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RESEARCH ARTICLE

GENETIC VARIABILITY AND GENETIC DIVERGENCE OF IMPORTANT RICE (*ORYZA SATIVA* L.) VARIETIES

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ABSTRACT

The present investigation was carried out during *kharief*- 2005 at the Research Farm, Division of Plant Breeding and Genetics, SKUAST-Jammu, Main Campus Chatha. The experimental material for the present investigation comprised of sixteen genotypes of rice (*Oryza sativa* L.) grown in a randomized block design with three replications. The study revealed that genotypes differed significantly among themselves for all the characters *viz*., morpho-physiological, biochemical, yield and yield attributing traits. A wide range of phenotypic variability was observed in most of the characters but was quite high for plant height, number of productivity tillers, harvest index, flag leaf area, crop growth rate (CGR) and net assimilation rate (NAR). The phenotypic and genotypic coefficients of variation revealed that there was good agreement between these two parameters. A number of characters such as flag leaf area, harvest index, grain yield, 1000 grain weight, peroxidase, leaf area duration (LAD) and □-amylase showed high genotypic coefficient of variation as compared to others. Apart from showing high genetic variability plant traits viz., plant height, flag leaf area, 1000-grain weight, grain yield, days to 50% flowering, kernel density, biomass yield, number of productive tillers, harvest index, CGR, RGR, NAR, LAD, peroxidase and □-amylase showed moderate to high heritability coupled with moderate to high genetics advance. Mahalonabis's D^2-statistic analysis revealed considerable amount of diversity in the material. Sixteen genotypes were grouped into six heterogenous clusters. Among these clusters, clusters B and cluster C had maximum number of genotypes (five each). The maximum average inter-cluster distance was recorded between cluster C and cluster F and minimum between cluster E and cluster F. Hence the selected material could be further utilized for future breeding programme

INTRODUCTION

Rice is cultivated in wide range of ecological environment in India. In Jammu Division of Jammu and Kashmir State it is cultivated as subtropical rice in plains of Jammu and Kathua districts. It is also grown in some temperate belts of the Division. The productivity of rice is very low (1.6 t/ha) [Anonymous, 2007) when compared to national and state average of 2.2 t/ha. Limited success has been achieved to break the yield plateau so far. This may possibly be due to narrow range of genetic variability and lack of adequate genetic information regarding the inheritance of quantitative traits controlling most important economic character i.e. yield.

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The ecogeographical diversity as a reasonable index of genetic diversity cannot be successful in discriminating between biological populations. Assessment of genetic divergence is important in plant breeding if there is no improvement by selection. For adoption to different ecological areas, the rice cultivars ought to differ for many characteristics. When the genotypes are differing for many characteristics it becomes important to document them. In present regime of World Trade Organisation (WTO) more characterisation of genetic diversity of the crop has attracted great importance of preserving the proprietary rights to particular geographical area. In the present investigation, an attempt was made to characterise the rice varieties grown in Jammu region for grain yield,

Table 1. Analysis of variance (mean squares) and genetic parameters for different yield and yield attributing traits in rice

