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# Genetic variability and interrelationship studies in green super rice

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## ABSTRACT

Field experiment was executed using 18 advance lines of green super rice (GSR) during Kharif 2015 at Agricultural Research Institute, D.I. Khan, KP, Pakistan. The aims of the study were to screen out genetic variability among GSR lines and to assess heritability and genetic advance and correlation between yield and related attributes. The experiment was laid down in a randomized complete block design with three replications and data on eight production traits were recorded and subjected to various statistical analysis. The results corresponding to analysis of variance revealed significant ( $P \leq 0.01$ ) differences among GSR lines for all the studied traits. 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. Similarly, the highest heritability (>60%) associated with genetic advance were assessed for all the traits, except panicle length, indicating better scope for improvement of these traits by an effective selection program. Correlation analysis revealed that paddy yield manifested significant correlation with days to panicle emergence ( $r=0.57^{**}$ ), panicle length ( $r=0.53^*$ ) and number of filled grains panicle<sup>-1</sup> ( $r=0.63^*$ ) hence, ample importance should be given to these traits during selection.

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## INTRODUCTION

Rice is the staple food and ranks second in production among cereals in Pakistan. It is also a good source of livelihood for farming community in its growing season as it secures a high proportion of foreign exchange after cotton. Rice accounts for 3.0 percent in the value added in agriculture and 0.6 percent of GDP. During 2016-17, rice crop was sown on area of 2724 thousand hectares showing a decrease of 0.6 percent over the last year's area of 2793 thousand hectares. Rice production stood at 6849 thousand tonnes achieving its targeted production of 6838 thousand tonnes and showing an increase of 0.7 percent over corresponding period of last year's production of 6801 thousand tonnes. Rice area decreased due to decline in domestic prices of rice which reduced the area under the crop and growers shifted to sugarcane and maize crop (Pakistan Economic Survey, 2016-17).

Asian rice, (*Oryza sativa*), is one of the most important and oldest crop species domesticated about 8,000 – 9,000 years ago (Liu *et al.*, 2007). It is a feeding source for more than one half of the world's population (Li *et al.*, 2006). Rice is the combination of several genetically differentiated groups, with the two most important groups being *indica* and *japonica*. *Indica* and *japonica*

are sometimes also described as sub-species. The archeological evidences had showed that it was grown in third millennium BC in Pakistan in the areas of Sindh and Punjab (Paikhomba *et al.*, 2015).

The rapid increase in population of the world demands for improvement in acreage and yield of the crop. It is expected that world population will possibly reach 9-11 billion during 2030-2050. With recent tendency of population growth and agriculture production the requirement of world food will be double in some part of the world. Development of high yielding varieties is the best way to ensure food security of increasing population (Bisne *et al.*, 2009). The challenge, above anything else, is to produce this additional rice with less land, less water, and less labour, in more efficient, environmentally-friendly production systems that are more resilient to climate change, among other factors. The success of fruitful breeding program usually depends upon the extent of genetic variability present in the breeding materials. Thus, knowledge on genetic variability along with heritability and genetic advance is very essential for a breeder to choose good genotypes for crop improvement.

Recognizing the stated importance and existing potentials to boost rice production and productivity to cope up with the

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fastest growing demand, utilization of genetic variability which exists among rice genotypes for grain yield will provide the basis for selection to improve productivity of rice in Pakistan. Hence, breeding for yield component to increase grain yield would be more efficient if the components involved are highly heritable and genetically independent (Akinwale *et al.*, 2011). In addition, the knowledge of heritability in the selection based improvement programs indicates the extent of transmissibility of a character in future generations (Sabesan *et al.*, 2009). It is also pertinent to note that high heritability alone does not guarantee large gain from selection unless sufficient genetic advance (GA) attributed to additive gene action is present (Akinwale *et al.*, 2011).

Therefore, efforts were made in the present study to determine the extent of genetic variability, heritability and possible amount of genetic advance for the agronomic traits as a basis for selection of high yielding genotypes and to generate information on relationship of yield and its component traits and their implication towards better selection.

