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Short Communication

Genetic studies for yield and nutritional traits in unpolished rice RILs of MTU1010 x BR2655

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Abstract

A study was carried out to access the genetic variability in a set of 190 recombinant inbred lines (RILs) of rice derived from MTU1010 and BR2655. Plant height and number of productive tillers per plant recorded high PCV and GCV during *kharif* 2016, whereas number of filled grains per panicle, grain yield per plant, grain zinc concentration and grain iron concentration during *rabi* 2016-17.The estimates of PCV were slightly higher than the corresponding GCV estimates for all the traits studied indicating that the characters were least influenced by the environment. High heritability coupled with high genetic advance as per cent of mean was noticed for traits like plant height, number of productive tillers, number of filled grains per panicle, 1000-grain weight, grain yield per plant, grain iron concentration and grain zinc concentration respectively during *kharif* 2016 and *rabi* 2016-17 indicating that traits are under additive genetic control, simple selection would likely be effective for further improvement of these traits in desirable direction. RILs J16, J144 and J146 have shown higher grain yield per plant with high iron and zinc concentrations.

Key words: F_8, F_9 RILs, genetic variability, heritability, genetic advance

Rice is considered as one of the important cereals which play very crucial role in providing food security and eradicating poverty. Deficiency of micronutriants such as Zn and Fe is rampant among Indian population particularly, in pregnant woman and children (Ritchie et al. 2018), therefore, identification of suitable material rich in Zn and Fe contents is of utmost need for rice improvement with respect to quality. Since rice is the principal food for more than half of the world's population (Sasaki and Burr 2000), it needs utmost attention for enhancing its productivity and production.

The information on heritability and genetic variability is essential for genetic improvement through selection. Plant breeding mainly relies on the extent of genetic variation present in a breeding population. The effectiveness of selection depends on the magnitude of heritability which enables the breeder to predict the genetic gain under selection. Both heritability and genetic advance are two selection parameters which were estimated during the course of present investigation. However, it is not necessary that a character showing high heritability should also exhibit high genetic advance (Johnson et al. 1955). It is well established that heritability estimates helps the breeders in selection of elite genotypes from multiple genetic populations. Genetic variability, heritability and selection intensity contribute to the success of genetic advance under selection (Johnson et al. 1955).

Present study was formulated with the objective to quantify the amount of the genetic variability present in the RIL population which may be exploited in genetic improvement of rice for grain zinc and iron in addition to grain yield.

The experimental material for the present study consists of a RIL mapping population (F8 generation) derived from a cross of MTU1010, a short duration

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(120-125days), long slender grain type with zinc 14.4ppm and iron 10.6ppm), and BR2655 (long duration (140-145days), medium bold grain type with zinc 23.7ppm and iron 18.3ppm). The Recombinant Inbred Lines (RISl) were produced from F_2 population and selfing till they attained complete homozygosity. The RIL population comprised of 190 individuals was planted along with parents in Randomized Complete Block Design with 3 replications at spacing of 20 x 15cm during *kharif* 2016 and *rabi* 2016-17. All the recommended agronomic practices were followed apart from providing plant protection measures to raise a healthy crop. Five plants were randomly selected and observations were recorded on yield attributing and nutritional traits, except for days to 50% flowering, which was recorded on plot basis. The traits studied were: days to 50% flowering, plant height (cm), number of productive tillers per plant, panicle length (cm), number of filled grains per panicle, grain yield per plant (g) and 1000-grain weight (g). Grain iron and zinc concentration were determined by X-Ray fluorescence Spectrometry (XRF) (EDXRF, model-X-supreme 8000) (Paltridge et al. 2012).

The mean data was subjected to statistical analysis. INDOSTAT software was used for analysis of variance (ANOVA) (Fishar 1954) and for the estimation of genotypic variance (s2g), phenotypic variance (s2g), phenotypic and genotypic coefficients of variation (PCV% and GCV%, respectively). The heritability was estimated according to the method of Falconer (1981) and the genetic advance was computed following the formula suggested by Johnson et al. (1955).

The analysis of variance (ANOVA) revealed mean sum of square due to genotypes were significant for all the traits studied *viz*., days to 50% flowering, plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle, 1000-grain weight, grain yield per plant, grain zinc concentration and grain iron concentration during *kharif* 2016 and *rabi* 2016-17 indicating the presence of considerable genetic variability. In this study, the relative values obtained for the genotypic and the phenotypic coefficient of variation indicate the magnitude of the variation present. Both the heritability and genetic advance as percent mean were estimated to obtain the knowledge about gene action for improvement of these traits (Figs. 1 and 2).

The GCV and PCV were low in both seasons indicating that less variability exist among RILs for days to 50% flowering. The observed heritability estimates were high coupled with low genetic advance during *kharif* 2016 while in *rabi*, the control of high heritability coupled with moderate genetic advance were noticed (Table 1), suggesting that trait is under non additive gene action, high heritability is being exhibited due to favorable influence of environment rather than genotype. Selection for this trait may not be rewarding as this was also pointed out by Singh et al. (2014).

