

**GENE ACTION OF SOME AGRONOMIC, YIELD AND QUALITY CHARACTERS IN AROMATIC RICE (*ORYZA SATIVA* L.) VARIETIES AND THEIR F<sub>1</sub> HYBRIDS UNDER LOWLAND AND UPLAND ENVIRONMENTS**

A. D. Jarwar<sup>1</sup>, Q. D. Dela Cruz<sup>2</sup>, G. S. Junejo<sup>1</sup> and M. Jarwar<sup>3</sup>

<sup>1</sup>Agriculture Research Institute Tandojam, Pakistan

<sup>2</sup>Department of Crop Sciences, Institute of Graduate Studies,  
Central Luzon State University Nueva Ecija Philippines

<sup>3</sup>Sindh Agriculture University, Tandojam, Pakistan

**ABSTRACT**

Gene action for twenty-one F<sub>1</sub> hybrids along with their parents were evaluated in a experiment designed with randomized complete block design having three replications in two environments. Significant differences were observed among parents, hybrids and hybrids versus parents for most of the agronomic, yield and quality characters of hybrids in both environments. Genotype x environment interaction was also significant in most of the traits studied. Results based on combining ability tests showed that, gene action for yield and agronomic traits was dominant while gene action for quality traits was additive. Results reveal that specific combining ability (SCA) variances were higher than the general combining ability (GCA) variances under lowland and upland environments for all the characters studied, except number of productive tillers per plant, number of non- productive tillers per plant, length of panicle, percent filled grains per panicle and grain breadth. These data suggest that non-additive gene action is important. Estimates of GCA effects under both environments of this study revealed that lines Sugdasi, Bengalo and DR65 were the best general combiners for grain yield and tester, Pandan was the best potential source of desirable genes for yield and yield related traits. Heterosis breeding may be utilized to improve quality traits with dominant gene action.

**Keywords:** Aromatic rice, F<sub>1</sub> hybrids, gene action, quality.

**INTRODUCTION**

Major population of the world depends on the rice crop, because rice is the staple food. In Asian population, rice has special position as a source of providing over 75% and more than three billion of world population meals and represents 50 to 80 percent of their daily calorie intake (Amirjani, 2011). Present rice production

---

Corresponding author: [adjarwar@yahoo.com](mailto:adjarwar@yahoo.com)

will not meet future demand. Production technology from the Green Revolution has been exhibiting diminishing returns; the 1990s saw a marked decline in yield and growth rate. Since 2000, annual withdrawals from rice stocks have been necessary to bridge the gap between rice production and demand (Khush, 2005). It is an estimate that the world population will increase upto 7.21 billion in 2015 and 8.27 billion in 2030, which requires the increase in rice demand from 680 million tons in 2015 to 771 million tons in 2030 (Badawi, 2004).

The challenge of overcoming the shortage of food in the world will require a coordinated effort. In future research on rice crop must be based on the development of high-yielding and early-maturing varieties in order to ensure the conservation and efficient use of natural resources (Swain, 2005). The "Basmati Rice", a specialty rice all over the world is the continuous selection by man for the diverse in quality with high aroma, (Singh *et al.*, 2000).

Ramalingam *et al.* (1993) carried out a study on combining ability in rice using line x tester analysis for yield and yield attributes. They observed a preponderance of non-additive gene action over additive gene action for all the traits, except for 1000 grain weight.

Bobby and Nadrajan (1993) conducted a study to deduce the nature of gene action in genetic analysis of yield components in rice involving CMS lines. They found that SCA variance was higher than GCA variance for all the characters studied. Genetic variation is due to the genotypic differences among individuals within a population and is the main concern of plant breeding. Genetic variability for important agronomic traits is mainly due to the additive genetic variance. The non-additive variance is generally smaller in magnitude than the additive component (Singh, 2000).

Akram *et al.* (2007) studied nature of gene action and inheritance of traits related to seedling vigor and grain yield in F<sub>1</sub> generation of a seven parent diallel cross. Genetic component analysis revealed that rate of germination index and seedling shoot length were influenced by both additive and non-additive gene action, however, the additive component was found to be more pronounced in the inheritance of these two traits. Wr-Vr graphic analysis indicated that rate of germination index was under the control of complete dominance gene effects. Over dominance appeared to be more important for seedling root length, seedling dry weight and 100 seed weight, while partial dominance was found controlling seedling shoot length, number of tillers per plant, panicle length and grain yield per plant.

