

Genetic Analysis and Traits Association in F₂ Intervarietal Populations in Rice Under Aerobic Condition

Farhad Kahani and Shailaja Hittalmani*

Marker Assisted Selection Laboratory, Genetics and Plant Breeding, University of Agricultural Sciences, GKVK, Bangalore 560065, India
Professor and University Head, Genetics and Plant Breeding, University of Agricultural Sciences, GKVK, Bangalore-560065, India

Abstract

Genetic variability 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 and genetic advance was computed in F₂ segregating populations of 15 crosses for 14 characters including drought and yield contributing traits under aerobic condition during dry season 2012. The estimates of phenotypic coefficients of variation (PCV) were high and moderate for days between flowering and maturity (10.71%), number of tillers plant (19.70%), number of panicles plant (21.44%), 100 grain weight (g) (27.01%), panicle exertion (14.75%), panicle length (cm) (12.90%), leaf width (cm) (20.96%), straw weight (g) (30.99%) and yield (g) (34.04%) in different crosses. High heritability coupled with high and moderate genetic advance was observed for all the plant traits observed. Correlation studies revealed that Grain yield plant⁻¹ was positively and significantly correlated with number of tillers, number of panicles, grain length and straw weight. However Grain yield plant⁻¹ was negatively significantly correlated with Days to flowering, Days to maturity, Plant Height, 100-grain weight, Grain width and Leaf width [1,2].

Keywords: Rice; Aerobic; Genetic variability; Heritability; Genetic advance

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. Except Antarctica, it is grown in all the continents, occupying 159 million hectare area and producing 683 million tones (equivalent to 456 million tons of milled rice); In Asia, more than 50% of all water used for irrigation is for rice. About 55% of the rice area is irrigated and accounts for 75% of the total rice production in the world. Being an extravagant consumer of water, rice uses around 5000 liters of fresh water to produce 1 kg of rice. The increase in depletion of fresh water resources is a major threat to the traditional way of rice cultivation. Efforts are therefore underway to develop water saving technologies such as alternate wetting and dry continuous soil saturation, irrigation at fixed soil moisture tensions varying from 0 to 40 kPa, or irrigation at an interval of 1-5 days after disappearance of standing water. To combat this problem water-saving rice production system like, aerobic rice cultivation is being popularized to obtain optimum yield with less water consumption. True aerobic rice system (ARS) is a new production system in which rice is grown under non-puddled, non-flooded, and non-saturated soil conditions. Thus in ARS, soils are kept in aerobic situation almost throughout the rice growing season. As already pointed out, ARS aims at growing rice without puddling and flooding under non-saturated soil conditions as other upland crops. The driving force behind ARS is water economy and reported a saving of 73% in land preparation and 56% during crop growth. The work on developing varieties suitable for ARS started only recently and is generally restricted to screening available varieties [3-15].

Moreover before launching any breeding programme, a breeder should have a thorough knowledge on nature and magnitude of genetic variability, heritability, genetic advance, genetic divergence and character association in a crop species. Since yield is inherited in a complex way and is influenced by the environment path coefficient

analysis will be an added advantage to the breeder in crop improvement programme. The study on above aspects is essential to identify superior genotypes. The crosses between the genotypes with maximum genetic divergence would be responsible for improvement as they are likely to yield desirable recombinants in the progeny. Keeping in view the genetic studies in aerobic rice were undertaken to estimate the genetic component of variance for yield and yield components involving aerobic cultivars and to compute the heritability, coefficients of variability and genetic advance in F₂ segregating populations of the 15 crosses for 14 characters.

Material and Methods

Crossing, development of f₁ and f₂ populations

Fifteen F₂ populations were generated using di allel mating design of rice by crossing 6parental genotypes viz., Moroberekan, Gandhasala, IR-50, IM-90, IM-114 and OYC-145. Staggered sowing of the selected parental genotypes was done to achieve synchronization in the flowering for effective crossing programme to generate F₁. The seedlings were raised during dry season 2011 following all the recommended agronomic practices. At panicle emergence and flowering stage, the florets of female parents were hand emasculated early in the morning, before 7 a.m. and later the pollen was collected from male parent and dusted on to the stigma around 11 a.m which is the ideal time for effective pollination. To avoid contaminations from

*Corresponding author: Shailaja Hittalmani, Professor and University Head, Genetics and Plant Breeding, University of Agricultural Sciences, GKVK, Bangalore 560065, India, Tel:91-8023624967, E-mail: shailajah_maslab@rediffmail.com

Received October 02, 2015; Accepted October 21, 2015; Published October 25, 2015

Citation: Kahani F, Hittalmani S (2015) Genetic Analysis and Traits Association in F₂ Intervarietal Populations in Rice Under Aerobic Condition. J Rice Res 3: 152. doi:10.4172/2375-4338.1000152

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foreign pollens, emasculated panicle were covered with butter paper packet. The seeds set on female plants were harvested, around 25-27 days after crossing event. Fifteen crosses were effected in a pair wise combination during dry season 2011, at K block, UAS, Bangalore.

