An assessment of early generation genetic variability and correlation for yield and quality traits in rice (*Oryza sativa* L.)

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ABSTRACT

The second filial generation of cross WGL 14 X CO47 was evaluated for its genetic potential of segregation during kharif 2018. The data were recorded on seven biometrical traits viz., days to flowering, plant height, panicle length, number of tillers/plant, number of productive tillers/plant, duration and single plant yield and three grain quality traits viz., grain length, grain breadth and length- breadth ratio.Wide range of variability was observed in number of tillers/plant, number of productive tillers/plant and single plant yield. The range for the characters days to 50 % flowering, number of productive tillers per plant, panicle length, single plant yield and duration expressed higher variations and offered scope for selection.The phenotypic variability is high in the population studied in comparison with genotypic variability conferring that environmental influence is present for the expression of traits. These characters have also manifested high heritability estimates with low or medium genetic advance as percent of mean. Correlation studies revealed that single plant yield exhibited a positive association with the number of productive tillers/plant, plant height and panicle length. The traits viz., days to 50 % flowering, grain length, grain breadth and grain length breadth ratio recorded negative association with single plant yield.Selection of entries based on number of productive tillers on positive side can improve single plant yield in this population.

Key words: Rice, transgressive segregation, second filial generation, variability, correlation

Rice is the staple food for the world population. More than half of the world population depends on rice for their calorie requirements. It contributes a greater amount of energy in the food basket. Nearly 100 countries are cultivating rice.India occupies the first position in rice area and the second position in production which almost tripled its production during the second half of the last century. However, rice production is threatened by increasing urbanization, biofuel policies and issues of climate change. All of these factors, directly or indirectly, influence both the quantity and the quality of rice that is available for consumption. In India, rice is being grown in 44.10 Mha area with the production of 106.5 million tonnes and productivity of 3.52 t/ha (USDA, 2016). In Tamil Nadu, the area, production, and productivity of rice was 17.9 lakh hectares, 55.4 lakh tonnes and 3100 kg per hectare respectively during 2013-14 (Directorate of Economics and Statistics, 2015).

In recent years, we are almost self-sufficient in production and efforts are concentrating on quality improvement. But yield and quality traits are negatively correlated and hence breeders are struggling in combining both the traits. Knowledge of genetic variability and heritability are basic requirement in crop improvement programme. Environmental effects influence the total observable variations of traits. Therefore, partitioning of overall variance due to genetic and non-genetic causes becomes necessary for an effective breeding programme. The genotypic co-efficient of variation estimates the heritable variability, whereas the phenotypic component measures the role of the environment on the genotype. High heritability indicates that it should be easy to conduct effective selection for the trait. Association studies reveal the degree and direction of the association between two or

more variables. Knowledge of the strength and type of association is an important prerequisite for the formulation of breeding procedures (Breese and Hayward, 1972). A knowledge of the association between yield and its component traits helps in improving the efficiency of selection. Early generation segregating populations are more important for improving plant types by operating further selection based improvement (Savitha and Ushakumari, 2015). The F_2 population provides wide scope for selection of genotypes since independent assortment of alleles acted on it. The traits governed by quantitative nature may express the transgressive segregants in earlier segregation generations. With this background, this experiment aims to select the superior genotypes in the F_2 population by studying the variability of yield, grain quality traits and the correlation among different biometrical traits.

The present investigation was carried out in the 'A' Block of Agricultural College and Research Institute, Madurai during kharif 2018. Warangal samba (WGL 14) IET is derivative of BPT 5204/ARC 5566// BPT3291, medium slender type of grain, straw glume, yield potential of 6.5 to 7.0 t/ha with duration of 140 days. It is moderately resistant to gall midge, Rice TungroVirus and has high head rice recovery with good cooking quality attributes. CO 47, a derivative of the cross IR 50/CO 43, is semi dwarf (80-90 cm), non-lodging and matures in 110-115 days. The average grain yield is 5.8 t/ha. It possesses medium slender translucent white rice, with acceptable cooking qualities. It is resistant to blast disease. The F_2 population of cross combination WGL 14 X CO47 was used for variability and correlation studies. Twenty-five days old seedlings were transplanted to the main field with a spacing of 20 cm between rows and 15 cm between plants. Single seedling per hill was adopted and no replicates were maintained. The recommended agronomic practices and crop protection measures were followed during the crop growth period. A total of 300 randomly selected plants in the cross combination in the F_2 generation was tagged. The following observations were recorded at appropriate growing stages of the crop *viz*., days to 50 per cent flowering (days), plant height (cm), panicle length (PL) (cm), number of tillers/plant, number of productive tillers / plant, days to maturity (days), single plant yield (SPY) (g) and quality observations *viz*., grain length (GL) (mm), grain breadth (GB) (mm) and length-breadth (GL/B) ratiowere recorded in the tagged plants.

