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Study of genetic variability and heritability for various morphological and yield attributed traits in RIL population of basmati rice (*Oryza sativa* L.)

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Abstract

In the present study, during kharif 2017 and 2018, genetic variable, the genotypic and phenotypic coefficients of variation and heritability for fifteen characters in one hundred and thirty RIL populations derived from a cross between Basmati 370 and Pusa basmati 1121 of rice was studied. All the characters taken under observations among the genotypes showed that there were highly significant differences for analysis of variance. Genotypic coefficients of variation were lower than the corresponding phenotypic coefficients in all the traits studied, indicating considerable influence of the environment on the expression of the traits. High heritability was estimated for panicle length (99%), grain length (75%), length breadth ratio (74%), plant height (67%), kernel elongation ratio (63%) and kernel elongation (60%) suggesting these traits are under high genetic control. High phenotypic variation was observed for yield per plant (65.73%), grain weight (40.24%), grains per panicle (20.20%) and plant height (18.39%) while number of effective tillers per panicle (11.02%) and remaining traits revealed low genotypic coefficient of variation (<10%) except for grain per panicle (14.53%). Therefore, the results suggest that these traits can be used for grain yield selection.

Keywords: Rice, genetic variability, heritability, RILs

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) [14]. 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) [7]. With the intensifications of diverse food demands and living standards of global populations, rice grain appearance and quality have become a primary concern for rice breeders. Therefore, there is an urgent need to increase the grain yield along with desirable grain nutritional quality (GQ) traits in rice (Sreenivasulu *et al.*, 2015 and Sun *et al.*, 2018) [22, 24]. The genetic variability components like GV, PV along with heritability are used to determine the heritable potential of the concerned genes as well as the effect of environment over them. The GCV and PCV are categorized into Low (0-10), moderate (10-20), High (≥ 20) (Johnson *et al.* 1995) [13] which suggests the possibility of improving the traits through selection. So keeping in view the above traits, the present study has been conducted to study the effect of genetic variability and heritability for various morphological and yield attributed traits in RIL population of basmati Rice

Materials and Method

Plant material

A F₇ recombinant inbred lines (RIL) population was developed by crossing Basmati 370 and Pusa Basmati 1121 by single seed descent (SSD) method by School of Biotechnology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, in the year 2017 and 2018.

Development of RIL population

For a self-pollinating species like rice, mapping populations likely originate from parents that are both highly homozygous (inbred). Inbreeding from individual F_2 plants allows the development of recombinant inbred lines (RIL's), which consist of a series of homozygous lines, each containing a unique combination of chromosomal segments from original parents. The major advantage of using an RIL population is that they produce homozygous or 'true-breeding' lines that can be multiplied and reproduce without any genetic change. Similarly, a breeding of individual F_2 plants obtained from crossing between the parents Basmati 370 and Pusa Basmati 1121 was carried out for the development of F_7 RIL population during the study.

Raising the crop

During *kharif* 2017, two parental lines, Basmati 370 and Pusa Basmati 1121 along with F_6 seeds (RILs) was sown and transplanted in a Randomized Block Design with three replication at the Experimental farm of School of Biotechnology, SKUAST-J. The nursery were transplanted in 5 meter row length with the planting density of 15×20 cm (length and breadth). One hundred thirty RILs were selected on the plot basis with three replication were used for phenotypic evaluation and the same protocol was followed during the *kharif* 2018 to develop F_7 population.

