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Assessment of genetic advance and correlation coefficient for yield and yield attributed traits of RIL population in basmati rice (*Oryza sativa* L.)

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Abstract

During *kharif* 2018, one hundred thirty (*Oryza sativa* L.) RILs derived from a cross between Basmati 370 and Pusa basmati 1121 were evaluated for fifteen quantitative traits related to grain quality and yield to examine the nature and magnitude of genetic variability, correlation coefficient analysis and genetic advance. Estimates of correlation coefficient, genetic variability, heritability and genetic advance in per cent of mean were also obtained for the above fifteen traits. Analysis of variance revealed that significant amount of genetic variability was present in the entire characters studied. The highest positive correlation was observed between PL and PH ($r=0.33$), ET and PH ($r=0.21$) followed by GW and GPP ($r=0.20$). Some of the traits showed then significant negative correlation with each other like YPP and PL ($r=-0.25$), KE and GW ($r=-0.02$) and KE and YPP ($r=-0.11$). High phenotypic variation was observed for yield per plant (40.25%), effective tillers per plant (42.28%) and amylose content (37.41%), Moderate phenotypic variations was recorded in plant height (12.23%), panicle length (11.99%) and so many other traits. Therefore, the present study was undertaken to find the genetic variability, correlation coefficient analysis, genetic advance through RIL population for the Selection criteria of fine rice lines.

Keywords: Rice, variability, heritability, phenotypic variation, correlation, genetic advance

Introduction

Rice (*Oryza sativa* L.), is one of the major staple food crops for more than 3.5 billion global population. The production and consumption of global rice accounted for almost 90% by Asian countries; mainly China and India alone contribute about 55% (Kong *et al.*, 2015) [12]. Among the cereals, rice provides up to 20% of their regular calorie intake for millions of global population. In order to ensure nutritional food security, the projected rice production must be increased to 852 million tons by 2035 (Brar *et al.*, 2018) [4]. Yield is a complex trait and various morphological and physiological characters contribute to grain yield. Many plant characters with the economic values are mostly and highly influenced by environmental conditions, the progress of breeding in such population is primarily conditioned by the magnitude and nature of variation and interrelationship of plant characters (Gandhi *et al.*, 1964) [7]. The correlation coefficient between yield and yield attributing traits has always been helpful as a basis for selection in breeding purposes. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. While selecting the suitable plant type, correlation studies would provide reliable information in nature, extent and the direction of the selection, especially when the breeder needs to combine high yield potentials with desirable agronomic traits and grain quality characters. A positive value of correlation shows that the changes of two variables are in the same direction, i.e., high value of one variable are associated with high values of other and vice-versa. When correlation is negative the movements are in opposite directions, i.e., high values of one variable are associated with low values of other. The knowledge of genetic variability present in the crop taken under observation for various characters under improvement is of significant importance for the success of any plant breeding programme. Heritability estimates along with genetic advance are very helpful in predicting the gain under selection than heritability estimates alone. Therefore, the present study was undertaken to find the genetic variability, correlation coefficient analysis, genetic advance through RIL population for the Selection criteria of fine rice lines.

Materials and Methods

Experimental Location, Experimental Design, and Planting Materials

The present study was conducted at the Research Farm, School of biotechnology, SKUAST- J, Chatha, Jammu. The material comprises 130 RILs developed from the cross between Basmati 370 and Pusa basmati 1121. The material was planted in the *kharif season* 2017 and 2018 along with parents in a Randomised Block Design with three replications. The five competitive plants from each of the replication were tagged and observations were taken from these tagged plants.

All the observations were taken as per the procedure given in Standard Evaluation System for Rice, IRRI, 2002. Correlation coefficient is used to find out the degree (strength) and direction of relationship between two or more variable and for fixing up the characters which are having decisive role in influencing the yield. Therefore, a field experiment was carried out to establish the extent of association between yield and yield components and others characters in rice. Analysis of variance revealed that significant amount of genetic variability was present in the entire characters studied. The present research work was taken up to assess genetic variability, phenotypic and genotypic associations between various components of grain yield to provide basis for selection and yield improvement in rice

Data Collection

Data were collected for all the fifteen traits taken under observation i.e Panicle length, yield per plant, 1000 grain weight, spikelet fertility, effective tillers per plant, Number of grains per panicle, grain quality traits like kernel elongation, kernel elongation ratio, grain length, grain breadth, length breadth ratio and morphological traits like plant height, days to 50% flowering, days to maturity.

