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GENETIC VARIABILITY, HERITABILITY AND CORRELATION COEFFICIENTS OF YIELD AND ITS COMPONENT TRAITS IN BASMATI RICE (*Oryza sativa* L.)

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SUMMARY

Rice is the premier staple food among the Indian population. Therefore, a better insight to the association of yield with its component traits can be helpful in improving the paddy yield. The present study was carried out using 140 F_7 recombinant inbred lines (RIL) population with the aim of determining the character association, genetic variability and the heritability of yield along with its 5 components. The RILs were evaluated for yield and its associated traits during *kharif* 2014 and *kharif* 2015. The results corresponding to analysis of variance showed highly significant differences prevail amongst all the RILs for yield and its component traits. The traits tillering ability, spikelet fertility percentage, number of grains per panicle and 1000-grain weight showed significant positive genotypic and phenotypic correlation with grain yield during 2014 and 2015. Panicle length exhibited significant positive and negative association with grain yield during 2014 and 2015 respectively. The presence of slightly higher phenotypic coefficient of variation than genotypic coefficient of variation indicated the negligible influence of environment on the expression of yield and its component traits. High heritability >80% had been observed for yield and associated traits during the study, suggesting that these traits would respond to selection owing to their high genetic variability and transmissibility. A thorough understanding of the inheritance of traits, their heritability and relationship with other important characteristics is important for the choice of breeding and selection methods for crop improvement.

Key words: Variability, heritability, recombinant inbred line, correlation coefficients, rice (*Oryza sativa* L.)

Key findings: Grain yield in rice is an economically important trait. For improvement of a quantitative trait like yield, it becomes imperative to determine the relationship between yield and its component traits as well as the genetic variability for such components in a population. This study concluded that RIL population can serve as an efficient genetic resource for improving grain yield in paddy by simple selection procedures.

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INTRODUCTION

Rice (*Oryza sativa* L.), is a monocotyledonous angiosperm having a diploid chromosome number 2*n* = 24. After maize and wheat, rice is the third highly preferred potent staple food for billions of people across the globe. The small genome of rice (430 Mb) made it a model plant for studying cereal genetics. With an alarming increase in the population throughout the world, the demand for rice will continue to increase in near future; therefore, rice breeders across the world aim at increasing the grain yield in rice (Song *et al.*, 2007). On the other hand, the area under rice cultivation has decreased with increased development and industrialization, hence increasing the grain yield per unit area is the only way to meet the target of increasing crop yield. Grain yield in paddy is a complex polygenic trait. Being quantitative in nature, it is controlled by several genes and is highly influenced by the environment (Ashfaq *et al.*, 2012). A better understanding of the relationship between grain yield and its component traits becomes necessary for making an efficient selection for the development of new varieties with improved economically important traits (Kumar *et al.*, 2014). The knowledge of heritability and genetic variability is a prerequisite for carrying out selection based improvement. The information about these help in the breeding programmes by broadening the gene pool of rice and gives an indication about the efficiency of transformation of characters into future generations respectively (Selvaraj *et al.*, 2011). Correlation (both phenotypic and genotypic) studies among yield and its component traits gives a better insight towards the relationship between them (Jayasudha and Sharma, 2010). Phenotypic correlation determines the extent to which the 2 variables are associated and is governed by genotypic and environmental correlation. The genotypic correlation on the other hand is the only heritable part and represents the genetic portion of the phenotypic correlation. Genotypic correlation plays a key role in the development and execution of suitable breeding programmes (Selvaraj *et al.*, 2011). For the improvement of economically important traits like yield in paddy, one of the utmost requirements is to widen the genetic base of the crop by introgression of genes from diverse sources. RIL populations, developed from sexual reproduction, which may evolve as superior seggregants can prove helpful in this context (Chaudhari *et al.*, 2014). A wide range of genetic variability has been reported for grain yield traits in the past by Singh *et al.* (2011); Idris *et al.* (2012); Nirmaladevi *et al.* (2015); Savitha and Usha Kumari, (2015), but still some unrevealed genetic variability prevails within the germplasm, which is of utmost importance for the selection of potential parents for obtaining superior seggregants in response to grain yield and its component traits. Keeping in consideration, the above background information, this study was undertaken with an attempt to estimate the genetic variability, heritability for yield and its component traits in a RIL population of rice and unravel the correlation between them.