Results and Discussion

Genetic variability components like genotypic and phenotypic variance along with heritability were estimated to determine the heritable potential of the concerned traits as well the effect of environment over them. The estimation of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are given in the table (1). GCV and PCV estimates were classified as low (0-10 percent), moderate (10-29 percent) and high (>20percent) (Johnson *et al.*, 1955) [13], which suggests the possibility of improving this trait through selection. In the present study, during *kharif* 2017, spikelet density (7.24) and yield per plant (7.02) showed the highest GCV values; followed by number of tiller per plant (5.87), panicle number per plant (5.84) and panicle length (5.21); days to maturity showed the lowest GCV value (2.61) whereas 1000- grain weight (3.92), days to flowering (3.89), plant height (3.81), grain weight (3.06), showed medium GCV values. In both the years, 2017 and 2018, the values recorded for genotypic variance was less than those obtained for phenotypic variance. In the year 2017, 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 (65.73%), grain weight (40.24%), grains per panicle (20.20%) and plant height (18.39%), Moderate phenotypic and genotypic variations was recorded in grain length (7.56%, 6.53%, respectively), kernel elongation (7.17%, 5.55%) and so many other traits. Days to maturity (2.18% and 0.72%), days to 50% flowering (3.26% and 0.94%) exhibited low phenotypic coefficient of variation (PCV) and genotypic of variation (GCV). Similar findings were earlier reported by Singh & Chakraborty (1996) [19], Devi *et al.* (2006) [9], Prajapati *et al.* (2011) [17]. Heritability is important selection parameter. Heritability is a good index of transmission of characters from parents to its progeny. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population. High broad sense heritability was estimated for panicle length (99%),

grain length (75%), length breadth ratio (74%), plant height (67%), kernel elongation ratio (63%) and kernel elongation (60%) suggesting these traits are under high genetic control. Grains per panicle (52%), grain breadth (56%) and amylose content (57%) showed moderate heritability in broad sense (Table 1). High heritability with high phenotypic coefficient of variation indicates the control of additive gene and scope and selection of genetic improvement those characters. Table 2 depicts the values of the genetic variability component for grain quality and various yield associated traits in the RIL population during the years 2018. Previous studies showed that greater variability in the initial breeding material safeguard better chances of producing favorable forms of a crop plant. The analysis of variation (ANOVA) for various traits taken under observation indicated that all the traits showed highly significant variation at 5 percent level of significance (Table 1). Significant genetic variability among rice genotypes for yield and major yield attributing traits were also reported by Poudel *et al.* (2014) [6], Gyawali *et al.* (2018) [10], Bekele *et al.* (2013) [6], Rashid *et al.* (2017), Summanth *et al.* (2017) [23], Abebe *et al.* (2017) [11] and Bandhi *et al.* (2018). 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 (65.73%), grain weight (40.24%), grains per panicle (20.20%) and plant height (18.39%), Moderate phenotypic and genotypic variations was recorded in grain length (7.56%, 6.53%, respectively), kernel elongation (7.17%, 5.55%) and so many other traits (Table 2). Days to maturity (2.18% and 0.72%), days to 50% flowering (3.26% and 0.94%) (table 2) exhibited low phenotypic coefficient of variation (PCV) and genotypic of variation (GCV). Similar findings were earlier reported by Singh & Chakraborty (1996) [19], Devi *et al.* (2006) [9], Prajapati *et al.* (2011) [17]. Heritability is important selection parameter. Heritability is a good index of transmission of characters from parents to its progeny. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population. High broad sense heritability was estimated for panicle length (99%), grain length (75%), length breadth ratio (74%), plant height (67%), kernel elongation ratio (63%) and kernel elongation (60%) suggesting these traits are under high genetic control. Grains per panicle (52%), grain breadth (56%) and amylose content (57%) showed moderate heritability in broad sense (table 2). High heritability with high phenotypic coefficient of variation indicates the control of additive gene and scope and selection of genetic improvement those characters. Most important agronomic traits of rice (*Oryza sativa* L.), such as heading date, yield, plant height and grain size, are controlled by quantitative trait loci (QTLs). Although multiple QTLs have been reported over the past few decades, few of them have been isolated or fine-mapped (Yano *et al.*, 2016; Huang *et al.*, 2009a; Ishimaru *et al.*, 2013; Li *et al.*, 2011; Ashikari *et al.*, 2006; Song *et al.*, 2007; Wang *et al.* 2015; Xue *et al.*, 2008) [27, 11, 13, 15, 4, 20, 26]. As the phenotypic manifestations of these quantitative traits show continuous variation and are always influenced by environmental factors and genetic backgrounds, only suitable genetic populations can provide a strong foundation for genetic and genomic research. To date, many types of genetic populations have been developed for QTL research and utilization. Primary genetic mapping populations, such as the F_2 , $F_{2:3}$ and BC_1 populations were often used for analyzing the genetic basis of QTL during early studies (Ahn *et al.*, 1993; Song *et al.*, 2005; Redona and

