

GENETIC ANALYSIS OF YIELD AND YIELD CONTRIBUTING TRAITS IN BORO RICE (*Oryza sativa* L.) OVER ENVIRONMENTS

K. PRIYANKA¹ AND H. K. JAISWAL²

Abstract

Hayman's component analysis was employed to estimate genetic components of variation for yield and yield related traits in *boro* rice. Nine diverse lines of *boro* rice were crossed in diallel mating design excluding reciprocals and all the parental lines along with their 36 crosses were evaluated in randomized block design over 3 seasons in 3 replication. Significant differences among genotypes were observed for all the traits over seasons. Component analysis indicated importance of both additive and dominance components. However, greater magnitude of dominance component than its corresponding additive component of variance exhibited greater role of dominance in the inheritance of these traits. The average degree of dominance was more than unity indicating over-dominance for all the traits. Most of the traits exhibited low to moderate narrow sense heritability.

Keywords: *Boro* rice, component analysis, diallel, gene action, heritability

Introduction

Rice is a major food crop for more than half of the world population. About 90 percent of all the rice grown in the world is produced and consumed in Asia. The largest rice producing countries include China, India, Indonesia, Vietnam, Thailand and Bangladesh. In Bangladesh, rice is cultivated in all the three seasons i.e. aus, aman and *boro*, accounting for around 34.5 million metric tons of rice. *Boro* rice is famous for high productivity. India is the world's second largest producer of rice after China, accounting for about 20% of the world rice production. To meet the food demand of the growing population and to achieve food security in the country, the present level of production need to be increased by 2 million tones every year. Amelioration of grain yield is primary objective in plant breeding experiments. It is a complex trait governed by polygenes and highly influenced by environment. Grain yield depends on a number of growth and yield component traits directly or indirectly. Therefore, selection of yield components would be more beneficial than yield per se.

Formulation of an effective breeding strategy requires the sound knowledge of nature and magnitude of gene action. Biometrically, Hayman's component analysis is an important tool which clearly provides information about various components of variance (Hayman, 1954) and in this way, helps to find the nature of various gene effects. Thus, the present study was conducted over three

^{1&2}Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi – 221 005, Uttar Pradesh (India).

seasons to have a reliable information of the various components of genetic variation for yield and yield related traits in *boro* rice.

Materials and Method

Seeds of nine diverse genotypes of *boro* rice (IR 8, IR 36, IR 64, HUR 36, HUR 105, MTU 1010, Jaya, Krishna Hamsa and Gautam) were sown in nursery at three different dates with 15 days interval between successive sowings to ensure synchronization in flowering for the purpose of hybridization. In *kharif*, raised nursery beds were made. Twenty one days old seedlings were transplanted in the crossing block. Raising a good nursery in *kharif* season was not a big deal in case of rice but in *boro* season special care was needed due to low temperature at vegetative stage. Firstly, seeds were soaked in water overnight and kept in moistened gunny bags for two days for sprouting. Then these sprouted seeds were spread uniformly in prepared seed beds (wet bed nursery) in last week of November. Nursery beds were covered with polythene sheets during night hours to avoid cold injury. Sixty days old seedlings were transplanted in the crossing block. A standard spacing of 20 x 15 cm was adopted for the planting. Row length was maintained at 2 m. Single seedling per hill was transplanted. Recommended agronomic package of practices for each season was followed to raise a good crop. At the time of flowering, crosses were made in 9 x 9 diallel mating design without reciprocals during *kharif*-2014, *boro*-2014 and *kharif*-2015 to generate 36 crosses. All the 36 crosses along with 9 parents were evaluated in randomized block design in three replications for three seasons i.e. *boro*-2014, *kharif*-2015 and *boro*-2015 at Agricultural Research Farm of Banaras Hindu University. All the genotypes were evaluated for days to 50% flowering, days to maturity, plant height, effective tillers per plant, main panicle length, flag leaf length, flag leaf width, grains per panicle, 100 seed weight and yield/plant. Data was recorded from ten randomly selected plants from each entry in each replication. Mean data over replications were used for statistical analysis.

The analysis of variance was performed as per method suggested by Panse and Sukhatme (1967) for randomized block design. Diallel component analysis was performed with the help of statistical software Windostat v.9.2 (Windostat Services, Hyderabad, A.P., India).