Sharat *et al.* (2006) conducted experiment to obtain information on gene action and reported that gene action is involved in expressing the different characters in basmati rice. The GCA variance is primarily due to function of the additive genetic variance and represents a fixable portion of genetic variation. If epistasis is present, GCA also includes additive × additive type of non-allelic interaction (Singh and Kumar, 2004).

Saleem *et al.* (2010) reported that panicle length was an important part of genetic variation for plant height, tillers per plant, secondary branches per panicle, grains per panicle, 1000-grain weight and yield per plant, except primary branches per panicle and panicle length.

This study was aimed to estimate the gene action and aids in selecting the desirable parents and crosses to develop the Basmati varieties of indica rice.

## **MATERIALS AND METHODS**

The experiment was conducted at the research area of the Research office, Central Luzon State University, Science city of Munoz, Nueva Ecija, Philippines. Hybridization carried out to produce F<sub>1</sub> hybrids from April, 2010 to October 2010. Evaluation of genotypes was conducted during the dry season, December 2010 to July 2011. Ten selected genotypes out of which seven were used as lines and three as testers while one was kept as check. Line (males) Local Roosi-2, Sugdasi, Mehak, JJ77, Rataria, DR65, and Bengalo were originated from Pakistan through selection. Whereas Testers (Females) Pandan and Vertin were originated from Philippines and Basmati 370 from India through selection, and the check variety Basmati 370 originated from Philippines.

The materials were grown in plastic pails for the production of crosses in the dry/summer season-2010. Staggered planting was done to synchronize flowering, to obtain the planned crosses. Hybridization was done as soon as the flowering appeared from the parental material. The F<sub>1</sub> cross combinations were made to produce hybrid seed, comprises, 1. LR2 x Pandan, 2. LR2 x Basmati 370, 3. LR2 x Vertin 4. Sugdasi x Pandan, 5. Sugdasi x Basmati 370, 6. Sugdasi x Vertin, 7. Mehak x Pandan, 8. Mehak x Basmati 370, 9. Mehak x Vertin, 10. J J 77 x Pandan, 11. J J 77 x Basmati 370, 12. J J 77 x Vertin, 13. Rataria x Pandan, 14. Rataria x Basmati 370, 15. Rataria x Vertin, 16. Bengalo x Pandan, 17. Bengalo x Basmati 370 18. Bengalo x Vertin, 19. DR 65 x Pandan, 20. DR 65 x Basmati 370, 21. DR 65 x Vertin.

Fertilizers were applied following the recommended rate into two splits at seedling and at panicle initiation stages. Flowers of female parents were emasculated. Emasculation was done in the afternoon between 4-6 p.m, one day before the anther is expected to dehisce or mature and the stigma is likely to become fully receptive. The emasculated flowers were then covered with butter paper bags to avoid natural cross pollination.

Pollination of emasculated flowers of each floret was done in the morning between 10 and 11 a.m. when the anthers were fully matured and ready to dehisce. Ripe anthers collected from the male parents were used to shed over the female parents (emasculated panicle). After pollination, the panicles were properly covered, again to protect from foreign pollen and were tagged just after bagging. The tags were marked with the date of emasculation, date of pollination, and the names of male and female parents. Seeds of the crossed material were harvested after 21-25 days of pollination. Evaluation of crosses along with their

parents and a check variety was done in two environments i.e. lowland and upland conditions with three replications, during the dry season in December 2010.

In both environments, each genotype was planted in a row plot of 1 meter length per row with a distance of 30 cm between rows and 20 cm between plants. The experimental plots in both the environments were fertilized at the rate of 132-42-42 NPK kg/ha, at 7 DAT while the remaining rate was applied into two splits at 30 and 45 days after transplanting. During transplanting, water level was maintained at 2-3 cm depth until 25-30 DAT, in the lowland condition. Under upland condition, irrigation was applied as alternate dry and wet. Aside from irrigation, weeding and appearance of insect pests and diseases were monitored regularly; no more infestation was observed in the experiments. In the upland condition, manual weeding was used to control the weeds.

The data of the following agronomic traits was recorded; days to flowering, days to maturity, plant height (cm), number of productive tillers per plant, and number of non productive tillers per plant. The data were collected for panicle length (cm), number of spikelet per panicle, number of filled grains per panicle, percent filled grains, weight of 1000 grains (g) and grain yield ha<sup>-1</sup> (kg) as yield and its related characters and grain length (mm), grain breadth (mm) and length per breadth Ratio as quality characteristics were recorded. The data collected from the experiment were subjected to statistical analysis for analysis of variance appropriate for RCBD.