Plant height is an important trait that affects grain yield (Piao et al. 2014). Most of the short stature rice varieties are high yielding, lodging resistant and have the *sd*-1 semi dwarfing gene from Dee-geo-woo-gen (Poehlman and John 1987). During *kharif* 2016 the estimates of GCV and PCV were high indicating the presence of wider range of variability for this character. Whereas moderate estimates of GCV and PCV were recorded during *rabi* 2016-17 indicating the environmental effect. High heritability coupled high genetic advance were noticed during both seasons indicating preponderance of additive gene action (Mamata et al. 2018) in governing the trait, suggesting selection for this trait would be effective in later generation.

Tillering in rice is a crucial trait for yield formation (Eixarch et al. 2015). The number of productive tillers per plant is closely associated with biomass production and grain yield in rice (Tanaka et al. 1966). Moderate to high per cent of variation (GCV and PCV) were noticed for tiller number during the seasons. High heritability with high genetic advance was also recorded during both the seasons, suggesting improvement through direct selection would be rewarding which is in accordance with earlier findings (Abebe et al. 2017; Mamata et al*.* 2018). However, in a recent study the PCV for grain nutritional traits ranged from 15.19 to 88.02% while GCV ranged from 15.16 to 71.57% in a large sample of brown rice germplasm (Bollinedi et al. 2020).

Panicle length is an important trait for improving panicle architecture and a key indicator for grain yield in rice (Liu and Hong 2016). During both the seasons the estimates of GCV and PCV for this trait were low indicating the presence of narrow range of genetic variability. Heritability was high while the genetic advance observed was moderate which limits the further improvement through direct selection which is in accordance with earlier findings (Abebe et al*.* 2017; Sameera et al*.* 2015).

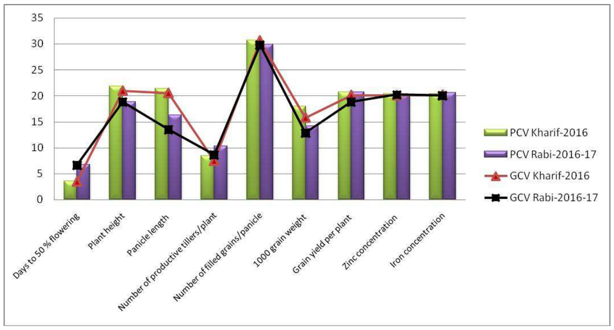

Fig. 1. **Graphical representation of PCV & GCV for yield, yield attributing and nutritional traits in RIL Population of MTU1010 X BR2655 for *kharif* 2016 and *rabi* 2016-17**

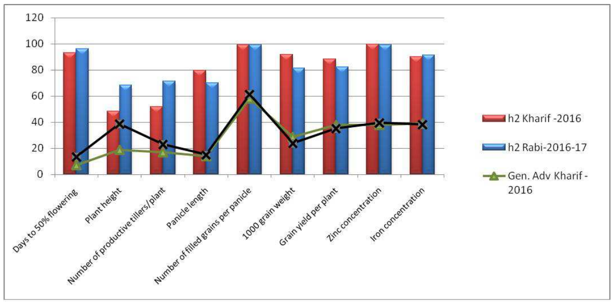

Fig. 2. **Graphical representation of Heritability & Genetic Advance for yield, yield attributing and nutritional traits in RIL Population of MTU1010 x BR2655 for *kharif* 2016 and *rabi* 2016-17**

Number of filled grains per panicle is one of the most important yield components used to estimate rice yields. Higher the spikelet number, higher is the yield (Zhao and Gu 2015). High GCV and PCV were observed for this trait in both seasons indicating the existence of wider genetic variability. High heritability coupled with high genetic advance was also recorded over the seasons. Sameera et al. (2015) and Lakshmi et al. (2017) had also recorded the similar results. Hence, directional selection could be effective for desired genetic improvement for this trait for high GCV and PCV, whereas Dhurai et al. (2014) reported high

Table 1. Range, variability, heritability, genetic advance for yield attributing and nutritional traits