Statistical analysis

Analysis of variance (ANOVA) was done as the first step to see if the significant genotypic differences exist and also to assess whether the traits studied were affected by the environment or not (table 1), PCV and GCV were calculated by the formula given by Burton (1952)^[3], heritability in broad sense (h^2) by Burton and De Vane (1953), and genetic advance i.e. the expected genetic gain were calculated by using the procedure given by Johnson *et al.* (1955)^[8]. Correlation coefficient was worked out as method suggested by Al Jibouri *et al.* (1958)^[2]. The estimated values were compared with table values of correlation coefficient to test the significance of correlation coefficient prescribed by Fisher

and Yates (1967)^[6].

Results and Discussion

Many of the traits showed the positive correlation with each other at $P \geq 0.05$ significant level. The highest positive correlation was observed between PL and PH ($r=0.33$), ET and PH ($r=0.21$) followed by GW and GPP ($r=0.20$). The significant positive correlation with medium value was observed between AC and PL ($r=0.18$), followed by KE and PL ($r=0.16$), KER and PL ($r=0.16$) and KE and PL ($r=0.15$). The minimum significant positive correlation value was observed between KE and ET ($r=0.005$), KE and GPP ($r=0.03$), KER and GPP ($r=0.02$) and GB and GW ($r=0.01$). Some of the traits showed then significant negative correlation with each other like YPP and PL ($r=-0.25$), KE and GW ($r=-0.02$) and KE and YPP ($r=-0.11$) (table 2). Steel and Torrie (1984)^[11] stated that correlations are measures of the intensity of association between traits. The selection for one trait results in progress for all characters that are positively correlated and retrogress for traits that are negatively correlated phenotypic variance was higher than the genotypic variances for most of the traits thus indicated the influences of environmental factor on these traits. High phenotypic variation was observed for yield per plant (40.25%), effective tillers per plant (42.28%) and amylose content (37.41%), Moderate phenotypic variations was recorded in plant height (12.23%), panicle length (11.99%) and so many other traits (Table). High GCV were observed in effective tillers per plant (26.90%), Amylose content (37.74%). Grain weight, grain length, grain breadth, kernel elongation exhibited low PCV values Similar findings were earlier reported by Singh & Chakraborty (1996)^[10], Devi *et al.* (2006)^[5], Prajapati *et al.* (2011)^[9]. High broad sense heritability was estimated for plant height (64%), and amylose content (53%), panicle length (44 %), grain length (38%), kernel elongation ratio (42 %) and kernel elongation (53%) showed the moderate range of heritability suggesting these traits are under high genetic control. Grain weight (17%), length breadth ratio (27%) and days to maturity (12%) showed low heritability in broad sense (table 3). The low heritability recorded for these traits indicates that direct selection for these traits will be ineffective. Since high heritability does not always indicate high genetic gain, heritability with genetic advance considered together should be used in predicting the ultimate effect for selecting superior varieties (Ali *et al.*, 2002)^[11].

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Table 1: Analysis of variance for different morphological and grain quality traits in basmati rice genotypes

Source of variation	Df	Plant height (cm)	Days to 50 % flowering (no.)	Days to maturity (no.)	Panicle length (cm)	Yield per plant (g)	1000 grain weight (g)	Spikelet Fertility (%)	Effective tillers (no.)	No. of grains per panicle (no.)	Kernel elongation (mm)	Kernel elongation ratio (mm)	Grain length (L) (mm)	Grain breadth (B) (mm)	L/B ratio	Amylose content %
Replication	2	53.03	50.864	126.23	0.074	1.16	153.52	248.89	151.20	34.53	673.97	0.882	0.094	0.0146	1.609	0.492
Genotypes	129	402.17	55.36	15.334	17.41	177.9	46.13	6.069	148.99	11.23	325.17	2.383	0.06	0.0116	264.82	0.278
Error	258	63.32	22.57	4.53	0.046	0.046	40.02	3.72	53.44	3.69	144.11	0.537	0.01	0.007	1.577	0.0131

*Significant at 5% level of significance

Table 2: Estimation of correlation coefficients between various grain quality and yield associated traits in Basmati 370 and pusa basmati 1121 and RIL population

