

Genetic studies of yield and quality traits in aromatic rice genotypes through Hayman's approach

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ABSTRACT

Hayman's approach analysis was employed to estimate genetic components of variation in aromatic rice genotypes for yield and quality traits by following 8 x 8 one way diallel mating design. Vr-Wr graphs were plotted for the traits viz., days to 50 % flowering, days to maturity, plant height at maturity, main panicle length, effective tillers per plants, 100 grain weight and yield per plant, that exhibited significant deviation of regression coefficient 'b' from zero, irrespective of significance of 't²' or deviation of 'b' from unity. Vr-Wr graph revealed over dominance for the traits viz., plant height, main panicle length, effective tillers per plant and yield per plant. Traits like days to 50 % flowering, days to maturity and 100 grain weight revealed partial dominance. Graphical and component analysis revealed over dominance type of intra allelic interaction for most of the yield and yield contributing traits. However, both additive and dominance types of genetic effects were observed for most of yield and quality traits.

Key words: Rice, Hayman's, Component, Diallel, Gene action

INTRODUCTION

Rice is one of the most crucial food crops in the world. As more than 50 per cent of the world population depends on rice for their staple diet. It is cultivated in 114 countries across the globe, but 90 percent of world's rice is grown and consumed in Asia. Global rice production for 2015-16 was estimated as 476.7 million tonnes (on milled basis), over an area of 161.0 million ha (USDA Rice Outlook, Feb 2017). Rice is the staple food for two thirds of Indian population and holds the key to food security. India has occupied largest area under rice of 43.5 M ha and it ranks second in production (106.6 Mt) after China with an area and production of 30.21 Mha and 145.77 Mt, respectively (USDA Rice Outlook, May 2017). Rice is grown in almost all the states of India, but major rice producing states fall in the regions of middle and lower Ganga plains, as well as the coastal lowlands of peninsular India.

Nowadays, the quality considerations assume enhanced importance, especially in the countries which are self-sufficient in their production. As per capita

income increases the consumption preference of common man is shifting towards quality rice. Aromatic rice constitutes a small but special group of rice which are considered best in quality. Among the quality rice varieties, Basmati is the unique aromatic quality rice. It is a nature's gift to Indian sub-continent. As living standards are improving steadily, human demand for high quality rice is continuously on an increase. This entails in incorporation of preferred grain quality features as the most important objective next to yield enhancement. Based on the survey of 11 major rice growing countries, (Juliano and Duff, 1991) concluded that grain quality is second only to yield as the major breeding objective. In the future, improvement of grain quality traits will be even more enhanced as once the very poor, many of whom depend largely on rice for their staple food become better off and begin to demand higher quality rice (Welch and Graham, 2002).

Genetic improvement for rice has thoroughly been studied worldwide. However, hybridization is the best means to create desirable variability and to fix the concerned gene. The estimation of heterosis provides

information about the type of gene action involved in the expression of various quantitative traits. Diallel mating design serves as one of the important breeding technique for yield and grain quality traits in rice such as grain length, grain width, grain shape and elongation, along with the better yield. Diallel cross analysis helps to identify the best parents and their combinations for further selection and suggests the breeder the appropriate stage for selection as some traits are fully expressed after generations become uniform. Keeping in view the above points the Diallel cross technique (Hayman, 1954) is the systematic method to study the nature of gene action for each character and distribution of gene among the parents.

MATERIALS AND METHODS

The present study was carried out during two seasons' viz., *kharif* 2015 and *kharif* 2016 at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (UP). The site of study is situated at 25° 18' N latitude and 83° 03' E longitude, at an elevation of 80.71 m above mean sea level. The research material consists of eight genotypes selected for crossing programme were namely Pusa Basmati 1, Pusa Sugandh 2, Pusa Sugandh 3, Pusa Sugandh 5, Type 3, Kasturi Basmati, Ranbir Basmati and Pusa-2517-2-51-1. Pusa Basmati-1 was used as check for yield traits and Taraori Basmati was used as check for quality trait. All the genotypes were obtained from the 'All India Coordinated Rice Improvement Project' (AICRIP) at the Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (U.P.).

