

Original Research Article

<https://doi.org/10.20546/ijcmas.2017.608.064>

Genetic Variability Analysis for Grain Yield and its Components Traits in Traditional Rice Varieties (TRVs)

B. Nandini^{1*}, E. Gangappa², M.P. Rajanna³, P. Mahadevu⁴, S. Ramesh²
and P.V. Shailaja Hittalmani²

¹Seed Unit, UAS, Dharwad-580005, India

²Department of Genetics and Plant Breeding, UAS, GKVK, Bangalore -560065, India

³Zonal Agricultural Research Station, V.C. Farm, Mandya, India

⁴Department of Genetics and Plant Breeding, College of Agriculture, Mandya, India

*Corresponding author

ABSTRACT

Three hundred and twenty four Traditional Rice Varieties (TRVs) were collected from different parts of Karnataka and were evaluated for grain yield and its attributes in two seasons (*kharif* 2011 and summer 2012) at ZARS, VC Farm, Mandya, Karnataka, India. The 14 quantitative traits studied were categorized into growth traits (days to 50% flowering, Plant height, Productive and tillers plant⁻¹), panicle traits (panicle length, spikelet panicle⁻¹, chaffy panicle⁻¹ and spikelet fertility), grain quality traits (grain length, grain breadth and L/B ratio) and grain yield traits (1000 grain weight, straw yield plant⁻¹, harvest index and grain yield plant⁻¹). Substantial variability among the accessions for quantitative traits was recorded. The variability parameters such as mean, range, standardized range, PCV, GCV, h²(bs) and genetic advance in TRVs were estimated. The pattern of genetic diversity was estimated using model based K means clustering approach statistics and formed four distinct clusters. The quantitative traits means and variances differed significantly among the clusters. Cluster I comprised of the maximum number of TRVs (137) and cluster IV consisted of 21 TRVs. The cluster IV followed by cluster II contributed maximum mean values for many traits. These results are discussed in relation to suitable strategies to be adopted for breeding rice varieties for increased productivity.

Keywords

GCV, PCV, Genetic advance and K means cluster.

Article Info

Accepted:

04 June 2017

Available Online:

10 August 2017

Introduction

Traditional Rice Varieties (TRVs) are an important component of crop genetic resources and are valued by rice breeders and farmers because of diversity, rarity and adaptability (Brush and Meng, 1998; FAO, 1998; Smale, 2006 and Gauchan *et al.*, 2006). TRVs are often highly variable in appearance, but they are each identifiable morphologically and have a certain genetic integrity. Farmers assign them local names

based on their distinct properties or particular characteristics as each TRVs has a reputation for adaptation to specific ecosystem. Hence farmers and researchers throughout the world continue to maintain and manage these TRVs within their production systems (FAO, 2010). Yet, their complete genetic potential has not yet been exploited in crop breeding programme (Gyawali *et al.*, 2010).

Undeniably, the success of green revolution has resulted in gradual erosion of genetic diversity of many crops, including rice, due to the replacement of TRVs with modern high-yielding cultivars. Owing to their adaptation to a wide range of agro-ecological conditions, TRVs provides tremendous genetic variability not found in modern varieties (Hanamaratti *et al.*, 2008). Increased use of TRVs in crop breeding programmes would help enhance genetic base of cultivars whose cultivation significantly contribute to stable and sustainable production. Under these premises, TRVs were collected from different locations and conserved at Zonal Agricultural Research Station (ZARS), Mandya, India. As a prelude to their use in breeding programmes variability among TRVs was assessed for traits of economic importance and the results obtained are reported in this article.

Materials and Methods

A collection of 225 TRVs constituted the material for the study. TRVs collected from different regions of southern Karnataka and maintained at AICRP on rice at ZARS, V.C. Farm, Mandya, Karnataka, India. The TRVs were sown following 15 x 15 Simple Lattice Design with two replications during *kharif* 2011 and summer 2012 at ZARS, Mandya, India. Each entry was sown in four rows each of 1.0 m length with spacing of a 0.3 m between rows and 0.20 m between plants within a row. All the recommended agronomic practices were followed during crop growth period to raise a healthy crop.

