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Elucidation of Genetic Parameters Controlling Yield and Quality Traits in Rice (Oryza *sativa* L.)

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ABSTRACT

Background: Forty two crosses involving seven lines and six testers were studied for economically important yield contributing and quality traits to test the magnitude of genetic components and diversity. Formulation of efficient breeding methodology is possible by targeting the genetic architecture of genotypes.

Methods: The systematic breeding programme involves generating genetic variability besides sorting off the diverse genotypes and utilizing the extreme phenotypes for producing stable varieties. Genetic diversity helps to achieve the greater continuum of genetic variability in segregating populations to reach for ideal selection of progenies. Heritability and genetic advance are other important selection parameters for retrieving better genotype through selection.

Result: Significant differences in analysis of variance were recorded for all the traits. The results signified the greater value of phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV) and environment coefficient of variation (ECV) pertaining to the test traits studied. Among agronomical characters, the GCV and PCV were reported to be in higher estimate for number of productive tillers per plant, number of grains per panicle, single plant yield and among quality characters for gelatinization temperature (GT), length breadth (LB) ratio, gel consistency and amylose content. The present study adverted that among the yield and grain quality characters *viz.,* number of productive tillers, number of grains per panicle, single plant yield, plant height, 1000 grain weight, milling percentage and grain length could be easily inherited to next generation due to high heritability. Whereas breadth elongation ratio and linear elongation ratio are influenced by environmental factors due to their low heritability. Further, the number of productive tillers, number of grains per panicle, single plant yield, plant height, Gel consistency and amylose content exhibited higher PCV, GCV, heritability and genetic advance and hence direct selection can be made for target traits.

Key words: First filial crosses, Genetic components, Grain quality, Seed yield.

INTRODUCTION

Rice (*Oryza sativa* Linn.) construed as an ideal food for people of Asiatic and African region and is chiefly targeted over 2.5 billion people. In India, rice is a cereal and staple food crop which occupies an area of 43.86 million ha and combats a prioritized task in food security of India contributing 46 per cent of the overall cereal production besides 43 per cent of total food grain production feeding more than 70 per cent population of the country. Globally, India constitutes the largest rice area to the tune of 36.9 million hectares shouldering second in production accounting 120.6 million tonnes. Evolution of rice hybrids exhibiting a productive advantage of 30 per cent compared to the existing hybrids contributed significantly for increasing production and productivity (Sharma *et al.,* 2013). Moreover, the yield potential of hybrids can be increased by improvement in parental lines. Hence, ensuring greater productivity is of prime factor in any breeding experiment. Traits *viz.,* reduced plant height, moderate tillering habit, large and compact panicles, increased number of grains per panicle, increased thousand kernel weight and higher yield construed significant rice characters for any trait based improvement (Ghara *et al.,* 2014). Grain quality is also a major factor to be considered for cooking and eating and plays a major role in marketing, foreign exchange and consumer preferences to increase the profitability.

Formulation of efficient breeding methodology for trait based improvement is possible by targeting the genetic architecture of genotypes. The systematic breeding programme involves generating genetic variability besides sorting off the diverse genotypes and utilizing the extreme phenotypes for producing stable varieties. Heritability and genetic advance are other important selection parameters for retrieving better genotype through selection. Segregating populations are more important for improving plant types

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by operating selection (Ashish, 2018). Further, it was an established fact that Line × tester analysis could be an excellent tool for harnessing selection of appropriate progenies in advance generation on target traits (Bhatti *et al.,* 2015).

MATERIALS AND METHODS

The experiment was conducted at B block farm of Plant Breeding and Genetics, Agricultural College and Research Institute, Killikulam during *Kharif* 2019. The materials comprised of forty two first filial crosses generated using seven lines (ADT 38, IR 20, ACK 14072, CO 50, CR 1009 SUB1, White ponni and TP 10106), six testers (Thuyamalli, Chandaikar, Norungan, Sivappumalli, ADT 39 and TPS 3). The rice genotypes, IR 20 and CO 39 were used as checks. Recommended agronomic practices were adopted in RBD with replicated thrice adopting a plant and row spacing of 20 × 20 cm. The biometric values on phenotypic traits *viz.,* plant height (cm), number of productive tillers, number of grains per panicle, panicle length, days for 50 per cent flowering, yield per plant (g), 1000 grain weight (g), milling per cent, head rice recovery, grain length (cm), grain breadth (cm), LAC(cm), BAC(cm), LER, BER, Gel consistency, Gelatinization temperature and Amylose content were recorded and their means were utilized for analysis. The phenotypic values were interpreted in WINDOSTAT biometric software to assess genotypic coefficient of variation (%), phenotypic coefficient of variation (%), heritability in broad sence (%), genetic advance and genetic advance as per cent of mean. Variability estimates treated as per the categorization proposed by Sivasubramanian and Madhava Menon (1973), heritability and genetic advance as per cent of mean were interpreted as per protocol given by Johnson *et al*. (1955).

