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RESEARCH ARTICLE

STUDIES ON GENETIC VARIABILITY AND DIVERGENCE FOR SOME METRIC TRAITS IN LOW LAND RICE WITH TOLERANCE TO SUBMERGENCE AND STAGNANT FLOODING

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ABSTRACT

Genetic variability and divergence were studied for yield and yield related traits in fifty one elite low land rice cultures, selected on the basis of their tolerance to situations like submergence and stagnant flooding. The experimental materials possessed considerable amount of variability for all the traits. Majority of the traits showed smaller difference between phenotypic coefficient of variation and genotypic coefficient of variation. Both GCV and PCV were high for number of fertile grains / panicle, 100-grain weight, harvest index, grain yield / plant and plot yield while, high heritability with moderate to high genetic gain for days to 50 % flowering, plant height, number of fertile grains / panicle, 100-grain weight, harvest index and plot yield indicating the presence of additive gene effect. The test genotypes were grouped into twelve clusters, where Cluster I and Cluster II were the largest accommodating ten genotypes. Maxim minter-cluster distance was noticed between the clusters VIII and XI, which could be used for recombination breeding to throw some transgressive segregants for varietal improvement. Days to 50 % flowering and plant height contributed maximum to genetic diversity.

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INTRODUCTION

Rice being the staple food for more than 70 per cent Indians and a source of livelihood for 120-150 millions rural households, the requirement of rice production by 2030 would be around 145 million tonnes from the present level of 105 million tonnes to sustain self-sufficiency in rice. More than 60% of rice produced in India comes from Eastern India. Out of the 26.8 mha rice area in eastern India, rainfed lowland rice constitutes 39% of the total rice area. About 8.0 mha of rainfed lowland areas are flood/submergence prone. Rainfed lowlands constitute highly fragile ecosystems, always prone to flash-floods and stagnant flooding submergence stress situations. Many Sub-1 introgressed lines developed by marker assisted back crossing (MABC) including Swarna Sub-1 and CR 1009 Sub-1 are valuable addition to the low land rice breeding programme and these genotypes could sustain tolerance to submergence. Since submergence and stagnant flooding stresses are unpredictable, therefore, there is a need to develop new varieties with high yield and tolerance to both submergence and stagnant flooding for greater stability of production under the diverse rainfed lowland ecosystems of eastern Indian states. The present investigation was, therefore aimed at evaluating fifty one such elite low land rice cultures including five different checks to study the genetic basis of yield variations in low land rice with tolerance to submergence and stagnant flooding. Different yield attributing traits were examined to study the availability and extent of genetic variability in yield and yield attributing characters present in the experimental material. These were also evaluated to assess the nature and magnitude of genetic diversity among the genotypes for further utilization in breeding programmes.

MATERIALS AND METHODS

The experimental material used in the present investigation consisted of fifty one elite low land rice genotypes including Sub 1 introgressed lines along with their parents, elite lines combining submergence tolerance with stagnant flooding, promising donors and four check varieties. The test genotypes were evaluated in a Randomized Block Design with two replications with the spacing of 20 x 15 cm at Rice Research Station, OUAT, Bhubaneswar during Kharif, 2014 under recommended cultural practices. Observations were recorded on5 randomly selected plants for Plant height (PH), Panicle

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length (PL), Panicle number (PN), Fertile grain number (FGN), Fertility percentage (F%), 100-grain weight (100-GW), Harvest index (HI), Grain yield / plant (GYP) while days to 50% flowering , days to maturity and Plot yield (PY)were recorded on whole plot basis. The data recorded were subjected to statistical analysis based on the sample mean of the various characters under observation. The data were analyzed by using ANOVA (Panse and Sukhatme, 1967) and the genetic parameters such as PCV and GCV were calculated by the formula given by (Burton, 1952), heritability broad sense (h2) by (Burton and DeVane, 1953), and genetic advance in percent of mean (genetic gain) were work out as suggested by (Johnson et.al., 1955). Multivariate analysis of genetic divergence among genotypes was done using Mahalanobis D^2 statistics and grouping of the genotypes into clusters by Toucher method (Rao ,1952).

RESULTS AND DISCUSSION

The analysis of variance showed significant variation existed among the test genotypes for all the traits studied, indicating presence of substantial genetic variation and thus provides enough scope for effective selection (Table 1). The magnitude of genetic variance was high for majority of traits except for panicle length, panicle number, 100-grain weight, harvest index and grain yield/ plant. However, the higher magnitude of genetic variance for grain number, days to 50% flowering, plant height, plot yield and fertility percentage which have direct bearing on yield may be sorted out as important selection criteria for realization of higher productivity in rice. The study on the result of coefficient of variations (CV) in different traits ranged from 1.68 per cent for days to 50 % flowering to 25.91 per cent for grain yield / plant (Table 2).

