1} and those such as PS-250, AC-35476, JBT-36/126, IET-17616 and JBT-38/109 with lowest expression for grain yield plant^{-1} (Table 3) would be prospective candidate parents for developing mapping populations for molecular dissection of genes controlling grain yield. DNA markers that are in near complete linkage disequilibrium with genomic regions affecting grain yield, would facilitate marker-assisted introgression of quantitative trait loci (QTLs) controlling grain yield into elite agronomic background. The accessions (PS-290 and PS-267) that are contrasting for plant height, number of productive tillers plant^{-1} and grain yield plant^{-1} are useful for developing multiple traits-based mapping population for molecular dissection, chromosomal localization and unraveling mode of action of genes controlling these traits simultaneously.

References

1. Subramanial E, James Martin G, Suburayalu E, Mohan R (2008) Aerobic Rice: Water saving rice production technology. IWMI Publ, pp 239—243.
2. Burton GW, De Vane EM (1953) Estimating heritability in tall Fescue (*Festuca arundinaceae*) from replicated clonal-material. Agron J 51 : 515—518.
3. Johnson HW, Robinson HI, Comstock RE (1955) Estimation of genetic and environmental variability in soybean. Agron J 47 : 314—318.
4. Singh RP, Kumar MS, Madhavilatha L (2007) Variability and relationship studies of yield and yield attributing traits in diverse lines of international irrigated observational nursery of rice (*Oryza sativa* L.). J Res ANGRAU 35 : 16—22.
5. Singh Sangam Kumar, Singh Chandramohan, Lal GM (2011) Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). Res Pl Biol 1 : 73—76.
6. Anandrao SD, Singh CM, Suresh BG, Lavanya GR (2011) Evaluation of rice hybrids for yield and yield component characters under North East Plain Zone. The Allahabad Farmer 67 : 63—68.
7. Prajapati M, Singh CM, Suresh BG, Lavanya GR, Jadhav P (2011) Genetic parameters for grain yield and its component characters in rice. Elec J Pl Breed 2 : 235—238.
8. Sravan T, Rangare NR, Suresh BG, Ramesh Kumar S (2012) Genetic variability and character association in rainfed upland rice (*Oryza sativa* L.). J Rice Res 5 : 24—28.
9. Sarma MK, Goswami RK, Sharma AK, Baruah Mayur, Sarma D, Neog P (2015) Genetic variability and diversity in indigenous rice germplasm of Assam under aerobic condition. Prog Agric 15 : 66—70.
10. Sedeek SEM, Hammoud SAA, Ammar MH, Metwally TF (2009) Genetic variability, heritability, genetic advance and cluster analysis for some physiological traits and grain yield and its components in rice (*Oryza sativa* L.). J Agric Res Kafer El-Sheikh Univ 35 : 858—878.
11. Vange T (2009) Biometrical studies on genetic diversity of some upland rice (*Oryza sativa* L.) accessions. Nature and Sci 7 : 21—27.
12. Pandey Praveen, Anurag P. John (2010) Estimation of genetic parameters in indigenous rice. Adv Agric and Bot 2 : 79—83.
13. Chahal GS, Gosal SS (2002) Principles and procedures of plant breeding: biotechnological and conventional approaches. Narosa Publ House, New Delhi, India, pp 604.