



Short communication

Genetic assessment of core set developed from short duration rice accessions held by Kerala Agricultural UniversityPawan Saini^{1*}, Rose Mary Francies¹, Jiji Joseph¹, Dijee Bastian¹ and Veena Vigneshwaran²¹Department of Plant Breeding and Genetics, College of Horticulture, Kerala Agricultural University, Thrissur, Kerala 680 656, India; ²RARS Pattambi, Palakkad, Kerala 679 306, India

Received 17 August 2013; received in revised form 9 October 2013; accepted on 29 October 2013

Abstract

A subset (core set) of the base collection comprising of 160 short duration rice germplasm accessions held by Kerala Agricultural University, Thrissur was formed based on twenty-four quantitative characters using the Power Core (v.1.0). Assessment of variability for yield and yield attributes in the core set pointed to the existence of high variability among the genotypes. High variability with respect to plant height, culm length, stem thickness, days to heading, leaf blade length, total tillers per plant, productive tillers per plant, panicle length, spikelets per panicle, grains per panicle, test weight of grain, grain length, grain width, straw yield per plant and grain yield per plant indicated good scope for improvement. The genotypic coefficient of variation, heritability and genetic gain estimates were high for all the traits studied, indicating that selection will be rewarding for improvement of these traits.

Key words: Core set, Rice, Variability, Genotypic coefficient of variation, Heritability, Genetic gain, Germplasm

Rice occupies the prime place among the food crops cultivated in Kerala. The undulating topography, the slopy terrain, high rainfall, the criss-crossing rivers and their deltaic formations, the backwater systems and saline water intrusion have all resulted in a variety of heterogeneous waterlogged ecosystems where rice alone could be cultivated. Diversity of cropping systems, the edaphic and climatic variations found among and within different regions, as well as among farmers within these regions have resulted in a cafeteria of diverse genotypes (Sasidharan et al., 2002).

Kerala Agricultural University (KAU), holds a rice germplasm collection of over 1000 accessions of varying duration assembled since its inception in 1972. However, a detailed, comprehensive and accurate characterization of the collection is wanting. In addition, selection of an appropriate

genotype for breeding programmes from this vast diverse collection often proves difficult and in turn becomes an obstacle to the effective and efficient utilization of the germplasm in crop improvement programmes.

Frankel and Brown (1984) proposed the concept of “core collection” as a collection that encompasses a representative sample of the entire collection with minimum repetitiveness and maximum genetic diversity of a crop species and its relatives. The concept of forming core collection serves as a very effective alternative from the point of enhancing the utility of this conserved germplasm, as it captures the complete diversity of the entire collection it was derived from.

Genetic variability is pre-requisite for any breeding material as it provides not only a basis for selection

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but also some valuable information regarding selection of diverse parents for use in hybridization programme. Thus improvement in any crop is based on the extent of genetic variation and the degree of improvement depends upon the magnitude of useful genetic variability. In the light of the above facts, the present investigation was carried out to assess the variability in yield and yield attributes in the core set formed from the short duration germplasm collection held by KAU.

An Augmented Blocks Design experiment was laid out with 16 compact blocks accommodating a total of 160 short duration germplasm accessions (Base collection) and three checks [Jyothy (PtB 39), Kanchana (PtB 50) and Harsha (PtB 55)] during *kharif* 2011-2012 in the Department of Plant Breeding and Genetics, College of Horticulture, Vellanikkara. Each block comprised of 10 accessions (unreplicated) and the three checks. Each accession was sown in two rows of 3 m length at spacing of 20 cm x 15 cm. Recommended agronomic practices as per package of practices of KAU (2007) were followed during crop growth period to raise a good crop.