RESULTS AND DISCUSSION

The present study insinuated the existence of significant variations on the test entries for targeted phenotypic traits implicating the presence of greater genetic variability among test crosses which is most ultimate for any crop improvement programme to schedule the selection process efficiently (Table 1). The range of phenotypic value for number of grains per panicle registered as 263 (IR 20 × ADT 39) to 72 (CR 1009 Sub 1 × Norungan) with a general mean of 139.28 followed by plant height as 161cm (White ponni x Norungan) to 52.65 cm (CR1009 Sub 1 × Chandaikar) with a general mean of 99.83 cm. As far as the qualitative traits are concerned, highest phenotypic value was recorded for gel consistency as from 97.4 (IR64) to 27.90 (Co 50 × TPS 3) and had mean value of 69.50 followed by head rice recovery percentage from 84 per cent (White ponni × Thuyamalli) to 48 per cent (Co 50 × Chandaikar) with a general mean of 66 per cent (Table 2a and 2b).

Genotypic (GCV), phenotypic (PCV) and environmental (ECV) coefficient of variation were calculated for each character and presented in Table 3. The results signified the greater value of phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV) and environment coefficient of variation (ECV) pertaining to the test traits studied (Chauhan *et al.,* 2020). Among

Table 1: Analysis of variance for 19 characters in rice.

df	Replication	Crosses	Line effect	Tester effect	Line × Tester effect	Error	Total
	2	41	6	5	3 0	82	125
Plant height	264.952**	1409.039**	7314.966**	1011.620*	294.090**	39.381	492.238
Number of productive tiller	0.18	173.711**	196.695	617.400**	95.166**	3.078	58.999
Panicle length	3.998*	32.817**	92.17 0	48.376*	18.353**	1.035	11.507
Number of grains per panicle	40.849	6187.943**	32030.168**	3234.301**	1511.771**	61.986	2070.962
Days for 50% flowering	14.913	547.056**	2492.630**	155.475*	223.204**	20.669	193.232
Plant yield	2.499	328.929**	1474.952**	246.454*	113.470**	10.148	114.586
1000 grain weight	1.618*	30.272**	79.945*	30.206*	20.349**	0.44	10.244
Milling per cent	12.951*	139.856**	603.003**	80.583*	57.106**	3.456	48.347
Head rice recovery	7.808	172.720**	876.168**	50.801*	52.350**	10.127	63.42
Grain length	0.006	1.209**	3.525**	0.172	0.918**	0.031	0.417
Grain breadth	0.036	0.208***	0.491*	0.25	0.145**	0.027	0.087
LB ratio	0.082	0.705**	2.706***	0.531	0.334**	0.078	0.283
Length after cooking	0.067	1.340**	4.429**	0.257	0.902**	0.049	0.473
Breadth after cooking	0.035	0.194**	0.424*	0.338*	0.124**	0.03	0.084
Length elongationratio	0.002	0.008**	0.005	0.007	0.009**	0.002	0.004
Breadth elongation ratio	0.006	0.023***	0.033	0.01	0.024**	0.007	0.012
Gelatinization temperature	0.911*	2.435**	8.480**	4.156**	0.939**	0.206	0.948
Gel consistency	62.538	742.041**	3655.811**	293.323	234.073**	25.637	261.208
Amylose content (%)	21.802**	52.055**	244.967**	38.56	15.721***	3.76	19.889