Statistical analyses

The variability was studied for genotypic and phenotypic variance and the coefficient of variability. The genetic variance was separated from the total variance according to Fisher et al. (1932). Environment variance was estimated from non-segregating population as illustrated by (Webber and Moorthy, 1952). Phenotypic and genotypic co-efficient of variation (PCV and GCV) were estimated using the formula suggested by Burton (1952) and expressed in percentage. The estimates of PCV and GCV were categorized based on the scale given by Sivasubramanian and Madhavamenon (1973). Heritability in the broad sense (h^2) was calculated according to Lush (1940) and expressed in percentage.

Table 1. Estimation of genetic variability parameters for seven quantitative and three qualitative traits in F_2 generation of WGL14 X CO 47.

Character	Range	Mean			Number of transgres-sive segre-gants	PCV	GCV	Herita-bility (%)	GA	GA as % of Mean
		WGL 14	CO 47	F_2 Pop ulation						
DFF	75.0-91.0	96.0	78.0	80.5	28	7.3	5.1	48.3	2.1	2.5
No of tillers	4.0-23.0	15.0	12.0	12.9	33	30.3	29.8	96.7	7.8	60.3
No. of productive tillers	1.0-22.0	13.0	9.0	10.4	17	39.7	34.1	73.8	2.2	21.2
Panicle length (cm)	20.3-27.9	29.0	25.0	25.4	11	6.9	5.7	68.1	1.4	5.5
Plant height (cm)	57.0-110.0	110.0	98.0	91.5	24	12.9	8.9	48.0	2.9	3.2
Grain length (mm)	4.0-8.5	7.3	7.7	7.0	14	18.3	18.0	97.2	0.3	42.2
Grain breadth (mm)	1.5-2.6	2.5	2.3	2.0	7	12.9	7.1	30.7	0.1	46.6
Grain L/B ratio	2.4-4.0	2.9	2.7	3.5	11	12.8	12.7	97.5	0.5	15.4
Duration	100.0-125.0	136.0	110.0	109.3	24	5.3	5.0	86.7	2.6	2.4
Single plant Yield (g)	11.5-26.4	25.1	24.5	17.3	21	26.1	20.8	79.6	13.3	12.8

The range of heritability, expected genetic gain or genetic advance (GA) under selection were calculated as suggested by Johnson et al. (1955). The variance and covariance components were utilized to calculate the correlation coefficient (Webber and Moorthy, 1952).

The experimental results generated from statistical analysis of mean data of various biometrical and quality traits in the F_2 population of WGL14 X CO 47 are presented in Table 1.

The descriptive statistics viz., mean and ranges concerning all the 10 characters are given in Table 1. Days to flowering varied from 75 to 91 days with a mean value of 80.50 days.The trait plant height ranged from 57 to 110 cm with a mean value of 91.50 cm. Panicle length ranged from 20.30 to 27.90 cm with a mean value of 25.40 cm. The trait number of tillers/ plant varied from 4 to 23 tillers/ plant with a mean value of 12.90. Similarly, the number of productive tillers/plant ranged from 1 to 22 tillers/ plant with a mean value of 10.40. Days to maturity ranged from 100 days to 125 with a registered mean value of 109.30 days and single plant yield recorded a minimum of 11.50 g to a maximum of 26.10 g with the mean of 17.30 g. The grain quality traits *viz*., length of grain ranged from 4.0 to 8.5 mm with a mean value of 7.0 mm and grain breadth 1.5mm to 2.6 mm with a mean of 2.0 mm. The trait GL/B ratio is ranged from 2.3 to 4.0 with a mean of 3.5. Total of 190 transgressive segregants were observed in F_2 population. Among them, number of tillers had the highest (33) and grain breadth had the lowest (7) in frequency.