Results and Discussion

Analysis of variance (ANOVA) showed significant variations for all the traits among seasons, genotypes and season x genotype interaction (Table 1). Significant season x genotype interaction indicated the differential response of genotypes over the seasons, so a separate analysis for each environment was carried out in order to assess the reliable estimates of various genetic components. Separate analysis for individual environment could also help in selection of traits which exhibited consistency in gene action, thus those traits could be reliably utilized in breeding programme irrespective of the environments. Analysis of variance indicated significant differences among the

treatments i.e. 9 parents and 36 crosses over the three seasons (Table 2). Significant variation for the yield traits in rice were reported by Hosseini *et al.* (2005), Sharma (2006), Dey *et al.* (2013) and Allahgholipour *et al.* (2015).

The estimates of components of genetic variation (\hat{D} , \hat{H}_1 , \hat{H}_2 , \hat{h}^2 , \hat{F} and \hat{E}) are presented in Table (3). The estimates of additive component of genetic variation were significant for most of the traits in all the growing seasons except days to 50% flowering (*boro-2015*), days to maturity (*boro-2015*), effective tillers/plant (in all the seasons), panicle length (in all the seasons), flag leaf length (*boro-2015*), flag leaf width (*boro-2015*), grains/panicle (*boro-2014*) and yield/plant (in all the seasons). The estimates of dominance components, \hat{H}_1 and \hat{H}_2 were highly significant for all the traits over all the three seasons (*boro-2014*, *boro-2015* and *kharif-2015*). In general, for yield traits estimates of additive component (\hat{D}) were smaller than those of dominance components (\hat{H}_1 and \hat{H}_2) for all the three seasons.

The estimates of net dominance effect, i.e. \hat{h}^2 , were positive and significant for days to 50% flowering (*boro-2014*), days to maturity (*boro-2014* and *boro-2015*), plant height (*boro-2015* and *kharif-2015*), effective tillers/plant (*kharif-2015*), panicle length (*kharif-2015*), flag leaf length (*boro-2014*), flag leaf width (*kharif-2015*), grains/panicle (*boro-2015* and *kharif-2015*) and 100 seed weight (in all the seasons). Positive and significant \hat{h}^2 for most of the traits was reported by Verma and Srivastava (2004).

The estimates of component \hat{F} were significant and positive for plant height (*boro-2015*), flag leaf length (*kharif-2015*), flag leaf width (*boro-2014*), grains/panicle (*boro-2015* and *kharif-2015*) and 100 seed weight (*kharif-2015*) suggesting an excess of positive genes controlling these traits. Raju *et al.* (2011) also reported an overall excess of dominant genes for most of the yield and quality traits except plant height, panicle length and kernel breadth.

Component \hat{E} was non-significant for most of the traits except flag leaf width (*boro-2014*). Verma and Srivastava (2004) and Kumar (2011) also reported non significant estimates of \hat{E} for all the yield traits under study which support the findings of the present investigation.

Most of the earlier studies reported significance of both additive and dominance genetic variance for most of the yield traits. Li and Chang (1970), Murai and Kinoshita (1986), Xu and Shen (1991), Mahmood *et al.* (2004), Verma and Srivastava (2004) and Kumar (2011) reported importance of both additive and dominant genes for all the traits under study. Raju *et al.* (2011) reported significant additive and non additive component of variance for the traits, plant height, panicle length, 1000-grain weight and kernel length/breadth ratio. The dominant component of variance was significant for days to 50% flowering, ear

bearing tillers, panicle weight and grain yield/plant and additive component was significant for kernel length and breadth. The non-additive component of variance dominated the additive one for most of the yield traits except 1000-grain weight. Verma and Srivastava (2004), Kumar *et al.* (2008) and Habib *et al.* (2014) reported involvement of both additive and dominance component of variance in the inheritance of the yield traits under study but the magnitude of dominance component was greater than the additive component of variance which indicated greater role of dominance in genetic control of these traits, which supports the present findings.

