Available online at www.ijpab.com

DOI: http://dx.doi.org/10.18782/2320-7051.6350

ISSN: 2320 – 7051

Int. J. Pure App. Biosci. **6 (2):** 384-392 (2018)

Research Article

International Journal of Pure & Applied Bioscience

OPEN ACCESS

Genetic Variability Studies in Swarna X Type 3 Ril Population of Rice (*Oryza sativa* L.)

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Received: 19.03.2018 | Revised: 15.04.2018 | Accepted: 20.04.2018

ABSTRACT

The present investigation is carried out to study the genetic parameters for yield, yield attributing and nutritional characters in Swarna x Type 3 RIL population of rice. Analysis of variance revealed significant differences among all the treatments under study. The characters viz., number of filled grains per panicle, panicle weight, grain yield per plant exhibited high Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV). Small differences between GCV and PCV were recorded for all the characters studied which indicated less influence of environment on these characters. The characters viz., plant height, number of filled grains per panicle, panicle weight, 1000-seed weight, grain yield per plant, grain iron and zinc concentration exhibited high heritability coupled with high genetic advance indicating the influence of additive gene action and simple selection could be effective for improving these characters.

Key words: *Micronutrient, Mineral, Phenotypic Coefficient, Yield*

INTRODUCTION

Rice is a major staple food for the world's population and also a model crop for a major group of flowering plants. Asia is the leader in rice production accounting for about 90% of the world's production. Micronutrient malnutrition has been designed as the most serious challenge to humanity as two-third of the world's population is at risk of deficiency in one or more essential mineral elements[6,51]. The mineral elements most commonly lacking in the human diets are Iron and Zinc[51].which ranked fifth and sixth, respectively, among the top ten risk factors contributing to burden disease.

Malnutrition is the most common cause of Zinc deficiency[33]. About 25% of the world's population is at risk of zinc deficiency[24]. In Asia and Africa, it is estimated that 500-600 million people are at risk for low Zinc intake.

Cite this article: Shivani, D., Cheralu, C., Neeraja, C.N. and Gouri Shankar, V., Genetic Variability Studies in Swarna X Type 3 Ril Population of Rice (*Oryza sativa* L.), *Int. J. Pure App. Biosci.* **6(2):** 384-392 (2018). doi: http://dx.doi.org/10.18782/2320-7051.6350

The reliance on cereal based diets may induce Zinc deficiency related health problems in humans, such as impairments in physical development, immune system, brain function, pneumonia, weight loss, growth retardation and delayed puberty in adolescents, poor appetite, delayed wound healing[52].

Iron is an important component in human diet because it regulates enzyme activity and plays an important role in the immune system[23]. It is also an important component of human blood because it is the central atom of hemoglobin[49].

Producing nutritious and safe foods sufficiently and sustainably is the present ultimate goal of modern agriculture. Past efforts were focussed only on increasing crop yields, but at present enhancing the concentrations of mineral micronutrients has become an urgent task. Once rice is biofortified with vital nutrients, the farmer can grow the variety indefinitely without any additional input to produce nutrient packed rice grains in a sustainable way. This is the only feasible way of reaching the malnourished population in India.

Hence the present investigation was taken up to study the genetic variability for yield, yield component traits and nutritional traits in RIL population of rice.

MATERIAL AND METHODS

The experiment was conducted at Indian Institute of Rice Research Farm, Ramachandrapuram, Hyderabad, India, during *kharif*, 2017. The experimental material comprised of 100 RILs of F7 population derived from Swarna and Type 3 along with four checks (Swarna, Type 3, BPT 5204, Chittimutyalu) laid out in Augmented Block Design. All the recommended package of practices was followed along with necessary prophylactic plant protection measures to raise a good crop. Five representative plants for each population were randomly selected to record observations on the quantitative characters under study. Data on days to 50% flowering (DFF) recorded at flowering stage while, plant height (PH), panicle length (PL), number of productive tillers per plant (NPT) were recorded at harvest and panicle weight, number of filled grains per panicle (FGP), test-weight (TW), grain iron content (Fe), grain zinc content (Zn) and grain yield per plant (GY) were recorded after harvest. Grain Iron and Zinc content were estimated by following recommended standard procedure i.e., X – Ray fluorescence Spectrometry (XRF) (EDXRF, model- X-supreme 8000).