During *kharif* 2015, eight genotypes were selected on the basis of their quality and quantitative traits for making F_1 crosses and all the genotypes were seeded in nursery at 3 dates, 10 days apart and transplanted in crossing blocks at 21 days after sowing. Crosses are made in diallel fashion (excluding reciprocals) developing 28 F_1 s, using model I and method II Griffings (1956). Thus, the set of 28 rice hybrids were generated. In *kharif* 2016, the seed of F_1 hybrids generated during previous season along with the parental lines and checks (Pusa Basmati-1 and Taraori Basmati) was raised at a standard spacing of 20 x 15 cm in 5 m rows in randomized block design with three replications. The recommended package of

practices was followed to raise a good crop.

Observations were recorded on eight randomly selected competitive plants in each replication for seven yield characters viz., days to 50 % flowering, plant height, ear bearing tillers plant^{-1} , panicle length, panicle weight, 1000- grain weight and grain yield plant^{-1} and other quality characters viz., kernel length, kernel breadth and length / breadth ratio. A statistical procedure as developed by Hayman (1954) was followed for genetic component analysis.

Kernel dimensional analysis was done with the help of graph paper and small millimeter scale. Alkali digestion was estimated by the test devised by Little et al. (1958). The simplified colorimetric method described by Juliano (1971) was followed for the estimation of amylose content.

RESULT AND DISCUSSION

The analysis of variance for all the traits revealed significant genetic differences among treatments (parent and crosses) for almost all the traits. Similar findings were also reported by Hasib (2005) and Mohammad et al. (2014) for different traits. In the Hayman's approach of diallel analysis a graph is drawn with the help of variance of arrays (V_r) and covariance between parents and their offspring (W_r). The array refers to crosses in which a particular parent is common. V_r - W_r graphs were plotted only for those seven traits viz., days to 50% flowering, days to maturity, plant height, main panicle length, effective tillers per plants, 100 grain weight and yield per plant that exhibited significant deviation of regression coefficient 'b' from zero, irrespective of significance of 't²' or deviation of 'b' from unity. Graphical analyses are a good estimator of the prepotency of parents and thus provide a basis for choosing parental combination for selective improvements of the character concerned (Sanjeev et al., 2007). Thus, the general conditions of diallel analysis were fulfilled for these traits. It reflects that these characters had a strong relationship between V_r and W_r of parental material and thus V_r - W_r was effective for genetical studies of parental material with respect to these traits. For the remaining traits the deviations of regression coefficient from zero were not significant, hence V_r - W_r graphs were not plotted.

Deviation of regression coefficient 'b' from zero

Table 1. Estimates of genetic components and other parameters for yield traits in F1 crosses

Components	DTF	DTM	PH (cm)	PL(cm)	ET/P	FS/P	US/P	100 SW	Y/P
D	100.01*	107.49*	728.13*	26.22*	4.26*	344.76	164.24*	0.08*	52.30*
H ₁	59.14*	65.03*	76.95*	30.37*	8.80*	1665.03*	695.39*	0.08*	70.07*
H ₂	50.99*	53.76*	72.89*	23.64*	7.51*	1490.06*	569.34*	0.06*	64.02*
h ²	0.85	0.32	-0.04	17.58*	9.88*	23.50	322.20*	0.03*	72.31*
F	39.98*	52.16*	-21.44	11.92*	3.26	30.96	238.92	0.04*	23.19*
E	0.31	0.30	0.26	0.27	0.19	1.74	1.29	0.00	0.55
Degree of dominance	0.77	0.78	0.33	1.08	1.44	2.20	2.06	0.96	1.16
H ₂ /4H ₁	0.22	0.21	0.24	0.19	0.21	0.22	0.20	0.21	0.23
KD/Kr	1.70	1.91	0.91	1.54	1.72	1.04	2.09	1.77	1.47
h ² /H ₂	0.02	0.01	-0.01	0.74	1.32	0.02	0.56	0.44	1.13