S.No.	Characters	Seasons	Mean	Range		Coefficient of variation (%)		Heritability $(h_2)_{bs}$%	Gen. adv as per cent of mean (at 5%)
				Min	Max	Phenotypic	Genotypic		
1	Days to 50% flowering	*Kharif* 2016	99.00	80.00	106.00	3.59	3.46	93.00	6.87
		Rabi 2016-17	93.00	70.00	101.00	6.73	6.60	96.20	13.34
2	Plant height (cm)	*Kharif* 2016	104.47	63.00	154.46	21.81	20.96	78.58	45.64
		Rabi 2016-17	101.91	61.30	145.46	18.80	18.77	68.30	38.60
3	No. of productive tillers/ plant	*Kharif* 2016	12.00	8.00	16.00	21.34	20.52	71.63	26.76
		Rabi 2016-17	11.00	7.00	19.00	16.34	13.51	71.30	23.00
4	Panicle length (cm)	*Kharif* 2016	25.34	16.49	31.38	8.39	7.48	79.60	13.76
		Rabi 2016-17	23.91	16.00	30.00	10.30	8.63	70.10	14.88
5	Number. of filled grains/ panicle	*Kharif* 2016	207.00	75.00	371.00	30.73	30.62	99.20	58.24
		Rabi 2016-17	205.00	75.00	365.00	29.87	29.77	99.30	61.12
6	1000 grain weight (g)	*Kharif* 2016	24.00	14.30	32.38	17.96	15.79	91.84	28.61
		Rabi 2016-17	23.89	13.70	32.70	14.19	12.79	81.20	23.75
7	Grain yield/ plant (g)	*Kharif* 2016	25.08	13.50	38.10	20.76	20.13	88.47	37.69
		Rabi 2016-17	25.11	13.56	36.63	20.72	19.80	82.30	35.14
8	Grain zinc concentration (ppm)	*Kharif* 2016	26.35	12.30	38.00	20.43	20.10	99.80	37.90
		Rabi 2016-17	23.77	13.06	37.13	20.26	20.19	99.30	39.39
9	Grain iron concentration (ppm)	*Kharif* 2016	8.63	5.30	18.13	20.40	20.18	90.10	38.90
		Rabi 2016-17	11.03	5.30	19.26	20.64	20.04	91.20	38.06

Table 2. List of RILs with high grain yield, grain iron and zinc cncentration

S.No.	Genotype	Grain yield per plant (g) *kharif* 2016	Grain yield per plant (g) *rabi* 2016-17	Zinc concentration (ppm) *kharif* 2016	Zinc concentration *krabi* 2016-17	Iron concentration *kharif* 2016	Iron concentration *rabi* 2016-17
1	J16	34.87	33.27	30.84	30.00	11.30	12.00
2	J17	30.57	30.51	31.85	32.20	9.50	10.90
3	J80	31.33	31.10	30.08	31.13	9.20	10.40
4	J128	30.83	33.37	33.57	33.13	13.10	12.30
5	J144	32.17	32.62	37.23	37.43	13.50	14.80
6	J146	33.87	32.86	38.00	37.10	12.70	14.00
7	J151	30.18	30.02	35.00	34.67	10.50	10.30
8	J174	31.63	32.50	30.00	30.04	11.40	12.90

heritability coupled with high genetic advance.

Thousand grain weight has shown a very wide distinctness among the RILs during both the seasons (Table 2). The wider distinctness indicates a good amount of genetic variability existed for this trait. In both seasons moderate GCV and PCV were recorded with high heritability estimate coupled with high genetic advance showing the presence of additive gene action governing the trait, suggesting simple selection will improve the trait.

Since grain yield in rice is a complex trait, the breeding of high-yielding rice varieties is crucial for meeting the food demand of the increasing world population. During both the seasons high GCV and PCV were noticed for this trait suggesting high range of genetic variability present among RILs. High heritability coupled with high genetic advance was recorded in both the seasons indicating that selection would be very effective through direct selection for this trait. Abebe et al. (2017) and Mamata et al. (2018) reported high GCV and PCV whereas, Khatun et al. (2015) observed high heritability and genetic advance.

A wide range for the mean grain zinc concentration was recorded over the season. High GCV and PCV were also observed suggesting high range of genetic variability. The heritability estimate for this trait was very high with high genetic advance in both the seasons indicating that this trait is controlled largely by additive type of gene action. Therefore, response to selection would be quite possible as reported by Ashok et al. (2016), as heritability and genetic advance were also high.

The mean grain iron concentration varied from one season to another. The mean Fe concentration was moderate (Table 1). Heritability estimate was very high with high genetic advance, indicating that this trait is controlled largely by additive type of gene action during both seasons. Therefore, response to selection would be positive. Bonninedi et al. (2020) reported a wide range of Zn and Fe contents in a large sample of germplasm. Eight RILs *viz*., J16, J17, J80, J128, J144, J146, J151 and J174 have shown higher grain yield per plant with high iron and zinc concentration presented in the Table 2. These RILs need to be evaluated in multilocation to access further of their yield and nutritional value in different environments. Stable high yielding in combination with high Zn and Fe lines can be a good source of useful genetic variability for the improvement of rice. These lines also serve as potenttial donor in further rice biofortification programme especially for enhanced grain zinc and grain iron content.

Authors' contribution

Conceptualization of research (RR, NCN, SLV, SK, MB); Designing of the experiments (RR, NCN, SK, MB, EKB); Contribution of experimental material (NCN, SLV); Execution of field experiments and data collection (RR, SK, MB, NCN); Analysis of data and interpretation (RR, SCD, EKB, SLV, SK); Preparation of the manuscript (RR, NCN, SLV, EKB).

Declaration

The authors declare no conflict of interest.

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