Variance

The genotypic and phenotypic variance was calculated as per the formulae[5].

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{(Mean sum of squares due to treatments – Mean sum of squares due to error)}}{\text{Number of replications}}$$

$$\text{Phenotypic variance } (\sigma^2_p) = (\sigma^2_g) + (\sigma^2_e)$$

$$(\sigma^2_e) = \text{Error variance}$$

Genotypic and phenotypic coefficients of variance

The genotypic and phenotypic coefficients of variation were calculated according to the formula given by falconer[11].

$$\text{Genotypic coefficient of variation} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Phenotypic coefficient of variation} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

Categorization of the range of variation was effected as proposed by Sivasubramanian and Madhavamenon[43].

<10%	:	low
10-20%	:	moderate
>20%	:	high

Heritability and genetic advance

Heritability

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population. Heritability (h²) in the broad sense was calculated according to the formula given by Allard[1].

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p}$$

Where

h^2 = heritability in broad sense

σ^2_g = genotypic variance

σ^2_p = phenotypic variance $(\sigma^2_g) + (\sigma^2_e)$

σ^2_e = environmental variance

As suggested by Johnson *et al.*[17],(h^2) estimates were categorized as:

Low : 0-30%

Medium : 30-60%

High : above 60%

Genetic advance

Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton[4].

$$GA = K.\ h^2\ (b).\ \sigma_p$$

Where

GA = expected genetic advance

K = Selection differential, the value of which is 2.06 at 5% selection intensity

σ_p = phenotypic standard deviation

h^2 (b) = heritability in broad sense

In order to visualize the relative utility of genetic advance among the characters, genetic advance as percent for mean was computed.

$$\text{Genetic advance as percent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

The range of genetic advance as percent of mean was classified as suggested by Johnson *et al*[17].

Low : less than 10 %

Moderate : 10-20 %

High : more than 20 %

RESULTS AND DISCUSSION

The results obtained from the present experimental study on evaluation of 100 RIL population of riceare furnished under theGenetic variability, Heritability and genetic advance.

Genetic Variability, Heritability and Genetic Advance

The genotypic and phenotypic coefficients of variation, heritability and genetic advance as per cent of mean were estimated for 100 RIL population. Results are furnished in Table 1 for GCV, PCV, heritability and genetic advance as per cent of mean respectively.

Days to 50 per cent flowering

The genotypic and phenotypic coefficients of variation were low i.e., 2.93 and 3.36, respectively. The results were in conformity with Singh *et al.*[42], Rahman *et al*.[32], Sravan *et al*.[45], Gangashetty *et al*.[13], Singh *et al*.[40], Vanisree *et al*.[50], Dhurai*et al*.[10], Rahman *et al*.[31], Suresh *et al.*[47], Mohan *et al*.[26], Sameera *et al*.[35], Shekawat *et al*.[38], Devi *et al*.[8], Lakshmi *et al*.[20], for low GCV and PCV.

The heritability observed for this trait was high (76.03%) with low genetic advance as per cent of mean (5.26%). Yadav *et al.*[53], Dhanwani *et al.*[9], Karande *et al.*[19], Shekawat *et al*[38]. Mohan *et al.*[25] and Lakshmi *et al.*[20], reported similar results for high heritability coupled with low genetic advance as percent of mean.

Plant height(cm)

The genotypic and phenotypic coefficients of variation estimates observed for this trait were moderate i.e., 12.566 and 12.645, respectively. The results were in conformity with Selvaraj *et al.*[37], Sravan *et al*.[45], Vanisree *et al*.[50], Dhurai *et al.*[10], Sravan *et al.*[44], Shrivastava *et al.* [39], Devi *et al*.[8], Lakshmi *et al.* [20], for moderate GCV and PCV.

The observed heritability estimates for this character was high (98.74%) with high genetic advance as per cent of mean (25.72%).Chandra *et al.*, Mohanty *et al.*[27], Singh *et al.*[41], Sravan *et al*.[45], Gangashetty *et al*.[13], Chakraborty and Chaturvedi[7], Dhurai*et al.*[10], Lingaiah *et al.*[22], Rahman *et al*.[31], Sravan *et al.*[44], Bhati *et al*.[2], Sameera *et al*.[35], Devi *et al*.[8], Lakshmi *et al.* [20],for high heritability coupled with high genetic advance as per cent of mean.

