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Research Article

Genetic analysis and trait association for yield related traits in $F_{2:3}$ biparental population of rice under slightly sodic condition

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Abstract

Genetic variability and correlation studies provide basic information concerning the genetic properties of the population based on which, breeding methods could be formulated for further improvement of the crop. The estimates of heritability, coefficients of variability, genetic advance and trait association were computed for eleven yield related traits in $F_{2:3}$ segregating populations of biparental crosses under slightly sodic condition. Analysis of variance revealed significant differences for the traits studied except, effective tillers per plant, panicle length and test weight, indicating the existence of high genetic variability among the lines. Estimates of phenotypic coefficients of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters studied, indicating considerable effect of environment. Moderate heritability accompanied with high genetic advance was recorded for filled grains and unfilled grains per panicle which, indicates heritability is most likely due to additive gene effect and selection for the traits will be effective. Traits like: effective tillers per plant, panicle length, filled grains per panicle and total grains per panicle that showed, positive and significant association with grain yield per plant, could be useful for breeders in any breeding program for further improvement of the traits under sodic condition.

Keywords: Genetic variability, PCV, GCV , Sodic condition

Introduction

Rice is the life and the prince among cereals as this unique grain helps to sustain two thirds of the world’s population. Asia is the biggest rice producer and consumer, accounting for 90 per cent of the world’s production and consumption of rice (Kahani and Hittalmani, 2015). Grain yield of rice in sodicity affected soils is much lower because of its high sensitivity to sodic stress (Gao *et al.*, 2007; Ismail *et al.*, 2007), high yield losses have been observed because of high mortality and poor crop establishment. Improvement in yield is the major objective in rice breeding programmes. The rice accessions are a rich reservoir of useful genes that rice breeder can harness for yield improvement programme (Singh *et al.*, 2015). The development of new genotypes requires knowledge of genetic variability presents in the crop to build efficient breeding programme.

Before launching any breeding programme, a breeder should have a thorough knowledge on nature and magnitude of genetic variability, heritability, genetic advance and character association in a crop species. Studies have also shown the potential to exploit the genetic variation in variable range of tolerance against sodic-salt stress without the general negative effect on yield. Moreover, it is the primary target for improvement of rice productivity in both favourable and unfavourable environments (Shah *et al.*, 2017). Grain yield is a complex trait, influenced by the environment and is the result of inter-action of many variables. The knowledge of genetic variability helps to ascertain the presence and absence of heritability of variations. Variability for yield in crop species will ultimately get exhausted; however thereby, limiting the prospects of further improvements in a crop species. Thus, variability is the prerequisite for any improvement in the crop species.

Effective improvement in yield may be brought through selection of yield component traits using the information from various variability parameters. Heritability is a good index of the transmission of character from parents to their offspring, which guide a breeder in the choice of parents from amongst diverse rice genotypes, for crop improvement programmes (Rashmi *et al.*, 2017). Estimation of heritability along with genetic advance, conjointly, is helpful in predicting the gain under selection than heritability estimate, alone (Moosavi *et al.*, 2015). Correlation is the measure of mutual relationship between two variables and measures the degree of relationship. Consequently, selection for yield may not be satisfying without taking into consideration yield component traits. Thus, positive correlation between yield and yield components are required for effective improvement. As $F_{2:3}$ population, derived from two contrasting parents for sodicity tolerance, provides an opportunity for two cycles of meiosis which minimizes linkage drag compare than F_2 population, where the chances of linkage drag is more due to single cycle of meiosis. Keeping these objectives in view, the present study was conducted to observe and evaluate genetic variability and correlation among $F_{2:3}$ population developed for conferring sodicity tolerance under slightly sodic environment.

Materials and Method

Experiment was carried out in *kharif* 2018, at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. Soil samples were collected randomly from different part of experimental fields, pre transplanting and post harvesting. Collected soil samples were mixed in equal proportion and subjected to analysis by pH and EC meter. pH at pre transplanting and post harvesting was recorded as 8.2 and 8.1, respectively while the EC recorded was 1.28 dS/m. Based on above readings the experimental site was categorized as slightly sodic.

A set of 298 $F_{2:3}$ families derived from the cross PUSA 44 (Sodicity sensitive variety) × CSR 43 (Sodicity tolerant variety), following single seed descent method, was transplanted on 31 July, 2018 @10 plants per family along with parents as check, in alpha lettice design with two replications maintaining a spacing of 15 x 20 cm plant to plant and row to row, respectively, under sodic condition.