*, ** = Significant at 0.05, and 0.01 levels, respectively. DTF-Days to 50% flowering; DTM-Days to maturity; PH- Plant height; PL-Main panicle length; ET/P- Effective tillers/plant; FS/P-Filled spikelet per panicle; UFS/P-Unfilled spikelet per panicle; 100 SW-100 seed weight and Y/P- Yield per plant

was significant for days to 50 % flowering and days to maturity. Vr-Wr graph plotted revealed partial dominance for days to 50 % flowering (Fig. 1 and Fig. 2). The scattered parental points on the regression line indicated diversity among parents. Most of the parental points fell away from the observed regression line which suggested the presence of G x E interaction. Pusa Sugandh-3 exhibited highest proportion of dominant alleles as it fell close to the origin and Kasturi Basmati revealed highest proportion of recessive allele due to farther distance from the origin. However, Pusa Sugandh-5 and Pusa -2517-2-51-1 revealed nearly closer to origin and Ranbir Basmati, Pusa Sugandh-2 and Type-3 was found nearly greater proportion of recessive alleles as they fall away from origin. Whereas, Pusa Basmati-1 exhibited equal proportion of dominant and recessive allele as they occupy intermediate position

in the regression line. Dwivedi et al. (1980) also reported partial dominance in the inheritance of the trait. Chaturvedi et al. (2015) and Priyanka et al. (2016) reported over dominance in case of days to 50 % flowering as the regression line intersected Wr axis below the origin in their study.

For plant height the regression coefficient 'b' showed significant deviation from zero. Over dominance was observed as the regression line intersected the Vr axis below the origin. Similar results reported by Raju et al. (2011), Chaturvedi et al. (2015) and Priyanka et al. (2016). Most of the parents are clustered around the regression line, revealed the absence of G x E interactions and diversity among the parents for plant height. Pusa -2517-2-51-1, Pusa Sugandh-5 and Pusa Sugandh-2 revealed highest proportion of dominant allele as it falls closer to the origin. Most of the parents

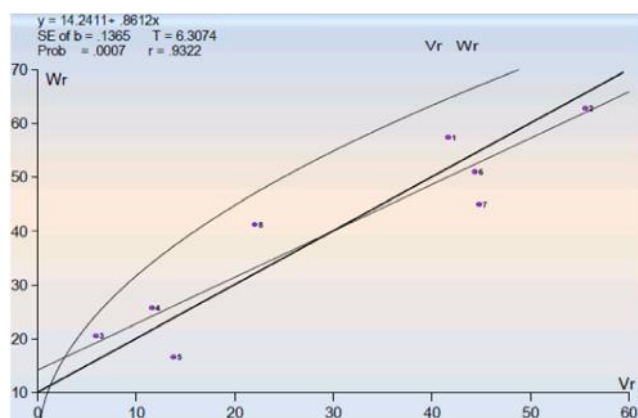


Fig. 1. Vr-Wr graph for days to 50 % flowering. 1. Ranbir Basmati; 2. Kasturi Basmati; 3. Pusa Sugandh-3;4. Pusa Sugandh-5; 5. Pusa -2517-2-51-1; 6. Pusa Sugandh-2; 7. Type-3; 8. Pusa Basmati-1

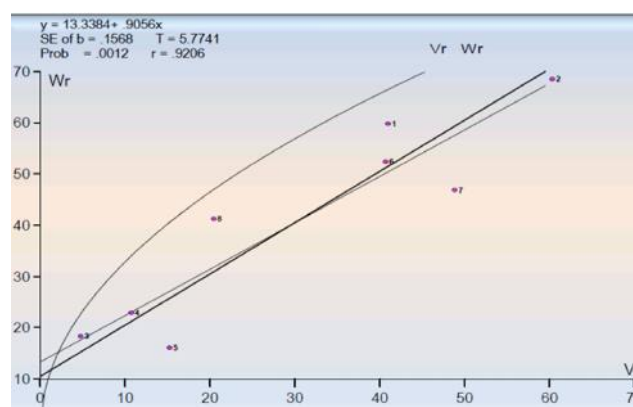


Fig. 2. Vr-Wr graph for days to maturity. 1. Ranbir Basmati; 2. Kasturi Basmati; 3. Pusa Sugandh-3;4. Pusa Sugandh-5; 5. Pusa -2517-2-51-1; 6. Pusa Sugandh-2; 7. Type-3; 8. Pusa Basmati-1