Panicle length (cm)

The genotypic and phenotypic coefficients of variation for this trait were low i.e., 7.10 and 7.66 respectively. Padmaja *et al*.[28], Singh *et al.*[42], Mohanty *et al.*[27], Pandey *et al.*[29], Sravan *et al.*[45], Vanisree *et al.*[50], Sravan *et al.*[44], Suresh *et al.*[47], Mohan *et al.*[26], Sameera *et al.*[35], Devi *et al.*[8], reported low GCV and PCV.

The heritability observed for this trait was high (85.84%) with moderate genetic advance as per cent of mean (13.56%). Yadav *et al*.[53], Parikh *et al*., Singh *et al.*[42], Biswash *et al.*[3], Shekawat *et al*.[38], and Mohan *et al.*[25], observed high heritability and moderate genetic advance as percent of mean.

Number of productive tillers per plant

The genotypic and phenotypic coefficients of variation for number of productive tillers per plant were low and moderate i.e., 9.168 and 10.385, respectively. The similar findings were reported by Garg *et al*.[14], Yadav *et al*.[53], Mohan *et al.*[26], for low GCV, Mohanty *et al*.[27], Sravan *et al*.[45], Dhanwani *et al.* [9], and Devi *et al*.[8], for moderate PCV.

The observed heritability estimate was high (77.93%) with moderate genetic advance as per cent of mean (16.67%). Jaiswal *et al.*[16], Selvaraj *et al.*[37], Singh *et al.*[42], Gangashetty *et al.*[13], Chakraborty and Chaturvedi[7], Dhurai *et al.*[10], Rahman *et al.*[31], Karande *et al.*[19],and Lakshmi *et al.*[20],observed high heritability coupled with moderate genetic advance as per cent of mean.

Number of filled grains per panicle

The genotypic and phenotypic coefficients of variation for this trait were high i.e., 33.21 and 33.58, respectively. The results were in conformity with Padmaja *et al*.[28], Chandra *et al*., Yadav *et al*., Singh *et al*.[41], Basavaraja *et al*., Singh *et al*.[40], Dhurai *et al.*[10], Lingaiah *et al.*[22], Patel *et al* .[30], Suresh *et al*.[47], Mohan *et al.*[26], Sameera *et al*.[35], Shekawat *et al*.[38], Devi *et al*.[8], Thippeswamy *et al*.[48] and Lakshmi *et al*.[20] for high GCV and PCV.

The heritability estimate for number of filled grains per panicle was high (97.79%) with high genetic advance as per cent of mean (67.65%). Padmaja *et al*.[28], Chandra *et al.*, Yadav *et al*.[53], Pandey *et al.*[29], Singh *et al.*[41], Sravan *et al*.[45], Kumar *et al*., Singh *et al*.[40], Chakraborty and Chaturvedi[7], Lingaiah *et al.*[22], Patel *et al*.[30], Rahman *et al*. [31], Devi *et al*.[8], Mohan *et al.*[25], Thippeswamy *et al*.[48], and Lakshmi *et al.*[20],for high heritability and genetic advance as per cent of mean.

Panicle weight

The genotypic and phenotypic coefficients of variation for this trait were high i.e., 22.10 and 22.18, respectively. The results were in conformity with Subudhi *et al*.[46], Satish Vangaru *et al.*[36], for high GCV and PCV.

The observed heritability estimate was high (99.23%) with high genetic advance as percent of mean (45.35%). Lestari *et al.*[21], Satish Vangaru *et al*.[36], reported high heritability and genetic advance as per cent of mean

1000-grain weight (g)

The genotypic and phenotypic coefficients of variation for this trait were moderate i.e., 14.29 and 15.05, respectively. The results were in conformity with Dhurai *et al.*[10], Patel *et al*.[30], Suresh *et al*.[47], Shekawat *et al.*[38], Devi *et al*.[8], for moderate GCV and PCV.

The observed heritability estimate was high (90.14%) with high genetic advance as per cent of mean (27.95). Chakraborty and Chaturvedi[7], Dhurai *et al.*[10], Lingaiah *et al.*[22], Patel *et al*.[30], Rahman *et al*.[31], Suresh *et al*.[47], Gampala *et al.*[12], Islam *et al.*[15], Sameera *et al*.[35], Devi *et al*.[8], Mohan *et al.*[25], Thippeswamy *et al*.[48], and Lakshmi *et al.*[20], reported for high heritability coupled with high genetic advance per cent of mean.