Table 1. Analysis of variance for quantitative characters in low land rice

Sl.No.	Characters	Mean sum of squares		
		Replication (d.f.=1)	Genotype (d.f.=50)	Error (d.f.=50)
1.	Days to 50% flowering	102.01	264.81**	78.35
2.	Plant height (cm)	15.55	163.37**	10.23
3.	Panicle length (cm)	2.12	6.86**	0.80
4.	Panicle number	5.29	4.17**	2.57
5.	No. of fertile grains/panicle	642.68	995.40**	334.85
6.	Fertility percentage	3.67	82.47**	22.45
7.	100-grain weight (g)	0.003	0.34**	0.044
8.	Harvest index	0.001	0.009**	0.003
9	Grain yield / plant (g)	11.77	22.54**	9.90
10.	Plot yield (q/ha)	70.42	112.58**	18.15

* and ** Significant at 5% and 1% level of probability respectively.

The coefficient of variation was less than 20 per cent for majority of the quantitative traits except grain yield /plant indicating a good index of reliability of the experiment for such traits. On the contrary higher values of CV (more than 20 %) were recorded only for grain yield per plant. However, the high CV value for grain yield/plant might have been attributed due to higher degrees of experimental error associated with the sampling procedures and measurement of the trait under study. The genotypic and phenotypic coefficient of variation in different traits maintained correspondence for most of the characters except for panicle number, number of fertile grains /panicle and grain yield / plant. Majority of the traits showed smaller difference between PCV and GCV indicating little influence of the environment, therefore, selection on the basis of phenotypic values for most of the characters is expected to be effective. In general, phenotypic coefficient of variation was higher than the genotypic co-efficient of variation suggesting the influence of the environment in the expression of these characters. High values of GCV and PCV were observed (>15%) for traits like number of fertile grains / panicle, 100-grain weight, harvest index, grain yield /plant and plot yield suggesting that these traits are under the influence of genetic control. Hence, these traits can be relied upon and simple selection can be practiced for further improvement. Moderate level of PCV and GCV for traits like days to 50 % flowering and panicle number implies comparatively moderate variability and which could be exploited for improvement through selection in advance generation. Lower values of these parameters for plant height, panicle length, and fertility percentage indicate narrow genetic base for these traits and improvement in these traits could be brought about by hybridization or induced mutation to widen the genetic base followed by pedigree selection in advance generation (Gangashetty *et al.,* 2013). A review of literature from published reports on genetic variability indicates very inconsistent and contrasting results by (Vange, 2009), (Ganta and Jyothula, 2010), (Selvaraj *et al.,* 2011), (Akhtar *et al.,* 2011), (Babu *et al.,* 2012), (Ovung *et al.,* 2012), (Tuwar *et al.,* 2013), (Aditya and Bharatiya, 2013), (Singh *et al.,* 2013), (Ganapati *et al.,* 2014), (Ketan and Sarkar, 2014),(Rai *et al.,* 2014), (Sarwar *et al.,* 2015) and (Kumar *et al.,* 2015). However in majority of the cases, these estimates were found to be low for days to 50 % flowering and fertility percentage; moderate to low for plant height and panicle length; moderate to high for panicle number, 100-grain weight and plot yield and high for number of fertile grains per panicle, harvest index and grain yield per plant. The contrasting and conflicting reports available for these two parameters for studying variability, is primarily ascribed to the type of experimental materials used in various experiments. In the present study heritability (broad sense) and genetic advance as per cent of mean estimated for all the traits are presented in (Table 2).