Variability in the F_2 population serves as base genetic materials for the selection process. In addition to that identification of transgressive segregants directs the breeding programmes in the right path. Knowledge of the nature and magnitude of genotypic and phenotypic variability present in any crop species play an important role in formulating a successful breeding programme (Allard, 1960). The success in a crop improvement programme depends on the ability of the breeder to define and assemble the required genetic variability and select for yield indirectly through yield associated and highly heritable characters after eliminating the environmental components of phenotypic variation (Mather, 1949). Therefore, it is necessary to have information on both PCV and GCV, to estimate

heritability, which helps the breeder to predict the expected gains through selection. Knowledge of the genetic advance that is expected by applying selection pressure to a segregating population is useful in designing effective breeding programme. Evaluation of segregating progenies helps in the estimation of various genetic and non-genetic components of variance.

The range and mean values do not reflect the total variance in the material studied. Hence, the actual variance has to be estimated for the characters to know the extent of existing variability. Genotypic variance measures the magnitude of genetic variability and phenotypic variance indicates the amount of variation which is due to phenotypic values. The absolute values of phenotypic and genotypic variance cannot be used for comparing the degree of variability in different characters because the characters differ in the unit of measurement. Hence, the co-efficient of variation (PCV and GCV) which is calculated by considering the respective means have been used for the comparisons. High values of these parameters indicate wider variability and vice versa. Accordingly, a narrow difference between the phenotypic coefficient of variation (PCV) and genotypic co-efficient of variation (GCV) implies a lesser effect of the environment on the expression of these traits. According to Johnson et al. (1955), heritability estimates along with genetic gain would be more useful than the former alone in predicting the effectiveness of selection. Therefore, it is essential to consider the predicted genetic advance along with heritability estimate as a tool in the selection programme for better efficiency.

In the present study, the phenotypic variability is high in comparison with genotypic variability conferring that environmental influence is present for the expression of traits studied except duration, L/B ratio and grain length and single plant yield in the F_2 population. This was in accordance with the findings of Balat et al. (2018). The physical traits of the grain *viz*., grain length and breadth do not show any significant variability implying that the parents involved in the F_2 population have similar grain shape. Similar findings were reported by Islam et al. (2015). This suggested the possibility of improvement of the highly variable characters created by segregation and recombination, whereas, it may not be equally effective for a character, namely grain length and breadth which exhibited a

Table 2. Estimates of correlation coefficient of grain yield with its component traits.

Traits	DFF	PH	PL	PT	GL	GB	GL/B	SPY
DFF	1.000	0.113*	-0.041	0.109*	0.009	-0.095*	0.004	-0.047*
PH		1.000	0.003	0.008	-0.029	0.017	-0.023	0.031
PL			1.000	-0.009	-0.071*	-0.091*	-0.008	0.009
PT				1.000	-0.048*	-0.043	-0.004	0.042*
GL					1.000	0.290*	0.055*	-0.221*
GB						1.000	-0.120	-0.205*
GL/B							1.000	-0.044*
SPY								1.000

*Significant at P= 0.05

DFF - Days to 50 % flowering, PH - Plant height , PL - Panicle length , PT - Productive tiller, GL - Grain length , GB - Grain breadth ,GL/B - Grain length and breadth ratio, SPY - Single plant yield.

narrow range of variability.

The traits *viz*., tillers /plant , productive tillers/plant, grain length, grain breadth and single plant yield expressed high heritability coupled with high genetic advance as percent of mean. This was in accordance with Gokulakrishnan et al. (2014).

The estimate of heritability is medium and the genetic advance as percent gain is low in the population for the trait plant height and days to fifty per cent flowering. This shows that their expression can be influenced very much by the environment. This was earlier reported by Srujana et al. (2017). Similarly, it suggested non-additive gene action for the expression of these characters High heritability values may be due to favourable influence of environment rather than genotype and as such simple selection based on these characters may not be rewarding. This was earlier reported by Srujana et al. (2017).