Observations were recorded on five plants selected at random from each entry in each replication for 14 metric traits. For the sake of convenience, the metric traits were classified into four sub groups such as (i) growth traits (days to 50% flowering,

plant height and productive tillers per plant) (ii) panicle traits (panicle length, spikelets panicle⁻¹, chaffy spikelet panicle⁻¹ and spikelet fertility) (iii) grain quality traits (grain length, grain breadth and L/B ratio) and (iv) yield traits (1000 grain weight, straw yield plant⁻¹, harvest index and grain yield plant⁻¹). The mean of five plants for each metric trait was considered for statistical analysis. Descriptive statistics such as range and variance and their standardized values - Standardized range [(Maximum-Minimum/Mean ×100)], Phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), heritability and genetic advance were estimated (Snedecor and Cochran, 1994) to quantify variability and compare across traits.

The TRVs were grouped into four cluster using K means model (Macqueen, 1967) based clustering approach. The metric traits mean and variances among TRVs included in each cluster were estimated. The significance of trait means and variance among the four clusters was examined following 'F' and Levene (1960) tests, respectively.

Results and Discussion

Pooled analysis of variance for 14 metric traits (Table 1) revealed significant differences among the TRVs for all the traits indicating the existence of ample variability among the TRVs all the traits.

Components of variability, heritability and genetic advance

Presence of genetic variability *per se* is of less significance in crop breeding programmes. Knowledge on relative contribution of genetic and non-genetic sources on the quantitative trait variability is useful in formulating appropriate selection strategies to breed improved rice varieties. The estimates of standardized range provide clues about the

occurrence of accessions with extreme expression which varied with the trait. However, standardized range *per se* does not reflect variability in the expression of all the accessions. The estimates of GCV and PCV which reflect average inter-accession differences are more useful statistics to understand variability among the germplasm accessions.

A higher PCV than GCV with narrow difference between them indicated a limited role of seasonal variation in the expression of most of the traits in TRVs (Table 2). High heritability coupled with high genetic advance indicated the effectiveness of selection for days to 50% flowering, grain length, grain breadth L/B ratio and straw yield plant⁻¹ (Mall *et al.*, 2005, Ganapathy *et al.*, 2007 and Karim *et al.*, 2007).

The traits such as chaffy spikelet panicle⁻¹, straw yield plant⁻¹ and grain yield plant⁻¹ exhibited low heritability with moderate genetic advance, indicating possible role of non-additive gene effects in the inheritance of these characters. Hence, simple selection for these characters would be less effective. The response to selection for traits such as days to 50% flowering, productive tillers plant⁻¹, L/B ratio and 1000 grain weight with high genotypic variance, high heritability coupled with high expected genetic gain would be encouraging.

Variability analysis

The efficiency and pace of rice genetic improvement programmes hinges on the precise information on magnitude of fixable (additive and additive based epistasis) component of genetic variability, $g \times e$ (both spatial and temporal) interaction, and DNA marker-assisted chromosomal localization and mode of action of genes controlling traits of economic importance. The identification of

accessions contrasting for traits of economic importance is a prerequisite for eliciting such information. Cluster analysis helps in grouping of accessions sharing similar characters in different clusters and to identify genetically diverse and desirable genotypes.

The information of genetic variability *per se* is not of much utility in crop breeding programmes. The organization of variability in terms of grouping TRVs based on their similarity and dissimilarity would help to choose the potential parents for hybridization and to obtain useful segregants.

The mean expression of growth traits such as days to 50% flowering, plant height and productive tillers plant⁻¹ of TRVs included in clusters I and IV was highest. Among panicle traits, means of TRVs included in cluster II followed by cluster IV was higher (Tables 3 and 4). A higher mean value was noticed for grain quality of TRVs included in cluster III followed by cluster II was better than that in other cluster. The grain yield potential of TRVs included in cluster IV was better than those included in other clusters. Effecting crosses among the TRVs of cluster II and cluster IV is expected to recover genotypes with combination of desired traits.

Traits-specific accessions

Exploitation of natural genetic variability help meet short-term objectives as very often breeders are forced to meet immediate requirement of the farmers, consumers and end-users. Continued crop genetic improvement to meet medium- and/long-term requirements requires availability of variability induced through deliberately planned crosses among the genotypes harbouring desired combination of traits. Evaluation of germplasm provides information about the accessions/genotypes with desired combination of traits.