## MATERIALS AND METHODS

The current research study was conducted at Agricultural Research Institute, D.I. Khan, KP, Pakistan during 2015 rice crop growing season. Eighteen advance lines of green super rice (GSR) were evaluated following RCB design with three replications. Thirty five days old nursery were transplanted into well puddled field with spacing of 20 cm each between rows and plants, respectively. Standard agronomic necessities were fulfilled to raise good crop. A composite of five plants were randomly selected in each  $3 \times 0.60$  m<sup>2</sup> plot to record observations on plant height, tillers plant<sup>-1</sup>, panicle length, filled grains panicle<sup>-1</sup> and 1000-grain weight, while for days to panicle emergence and physiological maturity and paddy yield, observations were recorded on plot basis. Finally, the mean values over three replications were used for statistical analysis and analysis of variance was performed as per Steel *et al.* (1997), GCV and PCV according to Burton (1952), broad-sense heritability according to Singh and Chaudhary (1999), genetic advance according to Allard (1960) and correlation according to Kwon and Torrie (1964). The magnitude of heritability was characterized as low (0-30%), moderate (>30-60%) and high (>60%) according to Robinson *et al.* (1949), while GCV and PCV values were characterized as low (0-10%), moderate (10-20%) and high (>20%) according to Deshmukh *et al.* (1986).

## RESULTS AND DISCUSSION

### Genetic Variability

Mean squares due to GSR lines manifested highly significant ( $P \leq 0.01$ ) variations for days to panicle emergence and physiological maturity, culm length, tillers plant<sup>-1</sup>, panicle length, number of filled grains panicle<sup>-1</sup>, 1000-grain weight and paddy yield (Table 1). These results suggested that the studied genotypes had considerable variability for effective selection. Similarly, it is obvious from fig. 1 that mean values for studied traits ranged from 83.67 to 101.33 days for panicle emergence, 113.58 to 153.09 days for physiological maturity, 82.76 to 110.28 cm for plant height, 8.87 to 20.72 for effective tillers plant<sup>-1</sup>, 21.10 to 28.82 cm for panicle length, 19.29 to 25.96 g for 1000-grain weight, 97.29 to 223.40 for filled grains panicle<sup>-1</sup> and 344.51 to 904.41 g for paddy yield.

The assessment of genetic variability revealed higher values for genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for all the studied traits. Presence of GCV and PCV in higher magnitude in all the studied traits is an implication of the prevailing variability, which opens up an opportunity for carrying out improvement through simple selection (Nirmaladevi *et al.*, 2015). GCV ranged from 33.61% in 1000-grain weight to 622.26% in paddy yield, while, PCV ranged from 35.61% (1000-grain weight) to 622.45% (paddy yield) (Table 2). The differences in genetic parameters ranged from 0.14 to 13.80%, indicating that genotypes had played an appreciative role rather than environment and indicating less influence of environment on these traits. It also suggested that selection based on these traits would be effective. Anis *et al.* (2016) assessed higher GCV and PCV values for plant height and filled grains panicle<sup>-1</sup>, while moderate GCV and PCV were estimated for panicles plant<sup>-1</sup>, panicle length and grain yield. Similarly, Tuhina-Khatun *et al.* (2015) conducted studies of genetic variation and diversity analysis of upland rice and estimated high GCV and PCV for plant height, number of tillers plant<sup>-1</sup>, filled grains panicle<sup>-1</sup> and seed yield, while moderate values were observed for days to heading and maturity. Study on morphological characterization of rice lines conducted by Augustina *et al.* (2013) also estimated highest GCV and PCV values for all the traits with less differences between them. Another study conducted by Manikya and Reddy (2011) reported less differences between GCV and PCV values for

**Table 1: Analysis of variance for various traits of 18 GSR lines**

Traits	Replications <i>df</i> =2	Genotypes <i>df</i> =17	Error <i>df</i> =34	CV (%)
Days to panicle emergence	0.46	93.25**	0.68	1.18
Days to panicle emergence	0.70	225.93**	0.27	0.55
Plant height	0.50	123.13**	7.31	3.73
Tillers plant <sup>-1</sup>	1.01	30.73**	0.55	6.54
Panicle length	4.09	18.17**	3.60	10.20
Filled grains panicle <sup>-1</sup>	13.96	3382.16**	21.46	3.78
1000-grain weight	0.39	7.38**	0.29	3.38
Paddy yield	5.75	63991.31**	13.16	0.82

\*\*= significant at 1% level of probability

Table 2: Components of genetic parameters for various traits of 18 GSR lines

Traits	$\sigma^2g$	$\sigma^2p$	GCV	PCV	PCV-GCV	$h^2_{(BS)}$	GA
Days to panicle emergence	30.86	31.54	56.69	57.31	0.62	97.85	7.69
Days to physiological maturity	75.22	75.49	77.35	77.49	0.14	99.65	12.12
Plant height	4.86	8.45	43.23	57.02	13.80	57.47	2.34
Tillers plant <sup>-1</sup>	10.06	10.61	79.73	81.89	2.15	94.81	4.32
Panicle length	4.86	8.45	43.23	57.02	13.80	57.47	2.34
Filled grains panicle <sup>-1</sup>	1120.23	1141.69	262.52	265.03	2.50	98.12	46.42
1000-grain weight	2.36	2.65	33.61	35.61	2.00	89.09	2.03
Paddy yield	21326.05	21339.21	622.26	622.45	0.19	99.94	204.39