agronomical characters, the GCV and PCV were reported to be in higher estimate for number of productive tillers per plant, number of grains per panicle, single plant yield and among quality characters for gelatinization temperature (GT), length breadth (LB) ratio, gel consistency and amylose content. The range of environmental coefficient of variation ranged from 2.29 (Milling per cent) to 13.47 (Gelatinization temperature). The genotypic and phenotypic coefficient of variation registered insignificant variant for most of the test traits investigated except LB ratio, breadth after cooking (BAC) and gelatinization temperature (GT) which was an indication of greater influence of the environment over these three characters. The traits investigated in the present study exhibited moderate and high values of PCV and GCV besides lesser ECV (Perween *et al.*, 2020). Hence, effective and careful phenotypic selection alone will be imperative for effective improvement of these traits. Most of the traits except breadth elongation ratio (41), linear elongation ratio (58), breadth after cooking (65), grain breadth (69), length breadth (74) pronounced higher heritability. Higher level of genetic advance as per cent of mean estimates was registered for grains per panicle (91.12), plant height (43.66), gel consistency (31.82), days to 50% flowering (27.90), Single plant yield (23.83), head rice recovery (14.02), number of productive tillers (13.61) and milling per cent (13.34).

The greater genetic advance coupled heritability for productive tillers per plant, grains per panicle and seed yield provides greater unswerving note about the efficacy of selection in among target traits in the developed progenies than the control entries. The traits that pronounced greater heritability coupled with higher genetic advance signified the presence of additive gene action and hence be improved through simple or progeny selection, but the characters which exhibited higher heritability coupled with moderate or lower genetic advance can be enhanced by intermating selected superior progenies among segregating population. In the present study, higher heritability associated with higher genetic advance for yield attributing characters was in accordance with the studies pronounced by Sidhya *et al.* (2014).

The present study adverted that among the yield and grain quality characters *viz.,* number of productive tillers, number of grains per panicle, single plant yield, plant height, 1000 grain weight, milling percentage and grain length could be easily inherited to next generation due to high heritability. Whereas breadth elongation ratio and linear elongation ratio are influenced by environmental factors due to their low heritability. Further , the number of productive tillers, number of grains per panicle, single plant yield, plant height, Gel consistency and amylose content exhibited higher PCV, GCV, heritability and genetic advance and hence direct selection can be made for target traits.

Table 2a: Mean performance of parents for quantitative characters.

Parents	Days to 50% flowering	Plant height (cm)	Tillers per plant	Panicle length (cm)	Grains per panicle	Single plant yield (g)
Lines						
ADT 38	70.30*	80.91*	14.05	21.51	76.39	47.49*
IR 20	103.60*	96.15*	14.89	21.45	105.74	22.53
ACK 14072	101.60*	80.97*	15.01	18.41	132.88*	32.76
CO 50	96.66*	89.59*	15.39	22.80*	119.27	32.36
CR 1009 sub 1	126.00	53.92*	15.47	16.65	83.93	25.80
White Ponni	109.00	127.59	20.02*	22.58*	172.29*	57.91*
TP 10106	63.33*	103.40	13.89	22.84*	83.14	24.77
Mean (L)	95.83	90.36	15.54	20.89	110.52	34.81
SEd	8.30	8.58	0.78	0.91	12.94	4.97
Testers						
Thuyamalli	91.33*	95.63*	14.49	22.59	145.34*	41.88*
Chandaikar	82.66*	70.93*	15.55*	18.78	96.17	32.81
Norungan	105.66*	121.26	13.26	22.5	105.74	23.45
Sivappumalli	112.66	146.93	11.45	25.69*	119.15	18.36
ADT 39	112.33	92.32*	15.24*	23.59	95.94	51.80*
TPS 3	105.66*	98.80*	15.05	22.61	92.48	31.47
Mean (T)	101.68	104.32	14.18	22.63	109.14	33.30
SEd	4.50	9.81	0.58	0.84	7.53	4.53
CD (0.05)	8.47	7.85	0.93	1.52	10.11	1.24

*significance at 5% level.

Table 2b: Mean performance of parents for qualitative characters.