Table.1 Pooled analysis of variance for grain yield and its component traits in Traditional Rice Varieties

Source of variation	df	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Productive tillers plant ¹	Spikelet's panicle ⁻¹	Chaffy panicle ⁻¹	Spikelet fertility (%)
Replications	1	6.74	139.80	12.44	7.57	463.77	347.46	59.48
TRVs	224	298.25	477.90	6.56	7.36	1440.50	138.14	78.30
Seasons	1	6977.81	11154.18	145.30	1136.81	20579.08	56368.89	45185.68
TRVs × Seasons	224	209.12	231.29	1.73	5.30	212.53	128.12	85.42
Error	448	4.76	103.75	2.06	2.14	214.90	76.62	47.15
Total	899							

* Significant @ P=0.05

** Significant @ P=0.01

Table 1: Contd...

Source of variation	Df	1000 grain weight (g)	Grain length (mm)	Grain breadth (mm)	L/B ratio	Straw yield plant ⁻¹ (g)	Harvest index	Grain yield plant ⁻¹ (%)
Replications	1	15.36	0.27	0.00	0.11	598.33	0.07	35.89
TRVs	224	35.34	5.75	0.70	2.30	33.53	0.01	26.85
Seasons	1	336.05	0.00	0.01	0.12	6312.52	0.65	1065.94
TRVs × Seasons	224	9.57	0.22	0.01	0.11	27.76	0.01	29.30
Error	448	8.01	0.10	0.00	0.00	18.15	0.00	13.10
Total	899							

* Significant @ P=0.05

** Significant @ P=0.01

Table.2 Estimates of descriptive statistics and components of variability for grain yield and its component traits of Traditional Rice Varieties

Classification	Traits	Mean ± SE	Range		Standardized range	Coefficient of variability		Broad sense heritability (%)	Genetic Advance as per cent of mean
			Lowest	Highest		GCV	PCV		
Growth traits	Days to 50% flowering	90.80 ± 0.57	71.75	115.75	0.48	9.42	9.59	96.53	19.07
	Plant height (cm)	120.28 ± 0.72	83.28	148.81	0.54	7.95	10.10	61.88	12.88
	Productive tillers plant ⁻¹	8.75 ± 0.09	5.36	14.98	1.10	13.43	17.33	60.05	21.44
Panicle traits	Panicle length (cm)	23.09 ± 0.08	18.80	27.35	0.37	4.75	6.24	57.79	7.43
	Spikelet panicle ⁻¹	128.23 ± 1.26	74.25	194.92	0.94	13.58	15.92	72.81	23.88
	Chaffy panicle ⁻¹	28.23 ± 0.39	11.00	47.83	1.30	13.57	26.12	26.98	14.52
	Spikelet fertility (%)	77.48 ± 0.29	59.58	87.83	0.36	3.49	7.28	22.92	3.44
Grain quality traits	Grain length (mm)	8.02 ± 0.07	4.14	11.24	0.88	14.82	15.07	96.72	30.02
	Grain breadth (mm)	2.58 ± 0.02	1.74	3.45	0.66	16.15	16.29	98.27	32.99
	L/B ratio	3.19 ± 0.05	1.32	5.78	1.40	23.89	24.07	98.49	48.84
Yield traits	1000 grain weight (g)	23.09 ± 0.19	14.87	30.28	0.67	11.29	14.27	62.50	18.38
	Straw yield plant ⁻¹ (g)	15.29 ± 0.19	8.85	27.03	1.19	13.72	23.00	35.58	16.86
	Harvest index	0.48 ± 0.01	0.33	0.66	0.68	9.60	15.34	39.20	12.38
	Grain yield plant ⁻¹ (g)	14.04 ± 0.17	6.94	20.75	0.98	13.54	22.29	36.87	16.93

Table.3 Estimates of traits means among Traditional Rice Varieties classified into different clusters