Source of variation		d.f.	Plant height (cm)	Days to 50% flowering	Flag leaf area (cm^2)	No. of productive tillers	Spikelets / panicle (No.)	Spikelet fertility (%)	Average panicle weight (g)	Biomass yield / plant (g)	1000-grain weight (g)	Kernel density (ml/g)	Harvest index (%)	Grain yield / plant (g)
Replications		2	157.95*	41.39**	4.21	5.21	460.58*	54.39	0.02	15.98	0.45	0.0002**	180.81	0.18
Genotypes		15	672.76**	70.89**	542.55**	5.57	516.93**	61.95**	0.48**	33.91**	17.05**	0.0001**	498.65**	15.73**
Error		30	36.37	2.50	14.83	3.69	87.88	16.86	0.12	6.30	0.79	0.00003	65.15	0.69
G.M.			106.34	95.72	36.15	10.22	135.50	78.95	2.48	21.76	22.30	0.54	65.47	13.86
	Minimum		85.48	90.00	22.71	7.40	94.06	72.00	1.69	14.38	17.91	0.53	44.07	11.08
	Maximum		142.31	104.33	71.10	12.26	154.33	87.33	3.09	25.37	26.66	0.55	89.36	18.45
αg^2			212.13	22.79	175.90	143.01	0.12	15.02	0.12	9.20	5.42	0.00	144.50	5.01
αp^2			248.50	25.30	190.74	230.89	0.24	31.89	0.24	15.51	6.21	0.0001	209.65	5.70
αe^2			36.37	2.50	14.83	87.88	0.12	16.86	0.12	6.30	0.79	0.00	65.15	0.69
h^2			0.85	0.90	0.95	0.61	0.49	0.47	0.49	0.59	0.87	0.53	0.68	0.87
GCV			13.69	4.98	36.68	8.82	13.99	4.90	13.99	13.94	10.44	1.21	18.35	16.15
PCV			14.82	5.25	38.19	11.21	19.88	7.15	19.88	18.09	11.17	1.66	22.11	17.23
GA			27.72	9.33	26.23	19.38	0.50	5.48	0.50	4.81	4.48	0.009	20.55	4.23

* Significant at 5% level, ** Significant at 1% level, αe^2 = Variance due to environment,αg^2 = Variance due to genotype, αp^2 = Variance due to phenotype, h^2 = Heritability in broad sense. GCV = Genotypic coefficient of variation. PCV = Phenotypic coefficient of variation. GA = Genetic advance

Table-2: Analysis of variance (mean squares) and genetic parameters for various physiological and biochemical traits in rice

Source of variation		d.f.	CGR (mg/pl/day)	RGR (mg/g/pl/day)	NAR (mg/dm^2/day)	LAI	LAD	Esterase	α-amylase	Peroxidase	Soluble proteins
Replications		2	17805.81*	3.51	978.00	0.006	8.62	0.01	0.02	0.04	0.003
Genotypes		15	25480.90**	14.01**	2662.71**	0.574**	1219.56**	0.08**	2.44**	3.01**	0.09**
Error		30	5254.05	3.28	734.71	0.01	33.85	0.006	0.06	0.02	0.002
G.M.			369.33	9.98	124.38	1.19	54.02	0.61	2.70	2.39	1.93
	Minimum		153.44	5.71	83.05	0.76	33.90	0.41	1.30	1.19	1.69
	Maximum		463.10	12.52	168.75	2.30	106.50	0.90	4.64	4.37	2.23
□ g^2			6742.28	3.57	642.66	0.18	395.23	0.02	0.79	0.99	0.03
□ p^2			11996.33	6.86	1377.38	0.20	429.09	0.03	0.85	1.01	0.03
□ e^2			5254.05	3.28	734.71	0.01	33.85	0.006	0.06	0.02	0.002
h^2			0.56	0.52	0.46	0.92	0.92	0.79	0.92	0.97	0.91
GCV			22.23	18.94	20.38	36.08	36.79	26.33	32.87	41.74	9.02
PCV			29.65	26.25	29.83	37.53	38.34	29.61	34.20	42.20	9.4
GA			126.80	2.81	35.67	0.85	39.30	0.29	1.76	2.03	0.34

* Significant at 5% at level, ** Significant at 1% level, □e^2 = Variance due to environment, □g^2 = Variance due to genotype, □p^2 = Variance due to phenotype, h^2 = Heritability in broad sense, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, GA = Genetic advance, CGR = crop growth rate, RGR = relative growth rate, NAR = net assimilation rate, LAI = leaf area index, LAD = leaf area duration