Moderate to high degree of heritability estimates were observed for majority of the traits except for panicle number indicating low or negligible influence of environment in the expression of these traits and may respond to selection for their improvement. Days to 50 % flowering, plant height, panicle length, number of fertile grains /panicle, fertility percentage, 100-grain weight, harvest index and plot yield exhibited higher heritability values where as grain yield /plant showed moderate heritability. Traits like number of fertile grains /panicle, 100-grain weight, harvest index, grain yield /plant and plot yield exhibited higher values of genetic advance whereas days to 50% flowering and plant height showed moderate levels of genetic advance. High heritability coupled with moderate to high genetic gain for days to 50 % flowering, plant height, number of fertile grains /panicle, 100-grain weight, harvest index and plot yield indicating the presence of additive gene effect and hence selection based on phenotypic performance for these traits would be effective This is in accordance with the reports of (Vange, 2009), (Nandan *et al.,* 2010), (Ganta and Jyothula, 2010), (Akinwale *et al.,* 2011), (Selvaraj *et al.,* 2011), (Thomas and Lal, 2012), (Augustina *et al.,* 2013), (Tuwar *et al.,* 2013), (Dutta *et al.,* 2013), (Ganapati *et al.,* 2014), (Rai *et al.,* 2014), (Shrivastava *et al.,* 2014) and (Sarwar *et al.,* 2015). The genotypes included in the present study showed considerable variation in respect of all the ten characters.

Table 2. Mean, Range, Coefficient of variation, Genotypic and phenotypic coefficient of variation, Heritability and Genetic advance estimates of various characters

S. No.	Characters	Mean	Range	CV(%)	GCV(%)	PCV (%)	h^2 (%)	GA (10%)	GA as per cent mean
1.	Days to 50% flowering	109.51	88.00 - 130.00	1.68	10.44	10.51	98.72	19.99	18.26
2.	Plant height (cm)	98.44	84.19 - 121.59	3.25	8.89	9.18	93.74	14.91	15.15
3.	Panicle length (cm)	23.97	20.67 - 29.00	3.73	7.26	7.73	88.32	2.88	12.01
4.	Panicle number	9.79	7.00 -13.00	16.38	9.14	14.76	38.40	0.98	9.97
5.	No. of fertile grains/panicle	100.69	58.40 - 144.70	18.17	18.05	22.16	66.36	26.06	25.88
6.	Fertility percentage	80.16	62.63 - 92.01	5.91	6.83	8.01	72.78	8.23	10.26
7.	100-grain weight (g)	2.41	1.38 - 3.36	8.66	15.98	17.12	87.20	0.63	26.27
8.	Harvest index	0.33	0.16 – 0.46	15.88	17.02	20.39	69.67	0.08	25.00
9	Grain yield / plant (g)	12.15	6.18 – 20.69	25.91	20.69	27.64	56.07	3.31	27.27
10.	Plot yield (q/ha)	31.94	16.38 -51.90	13.34	21.52	23.49	83.88	11.08	34.68

Table 3. Relative contribution (%) of individual character to the divergence among genotypes

Sl. No.	Characters	Rank total	Average D^2	Percent of total D^2
1.	Days to 50% flowering	3373	78.346	46.26
2.	Plant height (cm)	5618	23.070	13.62
3.	Panicle length (cm)	6712	13.111	7.74
4.	Panicle number	7095	10.659	6.29
5.	No. of fertile grains/panicle	7692	7.508	4.43
6.	Fertility percentage	7535	8.393	4.96
7.	100-grain weight (g)	7655	7.282	4.30
8.	Harvest index	6896	11.638	6.87
9	Grain yield / plant (g)	8466	5.046	2.98
10.	Plot yield (q/ha)	9083	4.310	2.54

Table 4. Grouping of fifty one lowland rice genotypes on the basis of D^2 analysis

Clusters	Genotypes
I	PSBRc 18-Sub 1(10), Samba Mahsuri(11), Samba Mahsuri Sub1 (12), Swarna-Sub 1(14), Pratikshya(27), IR 87098-55-2-1(33), IR 87439-BTN-145-2-1(37), IR 88763-SUB 177-1-1-2(45), IR 88776-SUB 8-1-1-2(47), IR 88789-SUB 64-2-2-3(48)
II	Ciherang(3), Ciherang-Sub 1(4), IR 64-Sub 1(8),PSRBc 18(9), IR 74(21), IR87439-BTN-88-3(36), IR 88234-STG 11-1-1-1(40), IR 89246-SUB 38-3-2-1(49), IR 89262-SUB 5-2-3-2(50), Lalat (51)
III	BR 11(1), Thadokkham- Sub 1(16), Inpara-3(17), PSBRc 68(22), PSBRc 70(23)
IV	Savitri(5), Savitri-Sub 1(6), OR 142-99(26), Jagabandhu(30), Upahar(29), IR 85086-SUB 33-3-2-1(31)
V	BR 11-Sub 1(2), IR 87118-39-1-1-6(34) , IR 88230-60-1-2-2(39) , IR 88250-20-1-1-3(42) , IR 88764-SUB 30-1-1-2(46)
VI	IR 68(19), NSICRc 214(25), IR 88243-17-1-1-3(41)
VII	Thadokkham(15), IR 86256-6-2-2-2(35), IR 88228-33-3-5-2(38), Mahanadi(28), IR 88762-SUB 51-3-1-3(44)
VIII	IR 64(7) , IR 72(20)
IX	IR 42(18) , IR 87092-26-3-1-3(32)
X	IR 88760-Sub-93-3-3-3(43)
XI	PSBRc 102(24)
XII	Swarna(13)