The accessions were characterized as per descriptor of rice (Rani et al., 2004; IRRI, 2007) with respect to forty one qualitative characters and twenty four quantitative characters. A subset (core set) of the Base collection capturing 87.08 per cent of the total diversity in qualitative traits and 107.32 per cent in quantitative traits was formed based on the twenty-four quantitative characters using the Power Core (v.1.0) (Kim et al., 2007). Power Core' is widely used for the establishment of core and allele mining set by the Advanced M (Maximization) strategy implemented through a modified Heuristic Algorithm. 'Power Core' by default classifies the continuous variables into different categories based on Struges's rule (Struges, 1926), which is described as: $K = 1 + \log_2 n$, where n = number of observed accessions. However, the software also allows modifying this rule to make desired number of classes for the continuous variables. Once classi-

fication of the continuous variables is performed, the software takes into account all classes, without omission of any of its variables. Thus, it possesses the capability to cover all the distribution ranges of each class. It minimizes the loss of useful alleles and effectively selects accessions with highest diversity reducing the repeated alleles.

Observations recorded on yield and yield attributes viz., plant height (cm), culm length (cm), stem thickness (mm), days to heading, leaf blade length (cm), total tillers per plant, productive tillers per plant, panicle length (cm), spikelets per panicle, grains per panicle, test weight of grain (g), grain length (mm), grain width (mm), straw yield per plant (g) and grain yield per plant (g) in the core set were analyzed for their variance as outlined by Sapra and Agarwal (1991). Analysis was done using "Augment 1" software (Sapra and Agarwal, 1995). The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) were classified as low, moderate and high as suggested by Subramanian and Menon (1973). Heritability and genetic gain were also classified into low, moderate and high according to Robinson et al., (1949) and Johnson et al., (1955) respectively.

Analysis of variance (Table 1) showed highly significant differences for all the characters studied, suggesting the existence of high variability among the genotypes.

The estimates depicting the statistical and genetic variability including mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic gain are presented in Table 2. The range of variability was wide with respect to plant height, culm length, days to heading, spikelets per panicle and grains per panicle. Moderate variability was observed for length of leaf blade, total tillers per plant, productive tillers per plant, panicle length, straw and grain yield. However, the range of variability with respect to grain width, test weight of grain, grain length and stem thickness was narrow.

Table 1. Analysis of variance for quantitative traits in core set of short duration rice accessions of Kerala

Source	Blocks	Treatments	Checks	Genotypes (unreplicated)	Genotypes v/s Checks	Error
df	3	36	2	33	1	6
Plant height (cm)	4.93	2263.58	7.17	2449.91**	627.64*	7.80
Culm length (cm)	6.07	3141.00	54.84*	2911.72**	16879.55**	13.38
Stem thickness (mm)	0.02	1840.08	0.36	1824.33**	6039.02**	0.13
Days to heading	3.42	2002.03	60.08**	1406.38**	25542.09**	1.75
Leaf blade length (cm)	10.38	1069.32	10.51	1117.26**	1604.93*	3.00
Total tillers per plant	1.80	1366.03	9.64	1417.60**	2376.96*	65.00
Productive tillers per plant	1.80	1440.40	9.64	1442.56**	4230.81*	0.65
Panicle length (cm)	0.11	1334.93	0.08	1438.96**	571.67*	0.13
Spikelets per panicle	119.20	5531.02	116.45**	1795.17**	139643.30**	200.73
Grains per panicle	139.88	4428.69	103.55**	4196.88**	20728.67**	230.80
Test weight of grain (g)	0.04	4373.98	0.02	4582.05**	6255.53**	0.03
Grain length (mm)	0.05	3033.35	0.96	2937.11**	12274.04**	0.03
Grain width (mm)	0	2989.89	0.06	2794.03**	15432.89**	0.01
Straw yield per plant (g)	2.66	3272.95	16.32	3472.72**	3193.99**	5.91
Grain yield per plant (g)	6.87	356.43	88.42**	238.26**	4791.99*	4.16

*P= 0.05 and P ** =0.01

All the characters studied in the present investigation exhibited high PCV and GCV values. The high phenotypic variations were accompanied by high genotypic variations indicating the presence of high genetic variability for different attributes and less influence of environment in expression of characters. This points out that there is great scope to improve these characters through selection. The results are in confirmation with the findings of Nair and Rosamma, 2007 with respect to plant height, days to flowering, tillers per plant, productive tillers per plant, panicle length, grains per panicle, test weight of grains, grain length, straw and grain yield.