$\sigma^2g$ =genetic variance,  $\sigma^2p$ =phenotypic variance, GCV=genotypic coefficient of variance (%), PCV=phenotypic coefficient of variance (%),  $h^2_{(BS)}$  = broad-sense heritability (%), GA=genetic advance

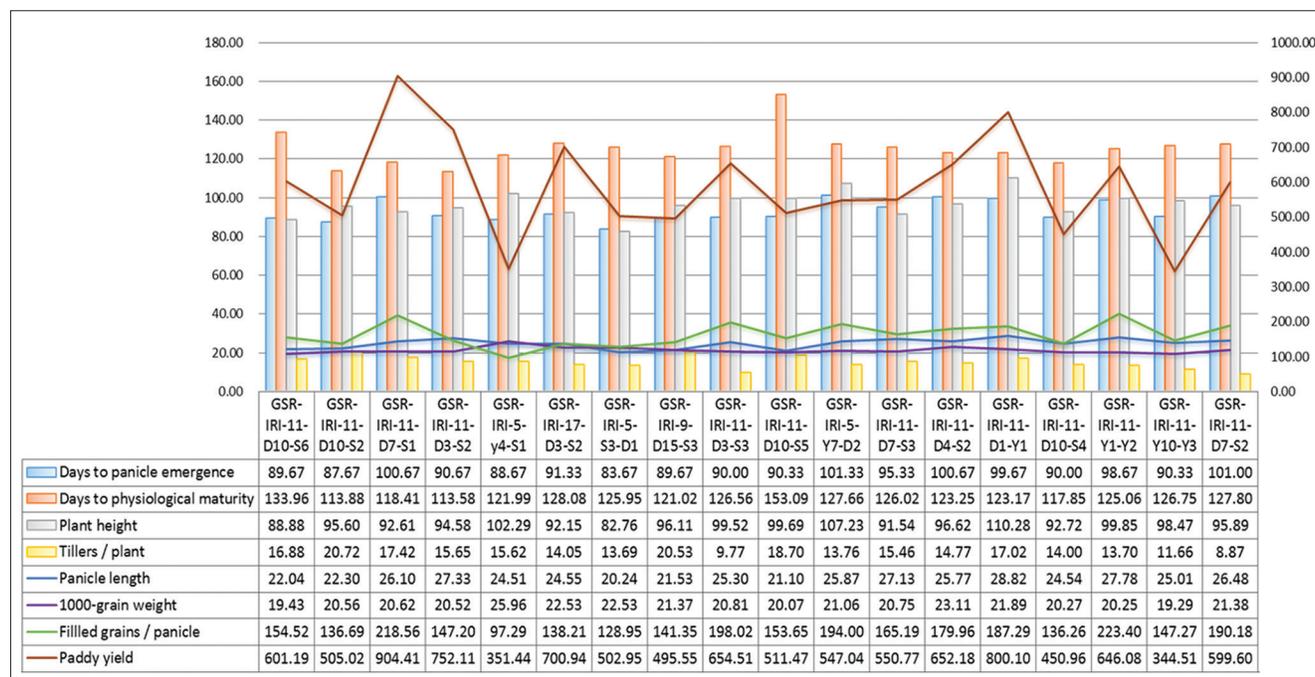


Figure 1: Mean performance of 18 GSR lines for yield and component traits

all the traits and concluded that there was less influence of environment on the expression of these traits.

### Heritability and genetic advance

Knowledge of heritability assists plant breeders in making selection more effective and simpler and together with heritability, genetic advance offer more realizable gain at specific selection intensity. In the present study, genotypic variances were higher in magnitude than corresponding environmental variances for all the studied traits, resulting in high heritability for most of the traits. Higher genetic variance indicates more chances of sustainable improvement through selection (Estehghari and Farshadfar, 2014). The highest heritability coupled with genetic advance were assessed for days to panicle emergence (97.85%, 7.69), days to physiological maturity (99.65%, 12.12), plant height (84.09%, 7.98), tillers plant<sup>-1</sup> (94.81%, 4.32), number of filled grains panicle<sup>-1</sup> (98.12%, 46.42), 1000-grain weight (89.09%, 2.03) and paddy yield (99.94%, 204.39), while moderate heritability along with genetic advance was observed for panicle length