MATERIALS AND METHODS

Experimental material

This study was carried out during *kharif* 2014 and 2015 at School of Biotechnology, Sher-e-Kashmir University of Agriculture Sciences and Technology, Jammu. The experimental material for the present study consisted of a RIL mapping population derived from a cross of agronomically superior line Pusa Basmati 1 which is a semi- dwarf, early maturing and high yielding aromatic rice variety with Basmati 370, a tall, late maturing and low yielding variety. The RIL population which comprised of 140 individuals was developed using single seed descent method. Each RIL along with parents was planted in a plot arranged in a randomized complete block design (RCBD) with 3 replications. All the recommended package practices were followed to raise a good crop. Five plants were randomly selected and were evaluated for yield and its component traits. The traits studied were: Tillering ability (Ti), Panicle length (PnL) in cm, 1000- grain weight (GW) in grams, Grain number per panicle (GNP), Spikelet fertility (SpFert) in percent and Grain yield (YLD) in grams. All the measurement techniques were based on IRRI standard evaluation system of rice (IRRI, 2002).

Statistical analysis

The mean values of the data recorded were subjected to statistical analysis. SPSS (version 20.0) software was used for the descriptive statistical analysis and analysis of variance (ANOVA) of yield and its component traits. For the estimation of genotypic variance (σ^2g), phenotypic variance (σ^2g), heritability in broad sense (h^2), and correlation coefficients (r^2) among yield and its component traits, R statistical package (R Core Team, 2013) was used. Phenotypic and genotypic coefficients of variation (PCV% and GCV%, respectively) were calculated according to the formula suggested by Burton (Burton, 1952).

RESULTS AND DISCUSSION

The recombinant inbred lines along with the parents were evaluated for yield and its component traits during the year 2014 and 2015. The mean ± SD and range obtained for the RILs is depicted in Table 1. The grain yield along with its associated traits showed a wide range i.e. tillering ability was found to range from (2.8 - 19.9) during 2014 and (3.0 - 21.2) during 2015. Another yield attributing trait, panicle length ranged between 22.7 cm to 31.4 cm during 2014 and 20.9 cm to 30.5 cm during 2015. The grain number per panicle was found to show a huge range of 63.0- 164.0 and 66.0- 132.0 during 2014 and 2015 respectively. The range for 1000-grain weight and spikelet fertility percentage during 2014 and 2015 was recorded as 9.9g-27.5g and 19.0g- 33.7g; 62.9% - 99.5% and 55.3% - 97.8%, respectively. The recorded maximum and minimum values for grain yield during both the years intimated the huge range varying between 5.3g- 40.9g during 2014 and 3.3g - 19.7g in the year 2015. The average values and the range for the traits clearly indicate that the recombinant inbred lines are of transgressive nature. The results obtained were in accordance to those observed by Tehrim *et al.* (2012); Chaudhari *et al.* (2014).

Table 1. Mean ± SD and range for yield and its component traits in RIL population of Basmati 370 × Pusa Basmati 1 during 2014 and 2015.

No.	Trait	Parents				RIL Population			
		2014		2015					
		Mean		Mean		2014		2015	
		Basmati 370	Pusa Basmati 1	Basmati 370	Pusa Basmati 1	Mean±SD	Range	Mean±SD	Range
1	Ti	7.6	9.2	9.1	10.0	8.8±2.6	2.8-19.9	9.9±2.8	3.0-21.2
2	PnL (cm)	25.7	28.3	25.8	27.7	26.6±1.2	22.7-31.4	26.4±1.6	20.9-30.5
3	GNP	91.0	118.0	109.0	133.0	102.0±17.0	63.0-164.0	95.0±12.5	66.0-132.0
4	GW (g)	19.0	21.1	20.2	22.4	22.1±2.9	9.9-27.5	22.5±1.4	19.0-33.7
5	SpFert (%)	88.7	90.1	87.9	91.4	86.9±6.2	62.9-99.5	84.6±7.5	55.3-97.8
6	GYD (g)	10.3	14.7	7.1	10.2	15.8±6.4	5.3-40.9	9.6±3.0	3.3-19.7

Ti: Tillering ability; PnL: Panicle length (cm); GNP: Grain number per panicle; GW: 1000- grain weight (g); SpFert: Spikelet fertility (%); GYD: Grain yield (g)

The analysis of variance revealed highly significant differences within the genotypes for all the 6 yield characters indicating the existence of significant amount of variability among the characters studies (Table 2). The presence of significant amount of variability in the initial breeding material assures the production of suitable recombinants for crop improvement. Previous studies in rice also found significant variation for these traits (Tiawari *et al.*, 2011; Yaqoob *et al.*, 2012; Anis *et al.*, 2016). Estimation of genetic variability components was done in order to determine the heritable potential of concerned genes as well as the

Table 2. ANOVA for yield and its component traits in recombinant inbred line population.