Mean data on days to 50 per cent flowering and days to maturity were recorded on plot basis. For remaining traits, data were recorded on five plants from each replication respectively, for plant height (cm), effective tillers per plant, panicle length (cm), filled grains per panicle, unfilled grains per panicle, total grains per panicle, Spikelet fertility per cent, test weight (g) and grain yield per plant (g). Data were subjected to statistical analysis.

Analysis of Variance (ANOVA) were performed using the PROC GLM procedure by SAS v9.2. Various genetic parameters such as genetic and phenotypic variance, genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) were worked out as per Burton and De-Vane (1953). GCV and PCV values were classified as per classification suggested by Sivasubramanian and Menon (1973), accordingly traits having <10 %= low; 10-20% = Moderate; >20 % = high.

Broad sense heritability (h^2), genetic advance (GA) were computed by using the formula given by Allard (1960). Heritability estimates were classified following the classification suggested by Johnson *et al.* (1955).

<30% = Low; 31-60% = Medium; >60% = High
Likewise, for genetics advance following classification was used:
<10% = Low; 10- 20% = Moderate; >20% = High
Correlation analysis was performed using the software packages ADEL-R and META-R developed by CIMMYT, Mexico. Following scales were used for categorization based values of correlation coefficient given by Searle, 1965
>0.65 = Very strong; 0.50 to 0.64 = moderately storng; 0.30 to .49 = moderately weak; <0.30 = very weak.

Results and Discussion

It is revealed from the analysis of variance that all 298 $F_{2:3}$ lines along with parents were highly significant at (P<0.01) for the traits under study except effective tillers per plant, panicle length and test weight (Table 1) confirming the existence of considerable amount of variability under sodic condition among the lines. Existence of significant variability present for a trait will be helpful for a breeder in selection and further improvement of the trait. Similar results were also reported by Fiyaz *et al. (*2011); Shah *et al.* (2017); Pallavi *et al.* (2017); Sandhya *et al.* (2017).

Estimates of various variability parameters are presented in table 2. The relative magnitudes of the phenotypic as well as genotypic variances between the traits were compared based on the phenotypic and genotypic coefficient of variation. In general, phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters studied indicating that apparent variation is not only due to genotypes but also due to the influence of environment and, the interaction of G x E. The difference between phenotypic and genotypic co-efficients of variation was quite variable suggesting a considerable effect of environment on the expression of these traits and the selection based on these will not be effective for further yield improvement. Results were in confirmation with the findings of Loitongbam *et al.* (2019); Maurya *et al.* (2018); Tuhina-Khatun *et al.* (2015). Unfilled grain per panicle showed highest genotypic as well as phenotypic coefficients of variation, meanwhile lowest GCV and PCV for test weight and days to maturity, respectively were observed among all the traits (Table 2). On the basis of suggested classification days to 50 per cent flowering, days to maturity, plant height and panicle length showed low GCV and PCV indicated that the breeders should go for other source of higher variability for these traits to make improvement. Likewise, effective tillers per plant, filled grains per panicle, total grains per panicle and grain yield per plant showed moderate GCV and high PCV, respectively suggested that these traits can be improved by the vigorous selection.

Heritability in broad sense is the relative magnitude of genotypic and phenotypic variances for the traits studied and plays a predictive role in selection procedures. This gives an idea of the total variation ascribable to genotypic effects, which are exploitable portion of variation (Sanghera *et al.,* 2013). The results revealed that heritability in broad sense was highest for Days to 50 per cent flowering (74.10%) (Table 2), suggesting the presence of a high component of heritable portion of variation which plays an important role in deciding the suitability and strategy for selection of this particular trait but, it may not be useful for improvement of days to 50 per cent flowering because, heritability is based on total genetic variation which includes both, fixable and non-fixable variances. Loitongbam *et al.* (2019) and Fiyaz *et al.* (2011) reported similar findings in their studies. Heritability was lowest for test weight (8.96%) indicating that, direct selection for this trait will be ineffective due to masking effect of the environment on the genotype. High heritability was recorded for days to 50 per cent flowering and days to maturity, medium heritability for filled grains per panicle, unfilled grains per panicle, total grains per panicle, spikelet fertility percent and grain yield per plant while, it was observed to be low for plant height, effective tillers per plant, panicle length and test weight.