(57.47%, 2.34) (Table 2). Traits with high heritability and genetic advance confirms their additive gene action, whereas low values are indicative of non-additive gene action (Singh and Narayanan, 1993). Thus assessment of heritability will be reliable if accompanied by high genetic advance. Studies conducted by Kalyan *et al.* (2017) and Limbani *et al.* (2017) found the highest heritability (>60%) for all the studied traits including paddy yield and suggested that these traits were mainly under genetic control and can be scored by phenotypic performance. Similarly, Konate *et al.* (2016) observed high heritability and genetic advance for days to flowering, plant height and paddy yield while studying genetic variability of agro-morphological traits in rice inbred lines. Pradhan *et al.* (2015) tested 30 low land rice genotypes and reported that the estimates of heritability and genetic advance were higher for days to heading, grains panicle<sup>-1</sup> and plant height, which signified additive gene effect. Prasad *et al.* (2015) assessed high heritability for days to maturity and plant height while evaluating genetic variability in fine rice genotypes. Lingaiah *et al.* (2014) evaluated 64 elite mid early genotypes of rice and reported high heritability (>60%) and

genetic advance for all the studied traits except productive tillers plant<sup>-1</sup>.

## Correlation

The assessment of correlation is useful in disclosing the direction and magnitude of relationship between yield contributing traits and yield. In the present study, assessment of correlation revealed that days to panicle emergence ( $r=0.57^{**}$ ), panicle length ( $r=0.53^*$ ) and filled grains panicle<sup>-1</sup> ( $r=0.63^{**}$ ) are most desired traits affecting paddy yield significantly (Table 3). These results indicated the simultaneous selection of these traits to enhance paddy yield. Paddy yield manifested no correlation with the remaining traits. Ratna *et al.* (2015), Eidi-kohnaki *et al.* (2013) and Surek and Beser (2002) pointed out that panicle length and number of filled grains panicle<sup>-1</sup> are important traits, significantly affecting paddy yield. Kole *et al.* (2013) reported that grain yield was significantly affected by panicle length. Similarly, a study conducted by Haider *et al.* (2012), Kiani and Nematzadeh (2012) and Seyoum *et al.* (2012) reported number of filled grains panicle<sup>-1</sup> being most important trait affecting paddy yield. In another study, Konate *et al.* (2016) and Nor *et al.* (2013) reported non-significant correlation between plant height and paddy yield, which is in line to this study. Significantly positive association of days to panicle emergence was also observed with plant height ( $r=0.49^*$ ), panicle length ( $r=0.73^{**}$ ) and filled grains ( $r=0.77^{**}$ ). Panicle length showed positive and significant association with number of filled grains ( $r=0.64^{**}$ ) and plant height ( $r=0.48^*$ ) (Table 3). Ratna *et al.* (2015) reported significant correlation between panicle length and plant height and non-significant association between panicle length and number of filled grains panicle<sup>-1</sup>.

## CONCLUSION

It is concluded that varying genetic variability exists in the germplasm provides opportunities for this collection to be useful for genetic improvement. Traits with high heritability and genetic advance are attributable to additive gene action, hence selection based on phenotypic performance would be effective. Days to panicle emergence, panicle length and filled grains panicle<sup>-1</sup> showed positive contribution towards paddy yield, hence it can be advocated to give priority to these traits in the selection program. Based on mean performance, GSR-

**Table 3: Correlation coefficients of paddy yield with component traits**

	DPM	DPE	PH	TP	PL	FG	TGW
DPE	-0.05						
PH	0.12	0.49*					
TP	0.08	-0.20	0.12				
PL	-0.37	0.73**	0.48*	-0.29			
FG	0.04	0.77**	0.41	-0.28	0.64**		
TGW	-0.20	0.13	0.04	0.13	-0.01	-0.20	
PY	-0.13	0.57**	0.27	0.12	0.53*	0.63**	0.22

\*\*,\*= Significant at 1% and 5% level of probability, respectively  
DPE=days to panicle emergence, DPM=days to physiological maturity, PH=plant height, TP=tillers plant<sup>-1</sup>, PL=panicle length, FG=filled grains panicle<sup>-1</sup>, TGW=1000-grain weight, PY=paddy yield

IRI-11-D7-S1, GSR-IRI-11-D1-Y1 and GSR-IRI-11-D3-S2 were identified to be most promising lines for paddy yield and some other traits, hence these lines may be good for future rice breeding programs.

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