The proportions of components of genetic variation are presented in Table 4. The estimates of degree of dominance (\hat{H}_1/\hat{D})^{1/2} were higher than the unity for most of the traits in all the three seasons, suggesting the presence of over-dominance type of intra-allelic interactions. The estimates were close to unity for days to 50% flowering (1.400 in *kharif*-2015), days to maturity (1.335 in *kharif*-2015), plant height (1.384 in *boro*-2014 and 1.337 in *boro*-2015) and grains/panicle (1.237 in *kharif*-2015) suggesting complete to over-dominance for the trait. Raju *et al.* (2011) reported over-dominance for days to flowering, ear bearing tillers per plant, panicle weight, grain yield/plant and kernel length and kernel length/breadth ratio and partial dominance for plant height, 1000 grain weight and kernel breadth. The average degree of dominance more than unity for most of the traits was also reported by Verma and Srivastava (2004), Kumar (2011) and Habib *et al.* (2014) which is in agreement with present findings. Mahmood *et al.* (2004) reported less than unity average degree of dominance for the trait plant height, number of productive tillers per plant and number of primary branches per panicle, suggesting partial dominance for these traits. Akram *et al.* (2007) reported over-dominance for panicle length, grain yield/plant and 100 seed weight, whereas partial to complete dominance for tillers per plant.

The ratio $\hat{H}_2/4\hat{H}_1$ was found close to the expected value of 0.25 for most of the traits, suggesting nearly symmetrical distribution of positive and negative alleles at loci showing dominance for the traits. An asymmetrical distribution of positive and negative alleles was observed in case of panicle length (0.178 in *boro*-2014), flag leaf length (0.155 in *kharif*-2015), flag leaf width (0.181 in *boro*-2015), grains/panicle (0.179 in *boro*-2014, 0.148 in *boro*-2015 and 0.140 in *kharif*-2015) and yield/plant (0.198 in *boro*-2014 and 0.181 in *boro*-2015). Various researchers have reported closeness as well as deviations from the value 0.25 for most of the yield and quality traits in their materials (Murai and Kinoshita, 1986; Xu and Shen, 1991; Verma and Srivastava, 2004; Akram *et al.*, 2007; Kumar, 2011 and Raju *et al.*, 2011) which is in agreement with the present findings. However, Habib *et al.* (2014) reported less than 0.25 for all the traits suggesting asymmetrical distribution of genes in the parents which may be due to differences among the materials under study.

Table 3. Components of genetic variation for yield and yield contributing traits for 9x9 diallel in *Boro* rice in three seasons

Component	Season	DTF	DTM	PH	ET/P	PL	FL	FW	G/P	100SW	Y/P
\hat{D}	<i>Boro</i> -2014	68.399*	36.061*	114.686*	1.738	2.891	65.288*	0.021*	891.203	0.164*	4.041
	<i>Boro</i> -2015	64.168	65.962	172.458*	1.219	1.161	37.875	0.006	794.003*	0.174*	2.680
	<i>Kharif</i> -2015	94.561*	93.392*	74.215*	1.095	4.568	93.667*	0.027*	1401.425*	0.162*	0.874
\hat{H}_1	<i>Boro</i> -2014	273.891*	270.448*	219.824*	14.759*	26.470*	288.402*	0.092*	4974.33*	0.507*	134.155*
	<i>Boro</i> -2015	356.004*	383.304*	308.144*	8.368*	24.934*	263.696*	0.087*	3081.517*	0.693*	211.363*
	<i>Kharif</i> -2015	185.261*	166.534*	232.242*	14.858*	30.738*	246.164*	0.124*	2143.826*	0.373*	55.574*
\hat{H}_2	<i>Boro</i> -2014	230.276*	236.944*	185.018*	14.213*	18.807*	233.170*	0.076*	3568.331*	0.420*	106.026*
	<i>Boro</i> -2015	314.359*	336.402*	258.698*	7.936*	20.781*	221.792*	0.063*	1827.368*	0.591*	153.380*
	<i>Kharif</i> -2015	162.649*	149.516*	191.881*	14.551*	24.360*	153.070*	0.107*	1199.832*	0.305*	48.465*
\hat{h}_2	<i>Boro</i> -2014	52.481*	69.741*	2.962	0.065	0.125	186.436*	0.0001	1068.599	0.177*	8.462
	<i>Boro</i> -2015	88.777	148.969*	127.377*	0.365	-0.206	8.730	0.010	1420.957*	0.32*	9.397
\hat{F}	<i>Kharif</i> -2015	11.519	20.586	62.36*	8.858*	12.045*	9.758	0.048*	2063.406*	0.257*	10.976
	<i>Boro</i> -2014	31.133	24.745	70.022	1.073	6.800	67.875	0.028*	2110.841	0.212	-9.881
	<i>Boro</i> -2015	26.402	34.786	149.561*	0.868	2.769	42.161	0.01	1903.741*	0.211	1.220
\hat{E}	<i>Kharif</i> -2015	17.430	20.934	38.553	-0.266	7.831	151.353*	0.037	2199.099*	0.180*	-4.095
	<i>Boro</i> -2014	0.546	0.467	0.253	0.525	0.588	0.922	0.005*	16.686	0.00014	1.979
	<i>Boro</i> -2015	0.474	0.538	0.438	0.440	0.548	0.495	0.004	12.556	0.00027	1.974
<i>Kharif</i> -2015	0.516	0.519	0.241	0.422	0.510	0.768	0.004	13.059	0.00009	1.350	