Table 3. D^2 Matrix

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	249.56	598.20	852.92	685.85	616.98	651.05	442.60	576.58	400.92	244.22	128.10	424.06	407.15	472.13	989.41
2		436.10	360.42	416.99	627.88	831.41	564.05	1163.12	928.67	515.82	407.69	945.34	673.27	463.15	1001.21
3			30.373	157.63	1311.83	1448.28	983.36	1997.29	1300.82	1201.24	851.01	1336.28	1478.59	268.68	266.49
4				243.84	1357.85	1601.29	1144.49	2294.26	1762.95	1389.66	1064.26	1722.05	1587.47	462.31	637.93
5					1201.99	1430.41	866.60	1992.27	1418.58	1323.71	962.31	1603.63	1456.40	253.30	400.58
6						84.41	141.57	903.81	1013.32	587.67	645.56	1153.49	930.61	1343.61	1852.80
7							206.54	773.06	843.29	595.28	649.60	978.03	940.89	1469.07	1944.45
8								709.44	657.42	683.17	448.33	1053.15	820.05	1004.04	1480.02
9									286.35	602.69	512.24	611.75	332.07	1611.45	2646.13
10										607.32	254.93	528.66	470.23	1103.20	1896.31
11											251.77	270.66	361.20	958.64	1647.19
12												403.73	358.57	649.02	1289.43
13													354.49	927.31	1599.58
14														922.44	2022.14
15															303.63

Value of V-statistics = 1929.14 for 345 degrees of freedom
1. RR-600. 2. RR-564, 3.Basmati-370, 4.Ranbir Basmati, 5.Sonnwal Basmati, 6. K-39, 7. K-343, 8. K-448, 9.Gizza-14, 10. IET-1410, 11. PC-19, 12.RR-377, 13.RR-389, 14. RR-8585, 15. Jaya, 16. Ratna

yield attributing traits, besides some morpho-physiological and biochemical traits in order to generate information which could be helpful in the formation of strategies to be adopted for genetic improvement of these cultivars. The information generated will be helpful in identifying parents to be used in future hybridization programme.

MATERIALS AND METHODS

The experimental material for the study comprised of 16 genotypes selected from diverse areas of Jammu Division which were grown during *kharif*, 2005 in a randomized block design with three replications at the Research Farm, Division of Plant Breeding & Genetics, SKUAST-Jammu, Main Campus, Chatha. Each plot consisted of three rows of 1.05 m length with inter- and intra row distance of 20 and 15 cm, respectively. Five plants were randomly selected from each plot in each replication for different morpho-physiological traits viz. plant height (cm), number of productive tillers, days to 50% flowering (on plot basis), flag leaf area (cm^2) [FLA], spikelets per panicle, spikelet fertility (%), average panicle weight (g), 1000-grain weight (g), biomass yield (g), crop growth rate (CGR) [mg/g/pl/day], relative growth rate (RGR) [mg/g/pl/day], net assimilation rate (NAR) [mg/dm^2/day], leaf area index (LAI), leaf area duration (LAD), kernel density (ml/g), grain yield per plant (g) and harvest index (%). Biochemical studies were analysed for various characters such as esterases, α-amylase, peroxidase and soluble proteins by the method given by Bemfield (1955). Analysis of variance was done by the procedure described by Panse and Sukhatme (1978). Genotypic and phenotypic coefficient of variation, heritability (broad sense), genetic advance was calculated following the procedure as described by Burton and Devane (1953). The intra and inter-cluster distances were calculated as per the method envisaged by Rao (1952).

RESULTS AND DISCUSSION

Analysis of variance for various morpho-agronomic and physico-biochemical characters revealed high significant differences among 16 genotypes except number of productive tillers which indicated the presence of considerable amount of variability in the experimental material (Table-1 & 2). The wide range of variation noticed in all the characters would offer good scope of selection for the development of desirable types. These results are in agreement with the findings of Majumdar *et al.* (1971) and Rasheed *et al.* (2002). Generally phenotypic variance was high for morphological traits, moderate for yield and yield attributing traits and low for biochemical characters with esterases and soluble proteins showing the lowest value. The genotypic variance closely followed the phenotypic variance and ranged from 0.00-6742.28 with higher values for morphological traits and lower values for biochemical traits. The present investigation further revealed that the genotypic variations contributed maximum to phenotypic variations for most of the characters and environmental deviation had minor contribution for almost all the characters. The variability present in these varieties for all the component traits can be exploited to improve the rice varieties. This suggested that available genetic variability can be successfully exploited through selection and hybridization among desirable lines for the development of superior genotypes.