Evaluation of F₂ generation population

The F₂ seeds of all the 15 crosses of rice were directly sown in the field under moisture scarce aerobic situation during dry season-2012 with single seeds per hill at spacing of 25 × 25 cm. On an average of 300 population size for each cross was maintained along with two rows parental lines. Mean values were utilized for statistical analysis and the characters observed for eliciting the information are: days to flowering, days between flowering and maturity, days to maturity, plant height (cm), number of tillers plant, number of Panicles plant⁻¹, productive tillers plant⁻¹, mother panicle weight (g), 100 grain weight (g), panicle length (cm), panicle exertion (± cm), leaf length (cm), leaf width (cm), grain length (mm), grain breadth (mm), straw weight (g) and grain yield plant-1 (g).

Statistical analysis

The observations recorded in respect of all the above quantitative traits were subjected to following standard statistical analysis: Descriptive statistics Sunderaraj et al. (1972), Mean, Range, Standard error, Variance, Skewness and Kurtosis. The mean values of quantitative traits were used to estimate coefficients of skewness and kurtosis using 'SPSS' software program, Genetic variability parameters, Coefficients of Variation Burton and, Phenotypic coefficient of variation (PCV), Heritability (h²)Johnson et al., (1955), Genetic advance (GA) [16-18].

$$PCV (\%) = \frac{\sigma_p^2}{\bar{X}} \times 100$$

$$h_{(bs)}^2 = \frac{\sigma_{bs}^2}{\sigma_p^2} \times 100$$

$$GA = K h^2 \sigma_p$$

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Results and Discussion

Genotypic coefficient of variation, phenotypic coefficient of variation, heritability in narrow sense, genetic advance and genetic advance as percentage of means were estimated for yield and quality in F₂ generation as presented in Table1. Expectedly phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) in all the characters studied. The difference between PCV and GCV is probably due to environmental effects. High heritability estimates for all the characters except panicle exertion and straw weight suggesting that the environmental factors did not affect greatly the phenotypic performance of these traits. Highest PCV (34.04%) and GCV (33.58%) were observed for grain yield plant⁻¹. PCV generally ranged between 2.67% for grain width to 34.04 % for grain yield plant⁻¹. Similarly, GCV ranged between 2.12% for grain width to 33.58% for grain yield plant⁻¹. A similar finding of higher PCV than GCV was also reported by [2,10,15]. Generally, heritability in broad sense estimate varied from 19.67% for panicle exertion and 99.95% for leaf width, respectively. Similarly, genetic advance was ranged between 0.16% for panicle exertion and 21.36% for plant height. A joint consideration of GCV, heritability broad sense and genetic advance revealed that 100-grain weight (27.01, 99.20 and 16.18%), leaf width (20.96, 99.95 and 11.46%) and grain yield plant⁻¹ (33.58, 96.12 and 16.04%) combined high GCV, high heritability broad sense and moderate genetic advance. Thus, high estimates of GCV and heritability could be good predictors of seed yield in rice. Hence selection based on the phenotypic performance will be reliable and effective. Furthermore, moderate to high heritability, GCV and GA% in a mean could be explained by additive gene action and their improvement could be achieved through mass selection [19-21] (Table 1).

Correlation studies revealed that Grain yield plant⁻¹ was positively significantly correlated with number of tillers, number of panicles, grain length and straw weight. These results suggest that selection to improve rice yield directed by phenotype of these traits may be effective [20]. However Grain yield plant⁻¹ was negatively significantly correlated with days to flowering, days to flowering, days to maturity, plant height, 100-grain weight, grain width and leaf width. Similar findings were also recorded by [22] for days to flowering (Table 2).

Characters	PCV	GCV	h ²	GA	GA% MEAN
DF	4.42	4.38	97.43	9.06	8.92
DFM	10.71	10.30	88.72	8.47	20.49
DM	6.17	6.11	97.69	17.78	12.48
PHT	14.49	14.33	97.45	21.36	29.22
NT	19.70	18.88	90.55	6.40	37.40
NP	21.44	20.73	93.16	6.13	41.33
100-GW	27.01	24.71	99.20	16.18	50.75
GL	15.31	11.03	72.57	0.24	19.08
GW	2.67	2.12	69.36	0.26	3.07
LW	20.96	20.96	99.95	11.46	43.16
PL	12.90	12.46	92.88	4.99	24.86
PE	14.75	16.88	19.67	0.16	5.48
SW	30.99	16.71	39.57	1.80	13.49
GYLD	34.04	33.58	96.12	16.04	68.30

Table 1: Estimates of PCV, GCV, heritability (broad sense) GA and GA%Mean in F₂ population.