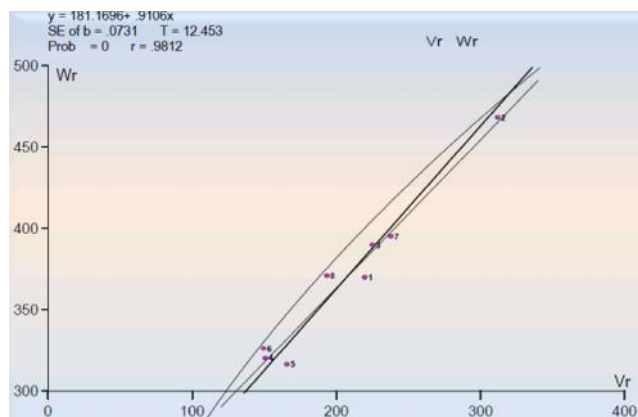


Fig. 3. Vr-Wr graph for plant height. 1. Ranbir Basmati; 2. Kasturi Basmati; 3. Pusa Sugandh-3;4. Pusa Sugandh-5; 5. Pusa -2517-2-51-1; 6. Pusa Sugandh-2; 7. Type-3; 8. Pusa Basmati-1

revealed equal proportion of dominant as well as recessive allele as they occupy intermediate position of the regression line. Kasturi Basmati revealed nearly higher proportion of recessive allele as it falls farther from the origin.

The regression coefficient 'b' deviated significantly from zero which indicates over dominance effect for the trait, main panicle length (Fig. 4). Similar results reported by Raju et al. (2011), Priyanka et al. (2016). Pusa Sugandh-5, Type-3 and Kasturi Basmati observed nearly closer to the origin, revealed presence more dominant allele. However, Pusa 2517-2-51-1, Pusa Sugandh-2 and Pusa Sugandh-3 clustered away from the origin showing the presence of more recessive allele for the trait respectively. On the other hand, Pusa Basmati-1 and Ranbir Basmati revealed equal proportion of dominant and recessive allele.

Over dominance effect was observed for effective tillers per plants as the regression line intersected below the origin on Wr axis (Fig. 5). Similar finding reported by Priyanka et al. (2016) in their studies. However, Mahmood et al. (2004) reported partial dominance in the inheritance of the trait. In Vr-Wr graph, Type-3 was very close to the origin showing the presence of dominant allele while Kasturi Basmati lies farthest from the origin showed the presence of highest recessive allele for the trait. Whereas, Pusa Basmati-1 and Ranbir Basmati revealed nearly closer to the origin suggesting more proportion of dominant allele for the trait. However, Pusa Sugandh-3, Pusa

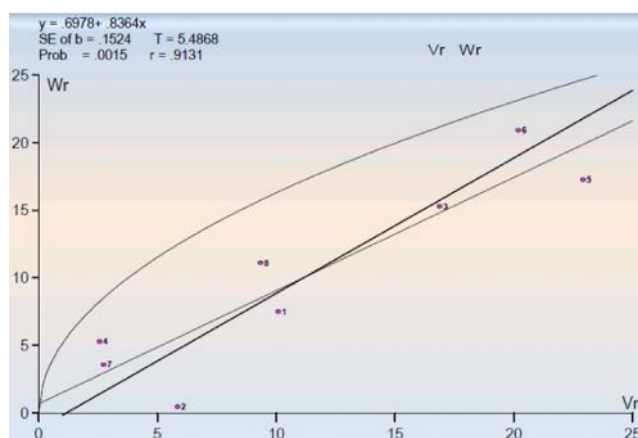


Fig. 4. Vr-Wr graph for main panicle length. 1. Ranbir Basmati; 2. Kasturi Basmati; 3. Pusa Sugandh-3;4. Pusa Sugandh-5; 5. Pusa -2517-2-51-1; 6. Pusa Sugandh-2; 7. Type-3; 8. Pusa Basmati-1

Sugandh-5 and Pusa Sugandh-2 occupy intermediate position suggesting equal proportion of dominant as well as recessive allele for the trait. Raju et al. (2011) reported that for effective tillers per plants, deviation of regression coefficient from zero was not significant. Hence, Vr-Wr graph not plotted.