*p<0.05; **p<0.01; ***p<0.001; SV-Source of variation; DF – Degrees of freedom; DTF – Days to 50% flowering; DTM – Days to maturity; PH- Plant height; ET/P – Effective tillers/plant; PL- Panicle length; FL – Flag leaf length; FW- Flag leaf width; G/P-Grains/panicle; 100SW- 100 seed weight; Y/P- Yield/plant; \hat{D} - variance component due to additive gene effects; \hat{H}_1 - variance component due to dominance deviations; \hat{H}_2 - estimate of dominance genetic variance due to proportion of positive and negative genes; \hat{h}^2 - net dominance effect; \hat{F} - mean of covariance of additive and dominance effects over all arrays; \hat{E} - environmental component of variation.

Table 4. Proportion of genetic components of variation for yield and yield contributing traits in *boro* rice over seasons

Component	Season	DTF	DTM	PH	ET/P	PL	FL	FW	G/P	100SW	Y/P
$(\hat{H}_1 / \hat{D})^{1/2}$	<i>Boro</i> -2014	2.001	2.071	1.384	2.914	3.026	2.102	2.117	2.363	1.759	5.762
	<i>Boro</i> -2015	2.355	2.411	1.337	2.620	4.634	2.639	3.697	1.970	1.996	8.880
	<i>Kharij</i> -2015	1.400	1.335	1.769	3.684	2.594	1.621	2.128	1.237	1.517	7.974
$\hat{H}_2 / 4 \hat{H}_1$	<i>Boro</i> -2014	0.210	0.219	0.210	0.241	0.178	0.202	0.206	0.179	0.207	0.198
	<i>Boro</i> -2015	0.221	0.219	0.210	0.237	0.208	0.210	0.181	0.148	0.213	0.181
	<i>Kharij</i> -2015	0.219	0.224	0.207	0.245	0.200	0.155	0.215	0.140	0.204	0.218
$\overline{KD} / \overline{KR}$	<i>Boro</i> -2014	1.257	1.209	1.566	1.237	2.271	1.657	1.960	3.010	2.165	0.650
	<i>Boro</i> -2015	1.191	1.246	1.960	1.314	1.693	1.535	1.506	4.109	1.872	1.053
	<i>Kharij</i> -2015	1.141	1.183	1.344	0.936	1.987	2.987	1.910	4.470	2.155	0.546
\hat{h}_2 / \hat{H}_2	<i>Boro</i> -2014	0.228	0.294	0.016	0.005	0.007	0.800	0.001	0.299	0.423	0.080
	<i>Boro</i> -2015	0.282	0.443	0.492	0.046	0.010	0.039	0.166	0.778	0.542	0.061
	<i>Kharij</i> -2015	0.071	0.138	0.325	0.609	0.489	0.064	0.447	1.720	0.843	0.226
\hat{h}_2 (ns)%	<i>Boro</i> -2014	41.0	37.6	46.1	12.9	26.2	30.8	14.8	9.30	15.7	42.5
	<i>Boro</i> -2015	33.4	31.6	35.7	13.9	18.1	25.2	34.2	13.3	18.0	42.4
	<i>Kharij</i> -2015	54.8	54.1	44.1	17.0	17.6	31.2	11.7	18.9	24.8	31.0