Table 5. Average intra and inter cluster distances among twelve clusters

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	50.975	130.921	80.079	197.473	118.632	107.605	89.411	250.811	112.525	229.941	241.496	99.097
II		54.498	146.070	433.960	291.379	98.510	172.710	80.130	243.453	443.953	517.197	312.444
III			39.698	157.465	97.018	102.202	62.824	284.445	123.745	171.818	192.811	150.862
IV				51.692	89.929	357.767	125.773	703.185	156.134	79.641	76.945	113.136
V					44.038	200.455	89.724	481.260	59.310	80.949	94.592	78.295
VI						29.879	172.269	134.837	180.316	296.778	366.063	277.507
VII							50.199	348.874	113.207	159.412	197.052	110.635
VIII								35.855	386.665	680.191	769.738	522.138
IX									51.581	136.097	165.676	98.947
X										0.000	72.752	193.512
XI											0.000	155.990
XII												0.000

Table 6. Mean performance of different clusters for different quantitative characters in low land rice

Sl. No.	Characters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
1.	Days to 50% flowering	109.30	96.05	108.60	125.83	119.00	98.50	111.40	88.25	118.00	123.00	129.50	121.00
2.	Plant height	93.32	95.78	104.52	109.72	96.19	96.18	105.98	86.88	87.45	112.05	101.50	86.89
3.	Panicle length	23.31	24.04	25.47	22.86	23.94	27.96	23.44	24.88	22.43	25.32	22.66	20.90
4.	Panicle number	9.99	10.21	9.46	9.52	9.00	10.13	8.80	11.70	12.00	8.40	9.30	8.30
5.	Fertile grain number	115.24	89.29	104.54	123.17	89.18	95.60	105.58	72.10	79.05	79.20	68.20	117.90
6.	Fertility percentage	77.48	78.74	77.97	83.05	84.29	75.78	84.52	75.35	90.88	81.32	70.38	82.38
7.	100-grain weight	1.97	2.51	2.95	2.37	2.53	2.39	2.69	2.53	2.29	2.13	2.11	1.92
8.	Harvest index	0.34	0.37	0.33	0.27	0.31	0.34	0.38	0.36	0.30	0.18	0.16	0.39
9	Grain yield / plant	11.92	11.62	15.86	13.78	10.85	11.89	13.36	9.99	10.39	6.18	6.36	12.11
10.	Plot yield	30.31	27.40	30.20	41.23	35.99	26.86	34.09	23.10	36.26	45.62	22.66	35.24

Days to 50 % flowering, grain yield /plant, fertile grain number, panicle length, panicle number, harvest index, fertility percentage were found to be major characters contributing to varietal divergence. The relative contribution of each character to the total divergence indicates that days to 50 % flowering and plant height had maximum contribution to genetic divergence of the test genotypes (Table 3). Therefore, the varieties chosen as parents for recombination breeding on the basis of such characters are likely to throw transgressive segregants for varietal improvement. The relative contribution of characters to genetic divergence has been reported by (Rashid *et al.,* 2009), (Thomas and Lal, 2012), (Senguttuvel *et al.,* 2013), (Kumar *et al.,* 2013) and (Haque *et al.,* 2014). The principal characters contributing towards genetic divergence were found to vary from report to report. However, in general days to flowering, 100-grain weight, plant height, panicle number, grain yield per plant and grain number were found to largely contribute to genetic divergence. This anomalous contribution of different characters towards genetic divergence might have resulted due to choice of characters for analysis, the extent of variability and fitness of characters associated with grain yield. Based on the relative magnitude of D^2 values, following Tocher's method, all the test entries were grouped into twelve clusters (Table 4). Cluster I and Cluster II were the largest accommodating ten varieties each. Grouping of large number of varieties in cluster-I and cluster II might have resulted due to similar selection pressure favouring identical expression of characters influencing grain yield during course of selection. The present study revealed that the cluster I and II comprised of genotypes like sub 1 introgressed lines, their recurrent parents and sub 1 derived lines indicating that there is no relationship between clustering pattern and geographical distribution of genotypes.