For meaningful genetic progress in crop improvement programmes, the selection of traits should be based on high heritability, coupled with high genetic advance (Shah *et al.,* 2017). The results revealed that reveals that high genetic advance was recorded for total grains per panicle (23.58%) (Table 2) followed by filled grains per panicle (21.52%) indicating the governance of trait by additive genes and selection will be rewarding for further improvement. Meanwhile, low genetic advance was observed for test weight (0.58%) followed by panicle length (0.68%) suggesting governance by non-additive genes thus heterosis breeding may be useful. For most of the traits, genetic advance recorded under nearly moderate to low category indicate the presence of non additive gene. Moderate heritability accompanied with high genetic advance was recorded for filled grains and total grains per panicle which indicates that heritability is most likely due to additive gene effect and selection for the traits will be effective. High heritability with nearly low genetic advance was observed for days to 50 per cent flowering and days to maturity which is indicative of non additive gene action. Further, high heritability is probably being exhibited due to favourable influence of environment rather than genotype. Selection for these traits may not be effective, therefore. Similar observations were also obtained by Shah *et al.* (2017) and Singh *et al.* (2012).

Correlation studies on association of most of the studied traits with grain yield per plant, revealed that genotypic correlation was higher than phenotypic correlation suggesting a strong association of these traits with grain yield per plant genetically and, the phenotypic value is lessened by the significant interaction of environment (Table 3). Similar trends of findings were reported by Shah *et al.* (2017); Pallavi *et al.* (2017) and Sudharani *et al.* (2013). In the present study, phenotypic correlation is observed higher than genotypic correlation for the association of plant height and total grains per panicle with grain yield indicating that, apparent association of these traits is not only due to genes but, also on account of favourable influence of environment.

At the genotypic level, effective tillers per plant showed a positively significant and moderately strong correlation (0.56) with grain yield per plant (Table 3), while positively significant and moderately weak correlation is revealed for grain yield per plant with days to 50 per cent flowering, days to maturity, plant height, panicle length, unfilled grains per panicle and total grains per panicle. Filled grains per panicle showed positively significant but very weak correlation with grain yield per plant. Correlation between spikelet fertility percent and grain yield per plant was non-significant at both genotypic and phenotypic levels. Results were in confirmation with the findings of Fiyaj *et al.* (2011); Singh *et al.* (2018); Gopikannan and Ganesh (2013).

Results of present investigation indicated that a wide range of genetic variability was found among 298 $F_{2:3}$ lines for the studied traits which means, there is ample scope for further improvement through selection of these traits. High PCV and GCV was observed for unfilled grains per panicle.

Likewise, effective tiller per plant, filled grains per panicle, total grains per panicle and grain yield per plant showed moderate GCV and high PCV. Moderate heritability accompanied with high genetic advance was recorded for filled grains and unfilled grains per panicle which indicates heritability is most likely due to additive gene effect and selection for the traits will be effective. Direct yield improvement under sodicity stress condition is difficult hence, yield improvement in sodic environment could be achieved by identifying secondary traits contributing higher yield and, selecting for these traits in a breeding programme. Thus, selection on the following secondary traits viz., effective tillers per plant, panicle length, filled grains per panicle and total grains per panicle will support the breeder in any breeding program for further improvement of the traits under sodic condition as these traits showed positive and significant association with grain yield per plant.

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Table 1. Analysis of Variance (ANOVA) for eleven yield related traits of $F_{2:3}$ population along with parents under slightly sodic condition

Source of variation	**d.f.**	**DF**	**DM**	**PH**	**ET**	**PL**	**FG**	**UFG**	**TG**	**SF**	**TW**	**GYPP**
Treatment	299	95.76**	87.48**	71.12**	11.11	6.59	606.62**	113.97**	759.858**	0.83**	10.7	59.62**

** Significant at 1% level of significance.
d.f. = degree of freedom

*(*DF) Days to 50 per cent flowering, (DM) days to maturity, (PH) plant height, (ET) effective tillers per plant, (PL) panicle length, (FG) filled grains per panicle, (UFG) unfilled grains per panicle, (TG) total grains per panicle, (SF) spikelet fertility per cent, (TW) test weight and (GYPP) grain yield per plant.