The amount of genetic variation alone does not give much information to the breeder unless supplemented with the heritability estimate which gives a measure of the heritable portion of the total variation. All the characters studied exhibited high degree of broad-sense heritability. High heritability observed in case of plant height, productive tillers per plant, days to flowering, panicle length, spikelets per panicle, grains per panicle, test weight of grain, grain length and width, and grain yield per

plant, is in concurrence with the results of Nair and Rosamma (2007) and Bisne et al. (2009). Likewise, high heritability was observed for leaf length, leaf width and total tillers by Singh et al. (2011) and Ovung et al. (2012). High degree of broad-sense heritability reveals that these characters are less influenced by environment and there could be greater correspondence between phenotypic and genotypic values.

The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. Genetic advance for all the characters under study was high. These findings with respect to plant height, productive tillers per plant, days to flowering, panicle length, grains per panicle, test weight of grain and grain yield per plant were in agreement with Selvaraj et al. (2011) and Rani et al. (2012). High genetic advance as per cent of mean for grain length and grain width was earlier observed by Singh et al. (2011).

Johnson et. al. (1955) reported that high heritability

Table 2. Estimation of statistical and genetic parameters of quantitative traits in core set of short duration rice accessions of Kerala

Sl. No.	Traits	Mean ± SE	Range		Coefficient of Variability		h^2 (Broad sense)	Genetic advance (%)	Genetic gain
			Minim-	Maxi-	PCV (%)	GCV (%)			
1	Plant height (cm)	180.14 ± 1.74	102.58	176.03	105.65	105.48	99.68	101.76	216.95
2	Culm length (cm)	95.92 ± 3.30	68.40	140.20	56.35	56.22	99.54	110.84	115.54
3	Stem thickness (mm)	4.19 ± 0.17	2.40	6.83	1019.16	1019.12	99.99	87.98	2099.32
4	Days to heading	85.00 ± 1.70	64.00	115.00	44.14	44.11	99.88	77.19	90.82
5	Leaf blade length (cm)	45.30 ± 1.40	30.25	67.48	73.85	73.75	99.73	68.74	151.73
6	Total tillers per plant	13.46 ± 0.69	9.50	29.60	284.46	278.08	95.57	75.37	560.01
7	Productive tillers per plant	9.46 ± 0.69	5.50	25.60	401.48	401.39	99.95	78.22	826.68
8	Panicle length (cm)	26.29 ± 0.85	17.92	50.21	144.29	144.28	99.99	78.14	297.21
9	Spikelets per panicle	166.02 ± 8.77	73.10	281.60	26.57	25.16	89.68	81.49	49.09
10	Grains per panicle	105.01 ± 8.92	9.42	223.20	62.95	61.26	94.72	128.99	122.82
11	Test weight of grain (g)	22.67 ± 0.08	21.38	23.65	298.49	298.49	99.99	139.44	614.89
12	Grain length (mm)	6.77 ± 0.18	4.29	9.25	758.06	758.06	99.99	111.64	1561.60
13	Grain width (mm)	1.21 ± 0.08	0.22	2.48	4351.46	4351.45	99.99	108.89	8963.97
14	Straw yield per plant (g)	37.85 ± 9.58	16.81	43.37	155.78	155.65	99.83	121.27	320.36
15	Grain yield per plant (g)	21.83 ± 1.62	8.00	46.96	71.19	70.57	98.28	31.45	144.11

should be accompanied by high genetic advance to arrive at a more reliable conclusion. High heritability coupled with high genetic advance was observed for all traits in the core set. This is considered advantageous for crop improvement through selection. Similar results in case of plant height, days to flowering, total tillers, productive tillers, panicle length and grains per panicle were reported by Rani et.al. (2012). This may be due to additive gene action and consequently high genetic gain can be expected through selection for these characters (Nadarajan and Gunasekharan, 2008).