Source of variation	DF	Year	Ti	PnL (cm)	GNP	GW (g)	SpFert (%)	GYD (g)
			Mean sum squares (MSS)					
Genotypes	139	2014	20.8**	5.4**	871.5**	24.4**	117.6**	152.8**
		2015	23.1**	7.3**	461.9**	5.8**	171.3**	26.7**
Replication	2	2014	35.0**	35.2**	34.9**	34.1**	35.2**	33.9**
		2015	35.5**	35.1**	39.1**	35.5**	36.6**	33.6**
Error	278	2014	0.0	0.0	0.0	0.0	0.0	0.0
		2015	0.0	0.0	5.9	0.0	0.1	0.0

**- Significant at 1% level of significance

influence of environment over them (Kumar *et al*., 2014). The relative values obtained for the genotypic and the phenotypic coefficient of variation indicate the magnitude of the variation present. In this study, both the heritable (genotypic variance) as well as non-heritable components (phenotypic variance and heritability) were estimated as depicted in Table 3. The values recorded for genotypic coefficient of variation (GCV) was less than those obtained for phenotypic coefficient of variation (PCV) for all the traits under observation, indicating that most of the portion of the phenotypic coefficient of variation was contributed by the genetic component as compared to that of the environment component (Nirmaladevi *et al*., 2015). Apart from this, both phenotypic and genotypic coefficient of variation were found to be in close agreement with each other. A wide range of phenotypic coefficient of variation (6.1% - 31.2%) and genotypic coefficient of variation (5.7% - 30.5%) was observed for the traits studied (Table 3).

Table 3. Genetic variability parameters for yield and its component traits.

No.	Trait	σ_2 g	σ_2 p	GCV (%)	PCV (%)	h^2
1	Ti	7.3	7.6	27.3	27.8	96.0
2	PnL (cm)	2.3	2.6	5.7	6.1	88.0
3	GNP	222.3	228.0	15.7	15.9	97.0
4	GW (g)	1.9	2.2	6.1	6.6	86.0
5	SpFert (%)	54.7	56.0	8.7	8.8	98.0
6	GYD (g)	8.6	9.0	30.5	31.2	97.0

σ2 g: Genotypic variance; σ2 p: Phenotypic variance; GCV: Genotypic component of variation, PCV: Phenotypic component of variation; h^2: Heritability (broad sense).

The observations recorded go well with the results obtained by Singh and Choudhary, (1996); Zahid *et al*. (2006); Pratap *et al*. (2012); Kumar *et al*. (2014); Naseem *et al*. (2014); Savitha and Usha Kumari, (2015); Anis *et al*. (2016). Presence of PCV and GCV in higher magnitude for the traits like Ti and GYD (g) is an implication of the prevailing variability, which opens up an opportunity for carrying out improvement through simple selection (Nirmaladevi *et al*., 2015). Lower values (less than 10) of genotypic and phenotypic coefficient of variation have been recorded for characters like PnL (cm), GW (g) and SpFert (%). Gokulakrishnan *et al.* (2014); Paikhomba *et al.* (2014); Lingaiah, (2015); Nirmaladevi *et al.* (2015) also reported similar results. Lower genotypic and phenotypic coefficient of variation obtained elucidate the presence of narrow genetic base for such traits and hence for their improvement, methods like hybridization and induced mutagenesis can be used to widen the genetic base, followed by pedigree selection in the advanced generations (Nirmaladevi *et al*., 2015). However, moderate value (10-20%) of GCV% and PCV% have been observed for traits like GNP hence is considered to have moderate amount of variability and hence could be improved through selection in later generations. Gokulakrishnan *et al.* (2014); Lingaiah, (2015); Hailu *et al.* (2016) reported similar results. Overall, the relative proximity observed between the phenotypic and the genotypic coefficient of variation for the traits indicate the meager influence of the environment on the expression of these traits, which is further supported by the higher values of heritability obtained.