For the trait, 100 grain weight, regression coefficient 'b' showed significant deviation from zero. Hence, Vr-Wr graph plotted revealed partial dominance as regression line intersected the Wr axis above the origin (Fig. 6). Raju et al. (2011) and Priyanka et al.

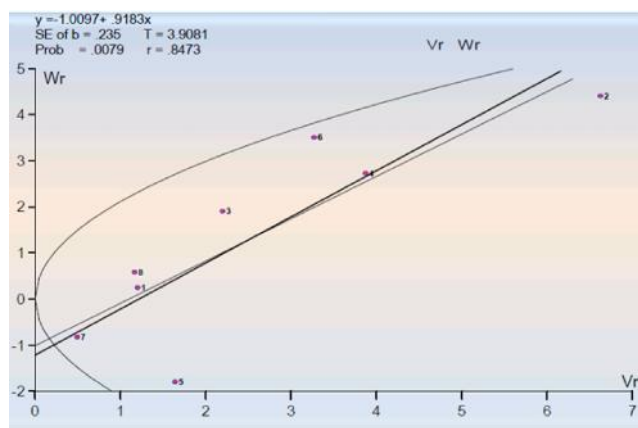


Fig. 5. Vr-Wr graph for effective tillers per plants. 1. Ranbir Basmati; 2. Kasturi Basmati; 3. Pusa Sugandh-3;4. Pusa Sugandh-5; 5. Pusa -2517-2-51-1; 6. Pusa Sugandh-2; 7. Type-3; 8. Pusa Basmati-1

Table 2. Estimates of genetic components and other parameters for quality traits in F_1 crosses??

Components	KLBC (mm)	KBBC (mm)	L/B BC	KLAC (mm)	KBAC (mm)	L/B AC	ER	EI	ASV/ GT Value	AC (%)
D	0.19*	0.01*	0.10	1.00*	0.01*	0.23*	0.01*	0.01*	3.01*	9.22*
H_1	0.46*	0.03*	0.29*	0.81*	0.03*	0.22*	0.04*	0.03*	6.34*	26.03*
H_2	0.40*	0.03*	0.30*	0.61*	0.02*	0.16*	0.03*	0.03*	4.47*	21.79*
h^2	0.16*	0.01*	-0.020	0.05	0.00	0.02	0.00	0.00	-0.00	-0.01
F	0.01	-0.01	-0.06	0.23	-0.00	0.11	0.00	0.01	4.41*	9.78
E	0.00	0.00	0.04*	0.01	0.00	0.00	0.00	0.00	0.01	0.02
Degree of Dominance	1.55	1.70	1.67	0.90	1.82	0.97	2.02	1.42	1.45	1.67
$H_2/4H_1$	0.22	0.24	0.25	0.18	0.22	0.18	0.19	0.23	0.17	0.20
KD/KR	1.02	0.78	0.69	1.29	0.77	1.68	1.21	1.23	3.03	1.92
h^2/H_2	0.42	0.39	-0.05	0.08	0.02	0.14	0.09	0.05	-0.00	0.00

*, ** = Significant at 0.05, and 0.01 levels, respectively. KLBC-Kernel length before cooking; KBBC-Kernel breadth before cooking; L/B BC- Kernel length/breadth ratio before cooking; KLAC- Kernel length after cooking; KBAC-Kernel breadth before cooking; L/B AC- Kernel length/breadth ratio after cooking; ER-Elongation ratio; EI-Elongation index; ASV-Alkali spread value; GT-Gelatinization temperature; AC-Amylose content. D- Variance component due to additive gene effect ; H_1 - Variance component due to dominance deviation; H_2 -Estimate of dominance genetic variance due to proportion of positive and negative genes; h^2 - Net dominance effect; F - Mean of covariance of additive and dominance effect overall array; E- Environmental component of variance; $H_2/4H_1$ - Proportion of dominant gene with positive and negative effect; KD/KR- Proportion of positive and negative genes; h^2/H_2 -Proportion of gene(s) /gene(s).