Classification	Traits	Mean of Clusters				'F' Statistics	Probability
		C1	C2	C3	C4		
	Size of cluster	137	41	26	21		
Growth traits	Days to 50% flowering	91.72	89.84	87.54	91.08	1.93	0.13
	Plant height (cm)	122.04	123.32	99.55	127.47	61.74	<.0001
	Productive tillers plant ⁻¹	8.77	8.83	9.90	8.41	2.09	0.10
Panicle traits	Panicle length (cm)	23.13	23.45	22.04	23.31	7.34	0.00
	Spikelet panicle ⁻¹	130.93	103.90	118.96	168.54	225.14	<.0001
	Chaffy panicle ⁻¹	28.96	23.24	28.30	33.72	21.01	<.0001
	Spikelet fertility (%)	77.37	77.49	76.04	79.47	2.31	0.08
Grain quality traits	Grain length (mm)	7.88	8.26	8.30	8.13	1.72	0.16
	Grain breadth (mm)	2.65	2.58	2.42	2.44	3.16	0.03
	L/B ratio	3.05	3.31	3.63	3.47	6.04	0.00
Yield traits	1000 grain weight (g)	23.38	22.95	21.44	23.56	3.37	0.02
	Straw yield plant ⁻¹ (g)	15.41	15.58	13.67	15.85	3.26	0.02
	Harvest index	0.48	0.49	0.59	0.49	3.04	0.03
	Grain yield plant ⁻¹ (g)	13.99	14.44	13.59	14.36	0.70	0.55

Table.4 Estimates of traits variances among Traditional Rice Varieties classified into different clusters

Classification	Traits	Variance of Clusters				Chi square	Probability
		C1	C2	C3	C4		
	Size of cluster	137	41	26	21		
Growth traits	Days to 50% flowering	84.36	49.60	67.46	63.81	4.29	0.23
	Plant height (cm)	57.24	71.49	96.89	125.84	8.18	0.04
	Productive tillers plant ⁻¹	1.64	3.46	31.16	1.53	155.20	<.0001
Panicle traits	Panicle length (cm)	1.44	1.69	1.99	1.87	1.62	0.65
	Spikelet panicle ⁻¹	62.43	105.27	108.06	238.25	22.21	<.0001
	Chaffy panicle ⁻¹	23.30	20.48	38.39	55.17	10.96	0.01
	Spikelet fertility (%)	16.69	26.45	31.24	14.32	7.62	0.05
Grain quality traits	Grain length (mm)	1.30	1.27	1.29	2.76	6.37	0.10
	Grain breadth (mm)	0.16	0.21	0.13	0.21	2.22	0.53
	L/B ratio	0.40	0.62	0.91	1.11	16.78	0.00
Yield traits	1000 grain weight (g)	8.44	8.04	5.19	15.64	7.15	0.07
	Straw yield plant ⁻¹ (g)	8.46	7.28	7.17	9.40	0.74	0.86
	Harvest index	0.00	0.00	0.22	0.01	344.80	<.0001
	Grain yield plant ⁻¹ (g)	6.86	5.96	8.68	5.90	1.32	0.72

Table.5 Traditional Rice Varieties with contrasting expression for selected traits

Sl.No	Characters	Identity accessions of lowest value	of with Mean value	Identity accessions of highest value	of with Mean value
1	Days to fifty % flowering	Tabandi sal	71.75	Anandi	114.75
		Dani sal	73.00	Gowrisanna	115.50
		Jeervel	74.25	Gowrisanna	115.75
		Rahodaya	74.75	Kaggali kervana	115.75
		Chinna pooni	75.25	Manila	115.75
2	Spikelet fertility(%)	Anekombu batta	59.58	Navara	85.96
		Kali katesi	61.18	Malkod	86.47
		Kempudadde gida	62.90	Guddani	86.52
		Anandi	65.04	Adikane	86.56
		Dodda alur	65.67	Kartha	87.83
3	1000 grain weight(g)	Bilikanna Hegge	14.87	Dodda batta	29.06
		Jeerige sanna	14.95	Sampoge	29.27
		Gandha Sale	15.55	Andra basumati	29.65
		Theertha halli local	16.21	Tiruvani	30.25
		Gowrisanna	16.86	Malkod	30.28
4	Straw yield plant ⁻¹	Kari Swarna	8.85	Rajboga	23.28
		Sampoge	9.31	Coimbathour	23.71
		Sanna mallige	9.37	K.N. local	24.39
		Nagabatta	10.09	Toranada batta	24.70
		Gandha Sale	10.10	Bangara Sanna	27.03
5	Harvest index	Bilidoddi	0.33	Ramgali	0.60
		Kali katesi	0.33	Kaduvelpe	0.60
		Bigan manji	0.34	Kundi pullan	0.61
		Toranada batta	0.35	Nagabatta	0.62
		Kalajeera	0.36	Sampoge	0.66
6	Grain yield plant ⁻¹	Kali katesi	6.94	Possugandhi	19.57
		Nirga samba	7.30	Kaduvelpe	20.01
		Kari Swarna	7.86	Bangara sanna	20.11
		Bigan manji	7.87	Kannur	20.22
		Kalajeera	8.20	Putta batta	20.75