Heritability of a trait is an 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, hence prior knowledge about the heritability of the traits is a prerequisite for the selection programme (Singh *et al*., 2011). Broad sense heritability explains both fixable (additive) and non-fixable (dominant and epistatic) variances which helps in estimating the inheritance of a character (Panse, 1957; Nirmaladevi *et al*., 2015). On the basis of heritability the traits are classified into 3 categories: Highly heritable (> 70%), medium heritable (50 - 70%) and low (< 50%), as per Robinson's classification (Robinson's, 1966). The entire 6 yield and its associated traits exhibited high heritability, greater than 70% during the study. The broad sense heritability estimates for the traits observed are Ti (96%), PnL (88%), GNP (97%), GW (86%), SpFert (98%) and GYD (97%). The heritability estimated for the traits was found to be in agreement with that seen by Sabesan *et al.* (2009); Jayasudha and Sharma, (2010); Selvaraj *et al*. (2011); Bornare *et al*. (2014); Paikhomba *et al*. (2014); Sabar *et al.* (2014). Highest value of heritability (98%) estimated for spikelet fertility indicated that it was predominantly governed by additive gene effect. Such traits can be improved by doing mass selection and adapting several other breeding strategies based on progeny selection. Panwar and Mathur, (2007) while studying variability in segregating populations of rice obtained similar values of heritability for traits like filled grains per panicle and biological yield per plant (g). The traits with lesser variation between GCV and PCV as well as higher heritability values should be considered while carrying out selection for grain yield improvement, because most likely such traits are controlled by additive gene effects.

The correlation analysis was done to reveal the association between yield and its component traits. Table 4 presents the phenotypic and the genotypic correlation between yield and its associated traits. The values below the diagonal indicate the correlation coefficients of the traits during the year 2014 while the values above the diagonal represent the correlation coefficients of the traits during 2015. The correlation studies for both the years indicate that the estimate of genotypic correlation coefficients was higher than the phenotypic correlation coefficients for entire 6 traits. During the year 2014, a significant positive correlation at $P < 0.05$ was found between yield and its component traits. Similar results were observed by Satyanarayana *et al.* (2005); Yoon *et al,* (2006); Sabu *et al.* (2009); Fu *et al.* (2010); Akinwale *et al*. (2011) and Ashfaq *et al*. (2012). In the year 2015, grain yield was found to have significant positive association with tillering ability and 1000- grain weight ($P < 0.05$). On the other hand, panicle length showed a negative but significant correlation with grain yield during the year 2015. A negative non-significant correlation between grain yield and panicle length was observed by Bornare *et al*. (2014); Venkata Lakshmi *et al*. (2014). This may be attributed to the lowest GCV%, PCV% and heritability of panicle length in comparison to other traits, indicating the slight influence of environment on it. From the correlation studies it was concluded that the characters like tillering ability (Ti), panicle length (PnL), grain number per panicle (GNP) and 1000- grain weight (GW) had positive significant correlation with grain yield (GYD). Therefore, improvement of such traits through selection will automatically result in increased grain yield.

Table 4. Estimates of correlation coefficients between yield and its component traits during 2014 (below the diagonal) and 2015 (above the diagonal).

Trait	Ti	PnL (cm)	GNP	GW (g)	GYD (g)	SpFert (%)
Tillering ability	1.00	-0.08*	-0.02*	0.24*	0.44*	-0.01*
	1.00	-0.12*	-0.03*	0.33*	0.63*	-0.02*
Panicle length (cm)	0.30*	1.00	-0.03*	0.06*	-0.07*	-0.02*
	0.42*	1.00	-0.05	0.08	-0.11*	-0.03
Grain number per panicle	0.11*	0.22*	1.00	-0.10*	0.04	0.07*
	0.15*	0.31*	1.00	-0.15*	0.07	0.10*
1000- grain weight (g)	0.12*	0.07*	-0.01*	1.00	0.33*	-0.03*
	0.17*	0.10*	-0.02*	1.00	0.48*	-0.06*
Grain yield (g)	0.66*	0.30*	0.21*	0.16*	1.00	0.00
	0.84*	0.43*	0.31*	0.24*	1.00	0.01*
Spikelet fertility (%)	0.09*	0.07*	-0.04*	0.07*	0.11*	1.00
	0.13*	0.10*	-0.07*	0.10*	0.16*	1.00

*- Significant at 5% level of significance

CONCLUSION

Presence of genetic variability in a crop is an utmost requirement for the improvement of economically important traits like yield in rice. From this study, we conclude that the recombinant inbred lines possessed adequate amounts of variability for yield and its associated traits. The traits tillering ability (Ti), panicle length (PnL), grain number per panicle (GNP), 1000- grain weight (GW) showed higher heritability and positive correlation with grain yield (GYD) and hence can be used as selection indices for improving grain yield in rice. In this study, the transgressive nature and the presence of high heritability and positive significant correlation between yield and its component traits in RIL population, confirm its suitability for such studies.

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