Grain yield per plant (g)

The complex character grain yield showed high GCV (20.22) and PCV (20.53) respectively. The results are in conformity with Padmaja *et al.*[28], Chandra *et al.* Yadav *et* *al*.[53], Singh *et al*.[42], Mohanty *et al*.[27], Singh *et al*.[41], Sravan *et al*.[45], Dhanwani *et al*.[9], Gangashetty *et al*.[13], Singh *et al*.[40], Vanisree *et al*.[50], Dhurai *et al.*[10], Patel *et al*.[30], Rahman *et al* .[31], Sravan *et al.*[44], Suresh *et al*. [47], Bhati *et al*.[2], Gampala *et al*.[12], Islam *et al.*[15], Karande *et al.*[19], Devi *et al*.[8], Thippeswamy *et al*. [48],and Lakshmi *et al.*[20], for high GCV and PCV.

High heritability estimate (96.98%) coupled with high genetic advance as per cent of mean (41.03). Chakraborty and Chaturvedi[7], Dhurai *et al.*[10], Lingaiah *et al.*[22], Patel *et al*.[30], Choudary *et al.*, Devi *et al*.[8], Suresh *et al*. [47], Biswash *et al*.[3], Karande *et al*. [19], and Lakshmi *et al.*[20], reported for high heritability coupled with high genetic advance per cent of mean.

Grain iron concentration (mg/kg)

The genotypic and phenotypic coefficients of variation for grain iron concentration were moderate i.e., 14.00 and 16.43, respectively. The result is conformity with Kalaimaghal *et al*.[18], and Sala *et al*.[34], for medium GCV and PCV.

The observed heritability estimate was high (72.56%) with high genetic advance as per cent of mean (24.57). Gangashetty *et al.*[13], also reported high heritability coupled with genetic advance as per cent of mean.

Grain Zinc concentration (mg/kg)

The genotypic and phenotypic coefficients of variation for grain zinc concentration were moderate i.e., 12.44 and 13.56, respectively. The result is conformity with Kalaimaghal *et al.*[18], and Sala *et al*.[34], for medium GCV and PCV.

The observed heritability estimate was high (84.18%) with high genetic advance as per cent of mean (23.515). The results are in conformity with Gangashetty *et al*.[13] for high heritability coupled with genetic advance as per cent of mean.

The knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding programme. Information on coefficient of variation is useful in measuring the range of variability present in the characters. Heritability and genetic advance are important selection parameters. Genotypic coefficient of variation (GCV) along with heritable estimates would provide a better picture of the amount of genetic advance to be expected by phenotypic selection[4]. It is suggested that genetic gain should be considered in conjunction with heritability estimates[17]. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone.

Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for days to 50% flowering, plant height, panicle length, number of productive tillers per plant, number of filled grains per panicle, panicle weight, 1000 grain weight, grain yield per plant, grain iron concentration and grain zinc concentration indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits.

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character.

High heritability for quantitative characters indicates the scope of genetic improvement of these characters through selection, which revealed that these characters are less influenced by environment and there could be greater correspondence between phenotypic and breeding values.

The genetic advance as percent of mean is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of selection value. It indicates the control of additive gene and selection may be effective for these characters.

Table 1: Estimates of variability, heritability and genetic advance in rice genotypes

Characters	PCV (%)	GCV (%)	Heritability in broad sense (h^2) %)	Gen. Adv as per cent of Mean (at 5%)
Days to 50% Flowering	3.36	2.93	76.03	5.26
Plant height (cm)	12.64	12.57	98.74	25.72
Panicle length (cm)	7.67	7.11	85.84	13.56
No. of Productive tillers per plant	10.39	9.17	77.93	16.67
Panicle weight (g)	22.19	22.10	99.23	45.35
No. of filled grains per panicle	33.58	33.21	97.79	67.65
1000 grain weight (g)	15.51	14.30	90.14	27.95
Grain Iron content (ppm)	16.44	14.00	72.56	24.57
Grain Zinc content (ppm)	13.47	13.02	93.47	25.93
Grain yield per plant (g)	20.54	20.226	96.98	41.03

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