The intra cluster distance ranged from 54.498 (cluster II) to 29.879 (VI) indicating limited genetic diversity in these clusters. Average inter-cluster distance (Table 5) revealed that most divergent clusters were VIII and XI and the minimum inter-cluster divergence was found between clusters V and IX .To realize much variability and high heterotic effect, (Mishra *et al*., 2003) and (Chaturvedi and Maurya ,2005) recommended that parents should be selected from two clusters having wider inter cluster distance. Therefore, it is suggested that in the present investigation parents should be chosen from the most divergent groups i.e., between cluster VIII and cluster XI for hybridization and these parental combinations are expected to throw transgressivesegregants for realization of high yield and better tolerance to submergence and stagnant flooding. The cluster mean values showed a wide range of variations for all the characters undertaken in the study given in (Table 6). Considering the average mean values of different clusters it is clearly evident that the clusters like II, III, IV, V, VI, VII and XII were quite distinguished for their characteristic features. It is interesting to note that the clusters III and VII consisted of genotypes combining many desirable quantitative traits and could be successfully employed in a breeding programme for genetic enhancement of yield in rice. Further the crosses involving parents from divergent clusters may exhibit higher heterosis and better recombinants are likely to be recovered in segregating generations for realization of higher productivity in rice.

Conclusion

The materials under the present investigation possess a highly significant difference among the test for all the traits, indicating presence of substantial genetic variation and thus provide enough scope for effective selection. The higher magnitude of genetic variance for grain number, days to 50% flowering, plant height, plot yield and fertility percentage which have direct bearing on yield may be sorted out as important selection criteria for realization of higher productivity in rice. Majority of the traits showed smaller difference between PCV and GCV indicating little influence of the environment, therefore, selection on the basis of phenotypic values for most of the characters is expected to be effective. Moderate to high degree of heritability estimates were observed for majority of the traits except for panicle number indicating low or negligible influence of environment in the expression of these traits and may respond to selection for their improvement. High heritability estimates were associated with moderate to high genetic gain for days to 50 % flowering ,plant height, number of fertile grains per panicle, 100-grain weight, harvest index and plot yield indicating the presence of additive gene effect and hence selection based on phenotypic performance for these traits would be effective .

The characters like number of fertile grains per panicle, 100-grain weight, harvest index and plot yield exhibited high GCV coupled with high heritability and high genetic advance indicates the preponderance of additive gene and such characters could be improved through selection .Panicle length and fertility percentage exhibited high heritability value and low genetic gain suggested that inheritance of such traits might be under the control of both additive and non additive gene effects. Therefore, selection of genotypes on the basis of phenotypic performance of the above traits may not be effective. Low to moderate heritability estimates with high genetic gain was observed for grain yield per plant indicated that inheritance of such traits is governed by additive gene effects. The low heritability as being exhibited due to high environmental effects, hence selection based on phenotypic performance may be effective. Low heritability with low genetic gain was observed for panicle number suggested that dominance and epistatic gene effects might be operating in the inheritance of these traits which indicates that this character is highly influenced by environmental effects and selection would be ineffective. In the present study days to 50 % flowering, grain yield per plant, fertile grain number, panicle length, panicle number, harvest index, fertility percentage, in descending order were found to be major characters contributing to varietal divergence.

The relative contribution of each character to the total divergence indicates that days to 50 % flowering and plant height had maximum contribution to genetic divergence of the test genotypes. Therefore, the varieties chosen as parents for recombination breeding on the basis of such characters are likely to throw transgressive segregants for varietal improvement. Based on the relative magnitude of D^2 values, following Tocher's method, all the test entries were grouped into twelve clusters. Cluster I and Cluster II were the largest accommodating ten varieties each. Grouping of large number of varieties in cluster-I and cluster II might have resulted due to similar selection pressure favouring identical expression of characters influencing grain yield during course of selection. The statistical distance (D2) represents the index of the genetic diversity among the clusters. D2 analysis based on all the characters together revealed that most divergent clusters were VIII and XI. Therefore, it is suggested that parents should be chosen from the most divergent groups i.e., between VIII and

XI for hybridization. The average cluster mean indicated that genotypes were grouped in twelve clusters. Considering the average mean values of different clusters it is clearly evident that the clusters like II, III, IV, V, VI, VII and XII were quite distinguished for their characteristic features. It is interesting to note that the clusters III and VII consisted of genotypes combining many desirable quantitative traits and could be successfully employed in a breeding programme for genetic enhancement of yield in rice

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