The mean estimates of various characters pertaining to individual accessions in the core set are presented in Table 3. Results showed that IC 263663 was the earliest in duration with 64 days to flowering followed by Dular, Cul 8714, Onam, Tulasi, PtB 10 and Thottacheera each with 76 days to flowering. Tall statured plants above 150 cm were observed in TKM 6, Reymuthika, Thottacheera, Panki, Karuthadukkan and PtB 10. Number of productive tillers per plant was highest at 25 in IC 263663 followed by 18 in Cul 8757.

Long panicles of 50.21 cm and 31.6 cm were recorded in Cul 8711 and Tkm 6 respectively. Panicles of length over 26 cm were recorded in Onam, PtB 46, Karuthadukkan, Cul 8714, Kasturi, Reymuthika, CSR 27 and Dular.

PtB 46 with 223 grains followed by PtB 35 with 199 grains recorded the maximum grains per panicle in the core set. Karangi, Cul 8757, Karuthadukan, Cul KAUM 20, Tulasi, SBRP-3, SBRP-4, IET 18886 and Cul 8757 recorded high test weight of grains of over 23 g. However, PtB 46 with 46.96 g followed by Karangi with 39.38 g recorded the highest grain yield per plant.

Results indicate presence of promising genotypes and high variability in the core set formed. Considering the estimates of statistical and genetic variability parameters, it may be inferred that the core set of thirty-four accessions has captured the variability in the original collection. According to Ovung et al. (2012) the presence of large amount of variability might be due to diverse source of materials apart from environmental influence