(2017) reported that for 100 grain weight deviation of regression coefficient from zero was not significant. Hence, Vr-Wr graph not plotted. Pusa Sugandh-3 and Pusa Sugandh-5 and Pusa Sugandh-2 being closer to the origin showed presence of more dominant allele while Ranbir Basmati and Type-3 showed presence of more recessive allele for the trait 100 grain weight as it falls most distant from the origin. Whereas, Kasturi Basmati and Pusa Basmati-1 revealed equal proportion of dominant and recessive allele for the trait as they occupy intermediate position of the regression line.

For yield per plant, deviation of regression

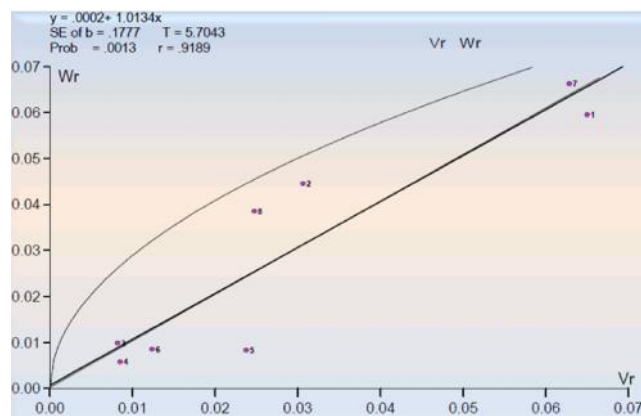


Fig. 6. Vr-Wr graph for 100 grain weight. 1. Ranbir Basmati; 2. Kasturi Basmati; 3. Pusa Sugandh-3; 4. Pusa Sugandh-5; 5. Pusa -2517-2-51-1; 6. Pusa Sugandh-2; 7. Type-3; 8. Pusa Basmati-1

coefficient 'b' from zero was significant. Regression line intersected the Vr axis below the origin indicating over dominance effect for the trait (Fig. 7). Ilieva et al. (2013) and Chaturvedi et al. (2015) also reported over dominance for the trait which is in agreement with present findings. Pusa Basmati-1 being closer to the origin revealed presence of highest dominant allele while Kasturi Basmati showed presence of highest recessive allele as it was most distant from the origin. Whereas, Ranbir Basmati, Pusa Sugandh-3, Pusa 2517-2-51-1 and Pusa Sugandh-2 revealed more proportion of dominant allele as they fall nearly closer to the origin. However, Pusa Sugandh-5 falls farther from the origin suggesting more proportion of dominant allele for the trait.

Component of genetic variation revealed that the traits main panicle length, number of effective tillers per plant, unfilled spikelets per panicle, 100 grain weight, yield per plant, kernel length before cooking, elongation ratio, elongation index, alkali spreading value and amylose content, were although influenced by both additive and non additive genetic components, the non additive gene actions was more important in controlling the inheritance of these traits. Only dominance component of genetic variance was significant for filled spikelets per panicle and kernel L/B ratio before cooking. In case of days to 50 % flowering and days to maturity both additive and non additive gene actions

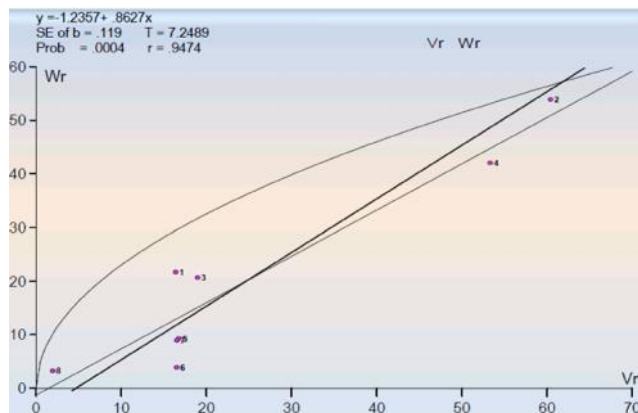


Fig. 7. Vr-Wr graph for yield per plant. 1. Ranbir Basmati; 2. Kasturi Basmati; 3. Pusa Sugandh-3; 4. Pusa Sugandh-5; 5. Pusa -2517-2-51-1; 6. Pusa Sugandh-2; 7. Type-3; 8. Pusa Basmati-1