Some of the TRVs were superior for six selected traits such as days to fifty per cent flowering, spikelet fertility, 1000 grain weight, straw yield, harvest index and grain yield/plant. The TRVs contrasting for these selected six traits were identified (Table 5). The TRVs such as Tabandi sal, Dani sal,

Jeervel, Rahodaya and Chinna pooni with fewer days to 50 per cent flowering, Navara, Malkod, Guddani, Adikane and Kartha with high spikelet fertility, Dodda batta, Sampoge, Andra basumati, Tiruvani and Malkod with high 1000 grain weight, Rajboga, Coimbathour, K.N. local, Toranada batta and

Bangara Sanna with high straw yield, Ramgali, Kaduvelpe, Kundi pullan, Nagabatta and Sampoge with high harvest index, Kali katesi, Nirga samba, Kari Swarna, Bigan manji and Kalajeera for high grain yield was identified. These TRVs are useful for developing populations for mapping genes controlling all these traits simultaneously.

References

- Brush, S., Meng, E. 1998. Farmers' valuation and conservation of crop genetic resources. *Genet. Res. Crop Evol.*, 45: 139–150.
- FAO. 1998. The state of the world's plant genetic resources for food and agriculture. United Nations Food and Agriculture Organization (FAO), Rome, Italy.
- FAO. 1998. The state of the world's plant genetic resources for food and agriculture. United Nations Food and Agriculture Organization (FAO), Rome, Italy.
- Ganapathy, S., Ganesh, S.K., Vivekanandan, P., Shanmugasundaram, P. and Babu, R.C. 2007. Variability and interrelationship between yield and physiomorphological traits in rice (*Oryza sativa* L.) under moisture stress condition. *Crop Res.*, 34(1/3): 260-262.
- Gauchan, D., Smale, M.M.N. and Cole, M. 2006. Managing rice biodiversity on-farms: The choices of farmers and breeders in Nepal. In: Small M (ed) Valuing crop biodiversity: on-farm genetic resources, economic change. CABI Publishing, Wallingford, UK, pp 162–176.
- Gyawali, S., Sthapit, B.R., Bhandari, B., Bajracharya, J., Shrestha, P.K., Upadhyay, M.P. and Jarvis, D.I. 2010. Participatory crop improvement and formal release of Jethobudho rice landrace in Nepal. *Euphytica*, 176: 59–78.
- Hanamaratti, N.G., Prashanthi, S.K., Salimath, P.M., Hanchinal, R.R., Mohankumar, H.D., Parameshwarappa, K.G. and Raikar, S.D. 2008. Traditional land races of rice in Karnataka: Reservoirs of Valuable traits. *Curr. Sci.*, 94(2): 242-247.
- Karim, D., Sarkar, U., Siddique, M.N.A., Khaleque Miah, M.A. and Hasnat, M.Z. 2007. Variability and genetic parameter analysis in aromatic rice. *Int. J. Sustain. Crop Prod.*, 2(5):15-18.
- Levene, H. 1960. Robust tests for equality of variances. In: Olkin *et al.*, (ed.). Contributions to probability and statistics: Essays in honour of Harold Hotelling. Stanford University Press, Stanford pp: 278–292.
- Macqueen, J. 1967. Some methods for classification and analysis of multivariate observations, *Fifth Berkeley Symposium*, pp. 281-297.
- Mall, A.K., Babu, J.D.P. and Babu, G.S. 2005. Estimation of genetic variability in rice. *J. Maharashtra Agril. Univ.*, 30(2): 166-168.
- Smale, M. 2006. valuing crop biodiversity: on-farm genetic resources and economic change. CABI Publishing, Wallingford, UK, pp no: 1-4.
- Snedecor, G.W. and Cochran, W.G. 1994. Statistical methods. 8th edition, Iowa state university press, Ames, Iowa, USA.

How to cite this article:

Nandini, B., E. Gangappa, M.P. Rajanna, P. Mahadevu, S. Ramesh and Shailaja Hittalmani, P.V. 2017. Genetic Variability Analysis for Grain Yield and its Components Traits in Traditional Rice Varieties (TRVs). *Int.J.Curr.Microbiol.App.Sci.* 6(8): 494-502.
doi: <https://doi.org/10.20546/ijcmas.2017.608.064>