Table-4 : Distribution of 16 varieties of rice in six clusters (A-F) (D^2 statistics)

Cluster	Total entries	Entry No.	Name
A	3	6	K-39
		7	K-343
		8	K-448
B	5	1	RR-600
		11	PC-19
		12	RR-377
		13	RR-389
		14	RR-8585
C	5	3	Basmati-370
		4	Ranbir Basmati
		5	Sonnwal Basmati
		15	Jaya
		16	Ratna
D	1	2	RR-564
E	1	10	IET-1410
F	1	9	Gizza-14

Table 5. Intra and inter cluster average D values of six clusters (A-F)

Cluster	A	B	C	D	E
A (6,7,8)	144.31	746.23	1362.67	674.45	838.01	795.44
B (1,11,12,13,14)		320.39	1183.63	558.34	452.41	527.07
C (3,4,5,15,16)			329.81	535.57	1496.37	2108.28
D (2)				0.00	928.67	1163.12
E (10)					0.00	286.35
F (9)						0.00

The phenotypic coefficient of variation (PCV) were, in general, higher than the genotypic coefficient of variation (GCV) which suggested profound influence of environment. The flag leaf area showed highest values of genotypic as well as phenotypic coefficient of variation followed by peroxidase, LAD, LAI and α-amylase. Moderate to low estimates of genotypic and phenotypic coefficient of variation were observed for harvest index, grain yield, average panicle weight, biomass yield, plant height, 1000-grain weight, esterase, CGR, NAR, RGR, number of productive tillers, days to 50 per cent flowering, spikelet fertility, kernel density and soluble proteins. Large range and high estimates of genotypic and phenotypic coefficient of variation observed in the present investigation point to existence of large amount of variability in the experimental material. Sharma and

Ghuyan (2004) also observed highest GCV and PCV for number of grains per plant and number of effective tillers per plant. Chauhan *et al.* (1984) and Gosh *et al.* (1981) also reported high GCV and PCV for various morphological, yield and yield attributing traits.

Further investigation revealed that the estimates of heritability in broad sense were highest for plant height followed by 1000-grain weight, grain yield per plant, days to 50% flowering, flag leaf area, soluble proteins, □-amylase, LAD and peroxidase. Moderate for kernel density, biomass yield, number of productive tillers per plant, harvest index, RGR, CGR and esterase. Low estimates of heritability for spikelet fertility, spikelet per panicle, average panicle weight and NAR. High estimates of genetic advance were observed for plant height, flag leaf area, harvest index, number of productive tillers per plant, CGR, LAD and NAR, moderate for 50% flowering, spikelet fertility, biomass yield, 1000-grain weight, grain yield per plant, RGR, peroxidase and □-amylase. Similar information was depicted by (Verma, 1967) and (Rao and Goud, 1969). Genetic variability may itself be due to additive and non-additive gene action. Obviously if the genetic variance observed is due to non-additive gene action, selection may not be effective, even though the estimated variability may be high. Thus genetic advance furnishes clue to the nature of gene action, infact, the additive gene action is expected to be associated with high genetic advance.

Sixteen genotypes grown for classifactory analysis differed significantly with regard to characters studied individually. The results of D^2 statistics displayed a marked divergence when subjected to Wilk's Lamda criterion taking all the characters together. D^2 values computed among lines ranged from 84.41 between entry 6 and 7 (K-39 and K-343) to 2646.13 between entry 9 and 16 (Giza-14 and Ratna). All the D^2 values were statistically significant (Table-3). Based on D^2 values all the sixteen genotypes of rice were grouped by Tocher's method into six clusters. The data relating to number of clusters formed and number of genotypes included in each cluster are given in Table-4. The results showed that cluster B and cluster C had maximum number of genotypes. Clusters like D, E and F comprised one genotype each. The intra and intercluster distances in terms of average D values are presented in Table-5. All the intra-cluster distances were lower than the inter-cluster distances. The maximum inter-cluster distance was observed for cluster C (329.81). The maximum inter-cluster distance was observed between cluster C and F (2108.28). Therefore, these genotypes are suggested to provide a broad spectrum of variability in segregating generations and would also yield higher amount of heterotic expression in hybrid combinations.

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