Mackill 1996) [3, 21, 18]. Large difference between GCV and PCV values reflect high environmental influence on the expression of traits. In this study, slight difference between GCV and PCV indicated the minimum influence of environment and consequently greater role of genetic factors on the expression of traits.

Conclusion

Rice is one of world's major cereal crop and it is used as staple food nearly half of world population. Usually rice is milled and cooked prior to consumption. Its composition may vary depending upon rice varieties. There are more than 1,200 varieties of rice under cultivation throughout the world. The differences in varieties are said to be related to morphology of the plants and grains, resistance to falling, precocity,

ramification, productivity, as well as resistance and tolerance to biotic and abiotic factors.

Phenotypic variability is the differences between individuals in a population due to genetic composition and growing environment (Sumanth *et al.*, 2017) [23]. Planning and execution of any breeding program for improvement on quantitative traits depends on magnitude of genetic variability. Therefore, success on plant breeding activities entirely depends on the existence of genetic variability with respect to desired traits and selection skill of plant breeder (Adhikari *et al.*, 2018) [2]. Variability, genetic diversity, expected genetic advances and heritability of the traits are therefore key basis for genetic improvement of the trait.

Table 1: Analysis of variance of morphological and yield associated traits

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	0.192*	1092.4*	0.70*	0.074*	1.16*	106.71*	0.88*	604.5*	579.98*	2.73*	0.067*	0.032*	0.011*	0.367*	0.0665*
Genotypes	129	313.41*	12.1*	11.69*	17.41*	177.9*	98.71*	239.40*	9.85*	843.32*	2.10*	0.064*	0.838*	0.017*	208.90*	0.4571*
Error	258	0.091	9.5	8.52	0.046	0.046	90.38	0.11	13.58	200.3	0.38	0.015	0.085	0.003	0.606	0.0478

*= Significance at p= 0.05 level

Table 2: Genotypic and Phenotypic Coefficient of Variability (GCV and PCV), heritability(h²) and Component of Variance for Morphological and Yield associated traits in Rice

	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	3
n	130	130	130	130	130	130	130	130	130	130	130	130	130	130	130
GM	129.55	26.31	32.12	100.78	23.99	14.81	84.84	7.67	1.69	4.55	98.76	142.14	26.93	13.64	1.79
MST	313.41	17.42	15.75	843.32	98.72	177.90	239.40	0.84	0.02	0.46	12.10	11.69	208.09	2.10	0.06
σ ² E	50.09	0.05	10.94	200.31	90.39	35.51	48.12	0.09	0.00	0.05	9.50	8.53	51.16	0.38	0.01
σ ² G	104.44	5.79	1.603	214.34	2.78	59.28	79.76	0.25	0.00	0.14	0.87	1.05	69.16	0.57	0.02
σ ² P	154.53	5.84	12.53	414.65	93.16	94.79	127.88	0.34	0.01	0.18	10.37	9.58	120.77	0.96	0.03
GCV	7.89	9.15	3.94	14.53	6.95	51.98	10.53	6.53	3.97	8.12	0.94	0.72	10.53	5.55	7.47
PCV	18.39	9.18	11.02	20.20	40.24	65.73	18.13	7.56	5.32	9.44	3.26	2.18	19.19	7.17	9.43
Heritability	0.67	0.99	0.124	0.52	0.03	0.63	0.62	0.75	0.56	0.74	0.08	0.11	0.57	0.60	0.63

*= Significance at p= 0.05 level

Author contribution

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

Declaration

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

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