Table 2. Genetic variability parameters for eleven yield related traits under slightly sodic condition

****Para-meters**	**Pusa 44**	**CSR 43**	**Range**		**Mean**	**V_g**	**V_p**	**GCV**	**PCV**	**h^2 (%)**	**GA (%)**
			Min	**Max**							
#DF	97.00	86.00	66.50	104.00	87.68	40.76	55	7.28	8.46	74.10 (H)*****	11.32 (M)
DM	129.00	117.00	101.5	135	118.35	35.42	52.06	5.03	6.1	68.03 (H)	10.11 (M)
PH	83.30	77.13	61.20	104.50	82.00	16.12	55	4.9	9.04	29.30 (L)	4.47 (L)
ET	12.40	21.90	5.25	23.40	12.42	1.8	9.31	10.81	24.57	19.33 (L)	1.21 (L)
PL	26.10	22.70	18.10	31.20	24.31	0.8	5.79	3.68	9.9	13.81 (L)	0.68 (L)
FG	87.50	93.34	31.33	141.33	73.02	208.49	398.14	19.77	27.33	52.36 (M)	21.52 (H)
UFG	30.25	10.50	5.33	47.49	19.50	27.6	86.38	26.94	47.67	31.95 (L)	6.11 (L)
TG	117.75	103.84	51.73	178.17	92.51	256.75	502.83	17.32	24.24	51.06 (M)	23.58 (H)
SF	74.63	89.97	48.51	92.96	78.8	27.89	78.07	6.7	11.21	35.72 (L)	6.5 (L)
TW	24.10	31.05	11.40	34.20	27.37	0.88	9.82	3.43	11.45	8.96 (L)	0.58 (L)
GYPP	28.09	33.74	9.28	45.77	23.96	14.65	44.98	15.97	27.98	32.56 (M)	4.49 (L)

*Alphabets in the parenthesis indicates: H = High; M = Moderate ; L = Low
**Vg = Genotypic variance, Vp = Phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, h^2 = Heritability (Broad sense), GA = Genetic advance

#(DF) Days to 50 per cent flowering, (DM) days to maturity, (PH) plant height, (ET) effective tillers per plant, (PL) panicle length, (FG) filled grains per panicle, (UFG) unfilled grains per panicle, (TG) total grains per panicle, (SF) spikelet fertility per cent, (TW) test weight and (GYPP) grain yield per plant.

Table 3. Genotypic and Phenotypic correlation coefficients among eleven yield related traits under slightly sodic condition

Traits	DF	DM	PH	ET	PL	FG	UFG	TG	SF	TW	GYPP
#DF	**1**	1.00*	0.06	-0.01	0.40*	0.14*	0.54*	0.31*	-0.40*	-0.21*	0.41*
DM	0.98*	**1**	0.05	-0.02	0.43	0.15	0.56	0.32	-0.42*	-0.20*	0.42*
PH	-0.06	-0.04	**1**	0.15	0.90	0.29	0.01	0.27	0.17*	0.13*	0.39*
ET	0.01	0.02	0.11*	**1**	-0.04	0.01	-0.17	-0.05	0.19*	0.12*	0.56*
PL	0.12*	0.13*	0.69*	0.05	**1**	0.18	0.37	0.28	-0.20*	-0.38*	0.49*
FG	0.08	0.09	0.30*	0.06	0.20*	**1**	0.15	0.95	0.54*	0.20*	0.28*
UFG	0.34*	0.34*	0.02	-0.05	0.12*	0.09	**1**	0.46	-0.74*	-0.22*	0.30*
TG	0.20*	0.22*	0.28*	0.04	0.22*	0.92*	0.47*	**1**	0.24*	0.11*	0.35*
SF	-0.27*	-0.27*	0.15*	0.10*	0.01	0.50*	-0.77*	0.15*	**1**	0.44*	-0.08
TW	-0.07*	-0.08*	0.12*	0.12*	0.00	0.20*	-0.07*	0.15*	0.20*	**1**	-0.30*
GYPP	0.22*	0.24*	0.46*	0.46*	0.39*	0.39*	0.16*	0.41*	0.07	0.11*	**1**

*Significance at 5% level of significance
Below diagonally- Phenotypic correlation coefficient
Above diagonally- Genotypic correlation coefficient
#(DF) Days to 50 per cent flowering, (DM) days to maturity, (PH) plant height, (ET) effective tillers per plant, (PL) panicle length, (FG) filled grains per panicle, (UFG) unfilled grains per panicle, (TG) total grains per panicle, (SF) spikelet fertility per cent, (TW) test weight and (GYPP) grain yield per plant.

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