Characters	DF	DFM	DM	PHT	NT	NP	100 GW	GL	GW	LW	PL	PE	SW	GYLD
DF	1													
DFM	0.17**	1												
DM	0.87**	0.63**	1											
PHT	0.21**	0.43**	0.38**	1										
NT	0.14**	-0.60**	-0.19**	-0.70**	1									
NP	-0.05	-0.67**	-0.37**	-0.72**	0.98**	1								
100 GW	0.25**	0.17**	0.28**	0.38**	-0.34**	-0.41	1							
GL	-0.14**	-0.58**	-0.40**	-0.33**	0.62**	0.66**	-0.22**	1						
GW	0.42**	0.00	0.33**	0.55**	-0.14**	-0.20	0.02	-0.07	1					
LW	-0.13**	0.45**	0.12	0.15**	-0.21**	-0.23**	0.05	-0.22**	0.22**	1				
PL	-0.21**	0.27**	-0.03	-0.11	-0.04	-0.03	0.38**	0.00	-0.16**	0.23**	1			
PE	0.28**	-0.05	0.19**	-0.05	0.07	0.02	-0.19**	0.36**	0.16**	-0.03	0.05	1		
SW	-0.50**	-0.21**	-0.50**	-0.44**	0.35**	0.41**	-0.37**	0.20**	-0.22**	0.45**	-0.11	-0.26**	1	
GYLD	-0.40**	-0.87**	-0.75**	-0.66**	0.67**	0.75**	-0.19**	0.58**	-0.22**	-0.17**	-0.02	-0.03	0.58**	1

*significant @ p=0.01, **significant @ p=0.05.

Table 2: Phenotypic correlations among traits in F₂ generations.

DF=Days to flowering	PHT=Plant Height	GW=Grain width	LW=Leaf width	SW=Straw weight
DFM=Days to flowering and maturity	NT=Number of tillers Plant ⁻¹	GL=Grain length	PL=Panicle length	GYLD=Grain yield plant ⁻¹
DM=Days to maturity	NP=Number of panicles	100-GW=hundred grain weight	PE=Panicle excretion	

Characters	DF	DFM	DM	PHT	NT	NP	100-GW	GL	GW	LW	PL	PE	SW	'r' values
DF	0.06	-0.10	-0.24	-0.03	0.04	0.01	0.04	0.01	0.02	0.01	-0.03	0.03	-0.21	-0.40**
DFM	0.01	-0.56	-0.17	-0.07	-0.18	0.15	0.03	0.02	0.01	-0.04	0.04	0.01	-0.09	-0.86**
DM	0.05	-0.35	-0.28	-0.06	-0.06	0.08	0.04	0.01	0.01	-0.01	0.01	0.02	-0.21	-0.74**
PHT	0.01	-0.24	-0.10	-0.15	-0.21	0.16	0.06	0.01	0.02	-0.01	-0.01	0.01	-0.19	-0.65**
NT	0.01	0.34	0.05	0.11	0.30	-0.22	-0.05	-0.02	-0.01	0.02	-0.01	0.01	0.15	0.67**
NP	0.01	0.38	0.10	0.11	0.29	-0.22	-0.06	-0.02	-0.01	0.02	0.01	0.01	0.17	0.75**
100-GW	0.01	-0.10	-0.08	-0.06	-0.10	0.09	0.16	0.01	0.01	0.01	0.05	-0.02	-0.16	-0.19**
GL	-0.01	0.33	0.11	0.05	0.18	-0.15	-0.03	-0.03	0.01	0.02	0.01	0.03	0.08	0.57**
GW	0.02	0.01	-0.09	-0.09	-0.04	0.04	0.01	0.01	0.04	-0.02	-0.02	0.01	-0.09	-0.19**
LW	-0.01	-0.25	-0.03	-0.02	-0.06	0.05	0.01	0.01	0.01	-0.08	0.03	0.01	0.19	-0.17**
PL	-0.01	-0.15	0.01	0.02	-0.01	0.01	0.06	0.01	-0.01	-0.02	0.13	0.01	-0.05	-0.01
PE	0.02	0.03	-0.05	0.01	0.02	0.01	-0.03	-0.01	0.01	0.01	0.01	0.09	-0.11	-0.03
SW	-0.03	0.12	0.14	0.07	0.10	-0.09	-0.06	-0.01	-0.01	-0.04	-0.01	-0.02	0.42	0.57**