DTF – Days to 50% flowering; DTM – Days to maturity; PH- Plant height; ET/P – Effective tillers/plant; PL- Panicle length; FL – Flag leaf length; FW- Flag leaf width; G/P-Grains/panicle; 100SW- 100 seed weight; Y/P- Yield/plant; $(\hat{H}_1 / \hat{D})^{1/2}$ – average degree of dominance; $\hat{H}_2 / 4 \hat{H}_1$ – proportion of dominant genes with positive and negative effects; $\overline{KD} / \overline{KR}$ – proportion of dominant and recessive genes; \hat{h}_2 / \hat{H}_2 – proportion of gene(s)/gene(s) blocks exhibiting dominance; \hat{h}_2 (ns)% – narrow sense heritability estimate

The ratio of dominance to recessive genes, i.e. $\overline{KD}/\overline{KR}$, was greater than unity for all the yield traits except effective tillers per plant (0.936 in *kharif*-2015) and yield/plant (0.650 in *boro*-2014 and 0.546 in *Kharif*-2015) in all the three seasons suggesting presence of an excess of dominant genes in parental lines. For effective tillers/plant (*kharif*-2015) it was close to unity indicating an equal proportion of dominant and recessive gene among parents. However, an excess of recessive genes were observed for yield/plant (*boro*-2014 and *kharif*-2015). Akram *et al.* (2007) also reported presence of dominant alleles in parental alleles for most of the traits as the ratio was more than unity. Verma and Srivastava (2004) reported occurrence of more recessive genes for the trait 50% flowering, panicle length, flag-leaf area and grain yield and occurrence of dominant genes in other yield traits. Raju *et al.* (2011) reported excess of dominant alleles for days to flowering, ear bearing tillers per plant, panicle weight, 1000 grain weight, grain yield/plant, kernel length and kernel length/breadth (L/B). Kumar (2011) reported distribution of more dominant alleles for the traits day to first flowering, plant height, grain yield/plant, 1000 grain weight, grain length and grain breadth and distribution of more recessive alleles for number of productive tillers, panicle length, number of grains per panicle and grain length/breadth (L/B). Habib *et al.* (2014) found less than unity value for plant height, number of tillers/plant, panicle length, total spikelets/plant, number of seeds/panicle, days to 50% flowering, days to maturity, panicle number/plant, grain weight/panicle, grain yield/plot and 1000 seed weight indicating excess of recessive alleles.

The ratio of \hat{h}^2/\hat{H}_2 denotes an approximate number of genes/group of genes controlling the trait exhibiting dominance. The estimate ranged from 0.001 (flag leaf width in *boro*-2014) to 1.720 (grains/panicle in *kharif*-2015) in various seasons, which indicated that at least one to two genes or group of genes showing dominance were present for different traits. In *boro*-2014, all the traits were controlled by single gene or gene group. In *boro*-2015, all the traits were controlled by single gene or gene group exhibiting dominance. In *kharif*-2015, all the traits were controlled by single gene or gene group except grains/panicle which was controlled by two gene or gene groups exhibiting dominance. Li and Chang (1970) reported one to five gene or gene groups exhibiting dominance for seeding to heading period, plant height, number of panicles per plant, panicle length, panicle weight and number of spikelets per panicle in rice. Murai and Kinoshita (1986) reported one to twelve gene or gene groups exhibiting dominance for different yield traits. Verma and Srivastava (2004) reported one major gene group involved in expression of panicle length and plant height in F_1 while the remaining traits showed the presence of at least one major group of genes controlling their inheritance. Kumar (2011) found the ratio less than one for all the traits under study and reported that all the traits were under the control of at least single group of genes. Xu and Shen (1991) and Akram *et al.* (2007) reported one to three gene or gene groups and Habib *et al.* (2014) reported three to five genes or gene groups showing dominance for traits under study.