were important but additive component was more predominant. Akram et al. (2007) observed predominant additive gene action for effective tillers per plant, predominant of dominant gene action for panicle length, 100 grain weight and only non additive gene action for grain yield per plant. Kaushik (1984) and Nematzadeh (1987) reported the importance of non additive gene effects in the inheritance of the panicle length and 100 seed weight which was in accordance to the present results. Raju et al. (2011) reported major role of non additive gene effects in controlling the inheritance of effective tillers per plants, kernel length before cooking and 100 seed weight which was similar to the present findings. Priyanka et al. (2017) studied greater magnitude of dominance component than its corresponding additive component of variance that exhibited greater role of dominance in the inheritance of various traits.

Major role of recessive genes was observed in the expression of the traits *viz.*, plant height, kernel breadth before cooking, L/B ratio before cooking and kernel breadth after cooking, which was confirmed by the negative estimate of \hat{F} and a less than one ratio of KD/Kr . The ratio of $H_2/4H_1$ was close to 0.25 for almost all the traits except main panicle length, kernel length after cooking, kernel L/B ratio after cooking and elongation ratio, suggesting nearly equal distribution of positive and negative genes among the parents for the respective traits. This report was in accordance with Raju et al. (2011)

The estimates of average degree of dominance

revealed partial dominance for days to 50 % flowering, days to maturity and plant height and complete dominance for main panicle length, 100 grain weight, kernel length after cooking and kernel L/B ratio after cooking and over dominance for effective tillers/ plants, filled spikelets per panicle, unfilled spikelets per panicle, yield per plants, kernel length and breadth before cooking, kernel L/B ratio before cooking, kernel breadth after cooking, elongation ratio, elongation index, ASV/GT value and amylose content. Akram et al. (2007) reported partial dominance for tillers per plant panicle length and grain yield per plant and over dominance for 100 seed weight which opposed the present results.

The proportion of h^2/H_2 ranged from -0.01 (plant height) to 1.32 (effective tillers) which indicated that at least one to two genes/group of genes showing dominance were present for different traits (Table 2.). Xu and Shen (1991) 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 proportion of h^2/H_2 for quality traits ranged from -0.05 (kernel L/B ratio before cooking) to 0.42 (kernel length before cooking) which indicated that the ratio less than one for all the traits under study reveals that all the traits were under the control of at least single or group of genes (Table 2.). Similar findings were also reported by Kumar et al. (2011).

CONCLUSION

The analysis of variance suggested that parents and their F_1 s exhibited high amount of genetic variation. So, this is in desirable direction for improving the traits concerned. Graphical and component analysis revealed over dominance type of intra allelic interaction for most of the yield and yield contributing traits. However, both additive and dominance types of genetic effects were observed for most of yield and quality traits. The pattern of inheritance was largely governed by non-additive gene action for yield and important yield components except 100 grain weight, day's to 50 percent flowering and days to maturity. So, there was limited scope for improvement of yield components, except 100 grain weight through progeny selections in early generations. For such traits heterosis breeding would be most effective followed by selection. And for other traits simple pedigree method is sufficient, as the additive

gene action played greater role as suggested by Raju et al. (2011). Parental lines having equal proportions of dominant and recessive genes may be exploited for getting improved populations. Components of genetic variances for yield and quality traits revealed non additive gene actions for the inheritance of most of these traits. So, heterosis breeding would be more effective to harvest the dominance gene effects of these traits. The low to moderate narrow sense heritability for some of the traits suggested that direct selection for these traits may not be effective and reliable.

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