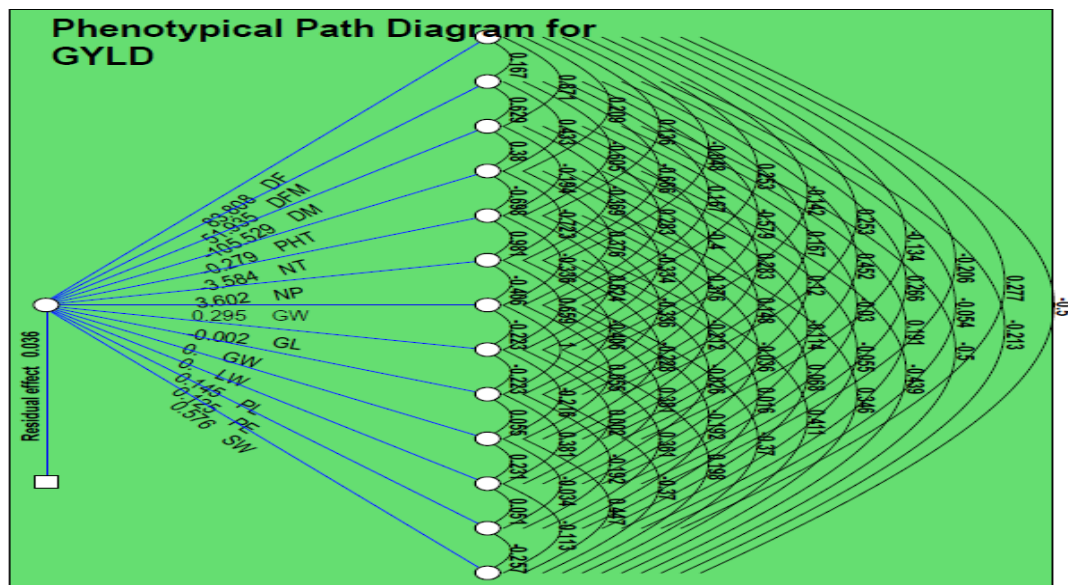
Residual Effect=0.0356.

Table 3: Genotypic direct (diagonal) and indirect effects of different quantitative traits in F₂ generation.

DF=Days to flowering	PHT=Plant Height	GW=Grain width	LW=Leaf width	SW=Straw weight
DFM=Days to flowering and maturity	NT=Number of tillers Plant ⁻¹	GL=Grain length	PL=Panicle length	GYLD=Grain yield plant ⁻¹
DM=Days to maturity	NP=Number of panicles	100-GW=hundred grain weight	PE=Panicle excretion	

The path analysis is a useful parameter to understand more clearly the association among different variables as recorded by simple correlation values. It helps to partition the overall association of particular variables with dependent variable into direct and indirect effects. While dealing with a more complex character like grain yield, it enables the breeder to specifically identify the important component trait of such a nature and differential emphasis can be laid on those characters for selection. Table 3 shows the results of the path analysis for the examined traits. Path coefficient analysis of yield and its component traits revealed that Straw weight (0.42) had the highest positive direct effect on grain yield. The Number of tillers Plant⁻¹(0.30) was the second most important character

it showed highest positive direct effect on grain yield [23] reported that indirect selection based on number of productive tillers per plant, harvest index and biomass per plant can be adopted for enhancement of grain yield as it showed positive direct effect on grain yield per plant. The number of tillers Plant⁻¹ had negative indirect effect on grain yield via number of panicles (-0.22), similar results were also reported by [24,25]. The traits that have direct affect on grain help to select them directly to enhance the yield. The lower residual effect indicated that different characters other than the characters considered in this study influence the grain yield considerably (Table 3 and Figure 1).



DF=Days to flowering	PHT=Plant Height	GW=Grain width	LW=Leaf width	SW=Straw weight
DFM=Days to flowering and maturity	NT=Number of tillers Plant ⁻¹	GL=Grain length	PL=Panicle length	
DM=Days to maturity	NP=Number of panicles	100-GW=hundred grain weight	PE=Panicle excretion	

Figure 1: Path diagram for F₂ population.

Conclusion

An overall consideration of the results revealed that grain yield plant⁻¹ could be improved through selection for traits number of tillers, number of panicles, grain length and straw weight which were positively correlated with grain yield plant⁻¹. High heritability estimates for all the characters except for panicle excretion and straw weight revealed that selection for these characters will have to be carried in advance segregating generations.

Acknowledgements

We express the opportunity to thank various funding agencies including DBT, New Delhi, NICRA, Hyderabad, India for carrying this work at University of Agricultural Sciences, GKVK, Bangalore, India.

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