Characters	PH	PL	ET	GPP	GW	YPP	SF	GL	GB	LBR	DF	DM	AC	KE	KER
PH	1.0														
PL	0.33*	1.0													
ET	0.32*	0.21*	1.0												
GPP	-0.008*	0.099*	-0.034*	1.0											
GW	0.121*	0.065*	0.0948	0.204*	1.0										
YPP	-0.015*	-0.251*	-0.0158	-0.056*	0.033*	1.0									
SF	-0.098*	0.004*	0.054*	-0.043*	-0.019*	-0.046*	1.0								
GL	-0.058*	-0.044*	-0.0038	-0.006*	-0.049*	0.046*	-0.087*	1.0							
GB	0.113*	0.078*	0.161*	0.001*	0.016*	0.120*	-0.085*	0.079*	1.0						
LBR	-0.105*	-0.079*	-0.036*	-0.053*	-0.006*	-0.006*	0.0148	0.659*	-0.301*	1.0					
DF	-0.268*	-0.021*	0.051*	-0.038*	-0.052*	0.013*	0.053*	-0.095*	-0.043*	-0.083*	1.0				
DM	-0.103*	-0.198*	-0.091*	0.061*	-0.025*	-0.032*	0.165*	-0.036*	0.016*	-0.001*	-0.150*	1.0			
AC	-0.128*	0.185*	-0.166*	0.055*	0.191*	-0.361*	-0.029*	-0.113*	-0.044*	-0.070*	-0.056*	-0.048*	1.0		
KE	0.116*	0.168*	0.005*	0.031*	-0.027*	-0.120*	-0.020*	0.150*	-0.040*	0.076*	0.027*	-0.037*	0.087*	1.0	
KER	0.139*	0.163*	-0.007*	0.024*	-0.001*	-0.126*	0.050*	-0.592*	-0.0948*	-0.411*	0.097*	-0.003*	0.146*	0.70*	1.0

*Significant at 5% level of significance

Table 3: Genotypic and phenotypic coefficient of variability (GCV and PCV), Heritability (h) and Component of Variance for grain quality and yield associated traits in RIL population

PH	PL	ET	GPP	GW	YPP	SF	GL	GB	LBR	DF	DM	AC	KE	KER	
R	3	3	3	3	3	3	3	3	3	3	3	3	3	3	
N	130	130	130	130	130	130	130	130	130	130	130	130	130	130	
GM	108.53	23.80	5.89	97.39	23.72	16.11	85.45	7.75	1.70	4.57	107.08	130.61	25.27	13.40	1.74
MST	402.17	15.33	11.23	325.17	6.07	46.13	149.00	0.61	0.01	0.28	55.37	90.30	264.83	2.38	0.06
σ^2E	63.32	4.54	3.70	144.11	3.73	40.02	53.45	0.22	0.01	0.13	22.58	64.90	1.58	0.54	0.02
σ^2G	112.95	3.60	2.51	60.35	0.78	2.04	31.85	0.13	0.00	0.05	10.93	8.47	87.75	0.62	0.01
σ^2P	176.27	8.14	6.21	204.46	4.51	42.06	85.30	0.35	0.01	0.18	33.51	73.37	89.33	1.15	0.03
Heritability	0.64	0.44	0.40	0.30	0.17	0.05	0.37	0.38	0.18	0.27	0.33	0.12	0.98	0.53	0.42
GCV	9.79	7.97	26.90	7.98	3.72	8.86	6.60	4.66	2.30	4.84	3.09	2.23	37.07	5.86	6.79
PCV	12.23	11.99	42.28	14.68	8.95	40.25	10.81	7.59	5.46	9.31	5.41	6.56	37.41	8.01	10.46
Genetic advance	0.16	0.11	0.35	0.09	0.03	0.04	0.08	0.06	0.02	0.05	0.04	0.02	0.76	0.09	0.09

Author's contribution

MS and AKS have proposed the concept of the research, designing of the experiment was finalized by MS, AKS, BKS, and RK. BKS has provided the material for research, MS has executed the field and lab experiments and collected the data, MS and SSG contributed to data analysis. MS wrote the whole manuscript. All authors reviewed the manuscript and provided suggestions.

Conflict of interest

All the authors don't have any conflict of interest.

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