The estimates of narrow sense heritability were low to moderate for most of the yield traits in all the three seasons. Days to 50% flowering showed highest heritability (33.4 to 54.8%) over the seasons followed by plant height (35.7% to 46.1%) and yield/plant (31.0% to 42.5%). Raju *et al.* (2011) also reported low to moderate narrow sense heritability for yield components such as days to 50% flowering, ear bearing tillers, panicle weight besides grain yield/plant indicating prevalence of non additive gene action i.e. dominant and epistasis in these traits. However, high heritability was observed by Raju *et al.* (2011) for 1000-grain weight indicating prevalence of additive gene action and direct selection for this trait can be done for genetic improvement. Direct selection is effective for the traits showing high heritability and desirable mean performance.

Conclusion

The present investigation indicated the importance of dominance type of genetic effects in inheritance of yield and yield related traits in rice over three seasons. Certainly, heterosis breeding would be more beneficial to harvest the dominance gene effects of these traits. The low to moderate narrow sense heritability for most of traits suggested that direct selection for these traits may not be effective and reliable.

Acknowledgement

The first author is grateful to the Department of Science and Technology, New Delhi, India for financial assistance as INSPIRE Fellowship and Department of Genetics and Plant Breeding, BHU for providing facilities for conducting of experiments during the course of present study.

References

- Akram, M., M. Munir, S. Ajmal, S. Mahmud and Y. Ashraf . 2007. Combining ability analysis for yield and yield components in rice (*Oryza sativa* L.). *Pak. J. Agric. Res.* **20**: 1-2.
- Allahgholipour, M., E. Farshdfar and B. Rabiei. 2015. Combining ability and heritability of selected rice varieties for grain yield, its components and grain quality characters. *Genetika.* **47** (2): 559-570.
- Dey, S.R., M.S.R. Bhuyan, M. Maniruzzaman, M.A. Islam and S. Begum. 2013. Heterosis in inter-ecotypic classes of rice (*Oryza sativa* L.), *J. Agrofor. Environ.* **7**(1): 111-114.
- Habib, M., G.A. Parray and Z.A. Dar. 2014. Component analysis of different traits in rice (*Oryza sativa* L.) under temperate conditions. *Agric. Sci. Digest.* **34** (4): 307-309.
- Hayman, B.I. 1954. The theory and analysis of diallel crosses. *Genetics.* **39**: 789-809.
- Hosseini, M., R.H. Nejad and A.R. Tarang. 2005. Gene effects, combining ability of quantitative characteristics and grain quality in rice. *Iranian J. Agric. Sci.* **36** (1): 21-32.

- Kumar, N.S. 2011. Genetics of grain yield and its component characters in rice. *Crop Improv.* **38** (1): 45-47.
- Li, C.C. and T.T. Chang. 1970. Diallel analysis of agronomic traits in rice (*Oryza sativa* L.). *Bot. Bull. Acad. Sinica.* **11**: 61-81.
- Mahmood, T. M., F. L. Turner, Stoddard and M.A. Javed. 2004. Genetic analysis of quantitative traits in rice (*Oryza sativa* L.) exposed to salinity. *Australian J. Agricul. Res.* **55** (11): 1173-1181.
- Murai, M. and T. Kinoshita. 1986. Diallel analysis of traits concerning yield in rice. *Japan. J. Breed.* **36**: 7-15.
- Panase, V.G. and P.V. Sukhatme. 1967. *Statistical Methods for Agricultural Workers*, ICAR, New Delhi, India.
- Raju, C.H.S., L. Krishna, C.H.D. Raju, S. Vanishree, P.N. Reddy and B.B. Reddy. 2011. Genetic studies of quantitative traits through Hayman's approach in rice. *Oryza.* **48** (4): 314-318.
- Sharma, R.K. 2006. Studies on gene action and combining ability for yield and its component traits in rice. *Indian J. Genet.* **66**: 227-228.
- Verma, O.P., and Srivastava, H.K. 2004. Genetic component and combining ability analysis in relation to heterosis for yield and associated traits using three diverse rice growing ecosystems. *Field Crop Res.* **88**: 91-102.
- Xu, Y.B. and Z.T. Shen. 1991. Diallel analysis for tiller number at different growth stages in rice (*Oryza sativa* L.). *Theor. Appl. Genet.* **83**: 243-249.