## **RESULTS AND DISCUSSION**

The nature and magnitude of gene action involved in the expression of quantitative and qualitative characters is important for successful development of crop varieties. These results indicate the importance of both additive and non-additive types of gene action in the control of these characters. The character wise types of gene action are presented in Table 1 and are discussed as under:

### **Agronomic characters**

Under lowland environment, variance due to SCA (29.011) was greater than variance due to GCA (0.896), for days to flowering which indicates the presence of non-additive gene action and dominant type of gene action governed this trait. The non-additive gene action was greater than the additive type of gene action for days to maturity and plant height indicates the dominant type of gene action for this trait. Number of productive tillers per plant and number of non-productive tiller per plant showed additive type of gene action as indicated by the GCA, and SCA ratio which was greater than GCA values (Table1).

Under upland environment, significant variation among lines, testers and their interactions for the characters days to flowering, days to maturity and plant height indicate the importance of both additive and non-additive type of gene action.

Results showed that the variance for GCA was greater than those of the ratio of GCA/SCA while the variance due SCA was greater than variance due to GCA and also its ratio indicates the additive type of gene action for the characters like number of productive tillers per plant and number of non-productive tillers per plant. The results agreed with the findings of Akram *et al.* (2007) who reported partial dominant type of gene found controlling the agronomic traits. Sharat *et al.* (2006) found that there was predominance of non-additive genetic components for expression of different traits in rice crop.

Table 1. Types of gene action on various agronomic, yield and yield related and quality traits under lowland and upland conditions.

Traits	$\sigma^2$ GCA		$\sigma^2$ SCA		$\sigma^2$ GCA/ $\sigma^2$ SCA		Gene action	
	Lowland	Upland	Lowland	Upland	Lowland	Upland	Lowland	Upland
<b>Agronomic Traits</b>								
Days to 50% flowering	0.89	0.65	29.01	59.81	0.04	0.01	$\sigma^2$ D	$\sigma^2$ D
Days to maturity	1.15	0.38	26.10	8.55	0.04	0.04	$\sigma^2$ D	$\sigma^2$ D
Plant height (cm)	3.16	2.15	61.21	145.24	0.06	0.01	$\sigma^2$ D	$\sigma^2$ D
No. of productive tillers plant <sup>-1</sup>	0.35	0.02	0.92	0.19	0.38	0.17	$\sigma^2$ A	$\sigma^2$ A
No. of non-productive tillers plant <sup>-1</sup>	0.04	-0.01	0.03	0.03	0.02	0.06	$\sigma^2$ A	$\sigma^2$ A
<b>Yield and Yield Related Traits</b>								
Length of panicle (cm)	0.03	0.03	0.34	0.05	0.09	0.02	$\sigma^2$ A	$\sigma^2$ A
Total number of spikelets panicle <sup>-1</sup>	2.42	3.21	190.17	140.91	0.01	0.02	$\sigma^2$ D	$\sigma^2$ D
Number of filled grains panicle <sup>-1</sup>	3.40	3.32	156.27	169.33	0.02	0.02	$\sigma^2$ D	$\sigma^2$ D
Percent filled grains panicle <sup>-1</sup>	0.35	0.02	0.25	8.06	0.09	0.01	$\sigma^2$ D	$\sigma^2$ D
Weight of 1000 grains (g)	0.24	0.29	0.55	0.86	0.44	0.34	$\sigma^2$ A	$\sigma^2$ A
Yield ha <sup>-1</sup> (kg)	38171.71	34476.48	133078.35	193535.56	0.29	0.18	$\sigma^2$ D	$\sigma^2$ D
<b>Quality Traits</b>								
Grain length (mm)	0.01	0.01	0.17	0.21	0.06	0.01	$\sigma^2$ A	$\sigma^2$ A
Grain width (mm)	0.01	0.01	0.01	0.01	-0.01	1.33	$\sigma^2$ A	$\sigma^2$ A
Length/breadth ratio (mm)	0.01	0.01	0.03	0.04	0.49	0.18	$\sigma^2$ A	$\sigma^2$ A

$\sigma^2$ A= Additive variance

$\sigma^2$ D= Dominant variance

### Yield and its related traits

Under lowland environment, the variation of GCA was greater than the variance of SCA for length of panicle and weight of 1000 grains (Table 1), indicating that these traits had additive type of gene action, while other yield traits, including total number of spikelets per panicle, number of filled grains per panicle, percent

filled grains per panicle and yield per ha had dominant type of gene action as indicated by the greater GCA/SCA ratio. The GCA variance was greater than SCA ratio.