Table 3. Grain yield and other quantitative traits of genotypes in core set

Sl. No.	Name	Plant height (cm)	Culm length (cm)	Stem thickness (mm)	Days to heading	Leaf blade length (cm)	Total tillers / plant	Productive tillers / plant	Panicle length (cm)	Grains/ panicle	Test weight of grain (g)	Grain length (mm)	Grain width (mm)	Straw yield / plant (g)	Grain yield / plant (g)
1	Ptb 46	120.18	75.90	5.51	86	36.28	11.7	7.7	28.97	223.2	22.52	6.85	1.75	22.55	31.99
2	Onam	117.49	81.87	3.46	76	38.29	10.9	6.9	29.04	98.0	22.77	7.13	1.98	19.85	39.38
3	Tulasi	107.66	71.58	3.76	76	45.12	12.8	8.8	24.29	128.9	23.19	8.77	1.97	21.17	22.87
4	Dular	141.68	106.40	3.33	75	44.32	11.5	7.5	26.21	38.2	22.92	7.25	1.68	16.80	22.50
5	Cul 8757	116.48	84.61	3.36	85	46.39	22.2	18.2	24.49	134.2	23.35	7.80	1.11	30.85	46.96
6	Cul 8714	102.58	68.42	4.07	76	43.86	18.3	14.3	28.27	92.1	22.41	7.02	1.11	21.56	36.09
7	Ptb 7	132.46	101.53	5.32	81	45.27	13.9	9.9	25.61	127.5	22.60	6.61	1.30	21.02	32.44
8	Ptb 10	152.80	117.95	4.92	76	43.87	14.4	10.4	26.79	37.3	22.78	6.56	1.56	34.13	25.04
9	Kargi	111.95	81.98	2.88	76	34.11	13.7	9.7	17.92	82.1	22.02	5.89	1.19	20.21	9.32
10	Reymuthika	171.75	140.17	3.66	88	46.07	9.5	5.5	28.06	146.2	22.14	4.29	1.16	27.34	13.84
11	Karangi	141.21	108.32	3.63	81	42.85	11.1	7.1	22.52	22.0	23.64	6.30	0.98	21.47	30.78
12	TKM 6	176.02	129.90	6.83	84	58.42	11.1	7.1	31.93	170.5	22.30	8.03	0.81	26.44	10.74
13	Cul 8711	125.08	87.15	3.79	83	46.40	12.1	8.1	50.21	105.2	22.46	6.93	0.97	20.09	25.47
14	Panki	162.15	137.52	5.02	96	59.57	10.8	6.8	27.13	98.6	22.60	6.76	1.51	43.37	12.99
15	IC 263662	125.11	99.85	3.23	64	39.41	29.6	25.6	24.31	94.0	22.01	7.58	0.99	19.95	17.31
16	IC 263665	103.74	76.26	4.18	81	36.58	18.4	14.4	23.11	28.1	22.59	7.65	1.16	23.15	27.39
17	AM 10-24	124.01	93.91	4.25	83	36.96	18.1	14.1	23.99	96.1	22.93	7.30	1.28	25.48	29.17
18	Cul 90-04	111.64	84.33	2.39	81	36.06	13.0	9.0	25.54	72.8	22.53	5.92	1.15	18.35	25.25
19	SBRP-3	145.45	109.99	4.42	91	54.07	10.4	6.4	25.45	79.1	23.54	7.63	1.32	24.43	18.37
20	SBRP-4	141.26	105.42	5.20	91	55.85	10.1	6.1	26.07	109.4	23.48	8.15	1.29	20.90	18.56
21	Moncumpu 519	121.32	73.19	4.58	88	57.04	11.3	7.3	24.29	165.0	22.76	8.09	0.79	22.04	13.79
22	Cul 9410-3-Sel 2	134.02	86.24	4.28	90	43.62	10.9	6.9	25.57	163.5	22.84	8.07	1.02	18.77	22.96
23	IET 18886	131.05	98.70	3.75	94	53.15	11.7	7.7	27.66	90.4	23.18	8.81	1.42	24.15	18.20
24	IET 18318-Sel 2	118.58	85.51	4.17	91	46.74	12.0	8.0	23.44	152.3	21.93	6.37	0.46	24.32	17.02
25	CSR 27	123.51	90.41	4.31	86	40.37	11.0	7.0	28.03	163.9	22.97	7.63	1.16	27.04	31.90
26	Indira Sugandhidhar	120.95	86.90	5.32	99	41.65	11.5	7.5	25.14	154.9	22.27	7.50	0.77	20.48	16.56
27	Kasturi	129.16	92.46	6.14	78	39.64	11.5	7.5	28.21	129.8	22.44	9.25	0.22	45.94	14.49
28	Ptb 35	117.88	78.22	3.20	81	49.01	11.3	7.3	25.36	199.8	22.61	6.33	1.43	22.68	32.76
29	Thottacheera	163.61	126.98	3.74	76	49.71	14.4	10.4	25.42	96.3	22.55	7.04	1.43	25.85	15.22
30	Karuthadukkan	157.34	124.53	4.23	82	47.04	16.5	12.5	28.60	111.0	23.09	7.84	1.41	23.40	9.69
31	Chomala	131.78	100.83	3.64	78	36.54	16.5	12.5	23.32	66.0	21.37	5.28	0.37	22.55	8.00
32	Cul KAUM-20	138.31	79.33	5.15	115	67.48	11.3	7.3	25.07	42.5	23.09	5.57	1.03	24.44	15.10
33	Cul M-20	111.81	86.85	2.82	96	30.25	12.3	8.3	22.31	85.6	22.32	7.39	0.89	22.87	15.07
34	Mo 7	103.00	88.39	3.78	106	48.38	11.9	7.9	21.56	50.7	22.76	7.33	2.47	21.22	14.69

affecting the phenotypes. As existence of variability is the basis for any crop improvement programme, the core set evaluated can prove highly useful in breeding programmes aiming to improve yield and yield attributes. The variability observed in the core set can be exploited through simple direct selection or other breeding approaches. Thus the study points out that the core set formed is a useful sub-set of short duration rice germplasm and improves its accessibility as was envisaged by Frankel and Brown (1984).

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