In general, the population studied had shown that a good amount of variability is present for the characters namely the number of tillers, productive tillers, and single plant yield enabling to exercise better selection pressure for the above-mentioned trait improvement. These characters have also manifested high heritability estimates with low or medium genetic advance as percent of mean. These characters are influenced by environmental effects and selection may not be useful in the immediate generation and may be postponed to later generations.

Correlation relationship among yield and quality traits

The results of the correlation among the biometrical and quality traits are presented in Table 2. Single plant yield exhibited a positive significant association with the number of productive tillers/plant (0.042). The traits *viz*., plant height (0.031) and panicle length (0.009) had positive association with single plant yield. Significant negative association with days to flowering (-0.047), grain length (-0.221), grain breadth (-0.205) and GL/B ratio (-0.044) were also observed. These results are in accordance with Islam et al. (2015), Allam et al. (2015) and Rawte and Saxena (2017).

This study concluded with a wide range of variability is observed in the number of tillers/plant, the number of productive tillers/plant and single plant yield. The range for the characters days to flowering, number of productive tillers per plant, panicle length, single plant yield and duration expressed higher variations and offered scope for selection. The productive tillers have a significant positive correlation with single plant yield. Selection based on the number of productive tillers on the positive side can improve single plant yield in this population.

REFERENCES

Allam CR, Jaiswal HK and Qamar A (2015). Character association and path analysis studies of yield and quality parameters in basmati rice (*Oryza sativa* L.). The Bioscan 9(4): 1733-1737

Allard RW (1960). Principles of plant breeding. John Wiley and Sons. Inc., New York

Balat JR, Patel VP, Visat ML and Bhagora RN (2018). Variability analysis in F$_2$ population of rice (*Oryza sativa* L.) for yield and related traits. Int. J. Pure App. Biosci. 6(1): 1021-1027

Breese EL and Hayward MD (1972). The genetic basis of

present breeding methods in forage crops. Euphytica 21(2): 324-336

Burton GW (1952). Quantitative inheritance in grasses. Proc. Int Grassland Congr 1: 277-283

Directorate of Economics and Statistics (2015). Department of Agriculture, New Delhi

Fisher RA, Immer FR and Tedin O (1932). The genetical interpretation of statistics of the third degree in the study of quantitative inheritance. Genetics 17: 107-124

Gokulakrishnan J, Sunil Kumar B and Prakash M (2014). Variability studies for some yield and qualitytraits in rice (*Oryza sativa*). Plant Archives 14 (1): 533-536

Islam MA, Raffi SA, Hossain MA and Hasan AK (2015). Analysis of genetic variability, heritability and genetic advance for yield and yield associated traits in some promising advanced lines of rice. Progressive Agriculture 26(1): 26-31

Johnson HW, Robinson HF and Comstock R (1955). Estimates of genetic and environmental variability in soybeans 1. Agronomy Journal 47(7): 314-318

Lush JL (1940). Intra - sire correlation and regression of offspring on dams as a method of estimating heritability of characters. Proc. Amer. Soc. Animal Production 33: 293-301

Mather K (1949). The genetical theory of continuous variation. Hereditas 35(1): 376-401

Rawte S and Saxena RR (2017). Correlation and path coefficient analysis of quality traits in selected rice (*Oryza sativa* L.) germplasm accessions. International Journal of Chemical Studies 5(5): 547-551

Savitha P and Ushakumarai R (2015). Genetic variability studies in F_2 and F_3 segregating generations for yield and its components in rice (*Oryza sativa* L.). Indian Journal of Science and Technology 8(17): 1-7

Srujana G, Suresh BG, Lavanya GR, Ram BJ and Sumanth V (2017). Studies on genetic variability, heritability and genetic advance for yield and quality components in rice (*Oryza sativa* L.). Journal of Pharmacognosy and Phytochemistry 6(4): 564-566

Sivasubramanian S and Madhava Menon P (1973). Genotypic and phenotypic variability in rice. Madras Agri. Journal 60: 1093-1096

USAD National Agricultural Statistics Service (2016). United State Government Printing Office. Washington

Webber CR and Moorthy BR (1952). Heritable and non-heritable relationship and variability of oil content and agronomic characteristics in the F_2 generation of soybean crosses. J. Agron. 44: 202-209