Under upland environment, the traits, length of panicle and weight of 1000 grains showed higher variation due to GCA than the ratio of variances due to GCA/SCA, which indicate the additive type gene action for these traits. While variances ratio of GCA/SCA were less than variance values of GCA indicating the dominant type of gene action for the total number of spikelet per panicle, number of filled grains per panicles, percent filled grains per panicle and yield per ha.

### **Quality traits**

Under lowland condition, all quality characters studied (grain length, grain breadth and length/breadth ratio) were controlled by additive gene action as the values of the variance of GCA were greater than GCA/SCA ratio values.

Under upland condition, the variances due to SCA were greater for the quality characters, grain length, grain width and grain ratio, than those due to GCA, which points out the pre-dominance of non-additive type of gene action. The ratio of variances GCA/SCA further proved the presence of pre-dominance of non-additive type of gene action.

### **CONCLUSION**

From the findings of the present study, it is concluded that, among the significant traits, the prevalence of non-additive type of gene action were present for traits like days to 50% flowering, days to maturity, plant height, weight of 1000 grains and grain length. Whereas, for yield and other yield related traits like number of spikelets/panicle, number of filled grains/panicle and percent filled grains/panicle, the prevalence of dominant type of gene action was present.

### **REFERENCES**

- Akram, M., A. Saifullah and M. Muhammad. 2007. Inheritance of traits related to seedling vigor and grain yield in rice (*Oryza sativa* L.). Pak. J. Bot., 39 (1): 37-45.
- Amirjani, M. R. 2011. Effect of salinity stress on growth, sugar content, pigments and enzyme activity of rice. Int. J. Bot., 7 (1): 73-81.
- Badawi, A. T. 2004. Rice-based production systems for food security and poverty alleviation in the Near East and North Africa: New Challenges and Technological Opportunities. 12-13 Feb-2004. FAO Rice Conference Rome, Italy.
- Bobby, T. P. M. and N. Nadarajan. 1993. Genetic analysis of yield components in rice involving CMS lines. IRRN 18:1.

Jinks, J. L. 1983. Biometrical genetics of heterosis. *In*: R. Frankel [ed.], Heterosis: Reappraisal of Theory and Practice. Springer-Verlag, Berlin, pp. 1-46.

Khush, G. S. 2005. What it will take to feed 5.0 billion rice consumers in 2030. *Plant Mol. Biol.*, 59: 1-6.

Ramalingam, P. V. and M. Subramanian. 1993. Combining ability in rice. *Oryza*, 30: 33-37.

Saleem, M. Y., J. I. Mirza and M. A. Haq. 2010. Genetic basis of yield and some yield related traits in basmati rice. *Pak. J. Bot.*, 42 (2): 955-961.

Sharat, K. P., K. B. Lotan and M. Jitendriya. 2006. Studies on gene action and combining ability analysis in basmati rice. *J. Central European Agric.*, 7 (2): 267-272.

Singh, R. K., V. S. Singh and G. S. Singh. 2000. Breeding aromatic rice for high yield, improved aroma and grain quality. *Aromatic Rice*. pp. 71.

Sarawgi, A. K., N. K. Rastogi and M. K. Munhot. 2000. Heterosis among Line x Tester for grain yield and quality components in rice. *Tropical Agric. Res. Ext.*, 3 (2): 2000

Singh, B. D. 2000. Estimation of components of genetic variance. *Plant Breeding* 6<sup>th</sup> ed. New Delhi-110002: Kalyani Printings. pp. 99.

Singh, N. K. and A. Kumar. 2004. Combining ability analysis to identify suitable parents for heterotic rice hybrid breeding. *IRRN*, 29 (1): 21-22.

Swain, D. 2005. Rainfed lowland and flood-prone rice a critical review on ecology and management technology for improving the productivity in Asia: Role of Water Sci. in Transboundary River Basin Mangmnt., Thailand.

(Received September 28, 2013; Accepted June 17, 2014)