Parents	1000 grain weight (g)	Milling (%)	Head rice recovery (%)	Grain length (mm)	Grain breadth (mm)	Length/ Breadth ratio	Kernal length after cooking (mm)	Kernal breadth after cooking (mm)	Length elongation ratio	Breadth elongation ratio	Gelatinization temperature (mm)	Gel consistency (%)	Amylose content
Lines													
ADT 38	22.13*	73.95	66.79	4.67	1.91	2.45	5.62	2.4	1.20	1.25	3.23	96.23*	30.92*
IR 20	20.39	77.84*	65.43	3.87	1.81	2.13	5.63	2.28	1.45*	1.25	2.25	91.94*	24.53
ACK 14072	18.62	78.53*	74.16*	5.12	1.88	2.72	5.95	2.38	1.16	1.26	2.76	65.48	23.10
CO 50	23.06*	63.79	53.05	5.32*	2.30*	2.31	6.23	2.63*	1.17	1.15	3.92*	66.86	36.98*
CR 1009sub 1	22.49*	64.54	54.56	4.80	1.82	2.64	5.57	2.19	1.16	1.20	4.49*	82.45	21.53
White Ponni	17.64	84.04*	78.86*	5.61*	1.87	2.99*	6.38*	2.44	1.13	1.31	3.33	91.76*	22.34
TP 10106	23.03*	73.95	72.03*	5.56*	1.93	2.89*	6.16	2.34	1.11	1.21	1.77	92.45*	22.17
Mean (L)	21.06	73.81	66.42	5.00	1.93	2.59	5.94	2.38	1.20	1.24	3.11	83.89	25.94
SEd	0.83	2.80	3.67	0.23	0.06	0.12	0.13	0.05	0.04	0.02	0.35	4.84	2.20
Testers													
Thuyamalli	22.34*	62.05	61.57	3.91	2.13	1.83	4.69	2.51	1.2	1.18	4.29*	96.19*	32.39*
Chandaikar	22.32*	69.47	66.18	4.22	1.86	2.27	5.29	2.33	1.25	1.25	3.61	95.16*	29.26*
Norungan	23.03	72.81*	67.42*	5.27*	1.82	2.90*	6.08*	2.38	1.15	1.31	3.11	90.31*	33.32*
Sivappumalli	22.01	75.32*	71.48*	4.71	2.21	2.13	5.60	2.63	1.18	1.19	3.17	41.20	18.67
ADT 39	17.85	66.39	63.76	4.42	2.15	2.06	5.39	2.73*	1.21	1.27	3.78*	93.58*	26.57
TPS 3	21.96	67.46	62.19	4.70	2.03	2.31	5.57	2.54	1.18	1.25	1.79	53.42	18.21
Mean (T)	21.59	68.92	65.44	4.54	2.04	2.25	5.44	2.52	1.20	1.24	3.29	78.31	26.40
SEd	0.70	1.76	1.39	0.18	0.06	0.14	0.17	0.06	0.01	0.02	0.32	9.10	2.47
CD (0.05)	0.70	1.30	1.56	0.24	0.18	0.22	0.31	0.19	0.07	0.11	0.33	0.96	1.11

*significance at 5% level.

Table 3: Genetic variability estimates for varied traits in rice.

Character	Coefficient of variation			Heritability	Genetic
	PCV	GCV	ECV	(h^2)%	advance
Plant height (cm)	22.69	21.92	5.89	93	43.66
Number of productive tillers	39.89	38.88	8.91	95	13.61
Panicle length (cm)	14.78	14.06	4.57	90	5.96
Number of grains per panicle	32.35	31.92	5.31	97	91.12
Days to 50% flowering	15.69	14.91	4.88	90	27.90
Single plant yield (g)	28.09	27.34	6.43	94	23.83
1000 grain weight (g)	13.95	13.65	2.88	95	5.84
Milling per cent	9.45	9.16	2.29	94	13.34
Head rice recovery (%)	11.67	10.88	4.20	87	14.02
Grain length (cm)	13.95	13.46	3.68	93	1.22
Grain breadth (cm)	14.64	12.18	8.12	69	0.39
LB ratio	20.22	17.50	10.13	74	0.77
Length after cooking	11.86	11.21	3.86	89	1.20
Breadth after cooking	11.61	9.39	6.81	65	0.36
Linear elongation ratio	5.99	4.58	3.86	58	0.08
Breadth elongation ratio	8.26	5.31	6.32	41	0.08
Gelatinization temperature	31.24	28.18	13.47	81	1.59
Gel consistency	20.54	19.81	0.73	96.43	31.82
Amylose (%)	20.29	19.15	1.14	94.38	8.72

Conflict of interest

All authors declare that they have no conflict of interest.

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