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# COMPONENTS OF GENETIC VARIATION AND GRAPHICAL ANALYSIS (VR-WR) FOR SOME YIELD AND QUALITY CHARACTERS IN BASMATI RICE (*ORYZA SATIVA* L.)

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## Abstract

Gene action for eight yield and six quality traits were evaluated through Hayman's analysis (graphical and component) for fifteen direct F1 hybrids along with their six parents of Basmati rice were studied in a randomized complete block design with three replications. Significant differences were observed among parents, hybrids and hybrids versus parents for most of the agronomic, yield and quality characters of hybrids. Valid graphical analysis were explained for characters like plant height, 100 grain weight, days to 50% flowering, days to maturity, kernel length before and after cooking and alkali spread value, showing significant deviation of regression coefficient, 'b' from zero and non significant deviation of 'b' from unity and all these traits revealed over dominance type of intra allelic interaction. Furthermore, component analysis were done for all the traits by examining estimates D, F, $H_1$, $H_2$, $h^2$ and E and proportion of components *i.e.* $(H_1/D)^{0.5}$, $H_2/4H_1$, KD/KR, $h^2/H_2$ and $h^2n$. The component D, reflecting additive genetic variance was significant for all the characters studied except for effective tillers per plant, seeds per panicle, grain yield per plant, kernel breadth after cooking and amylose content. The ratio $(H_1/D)^{0.5}$ which measured the mean degrees of dominance over all loci was more than one indicating over dominance for all the characters. The ratio, $H_2/4H_1$, close to 0.25 for characters effective tillers per plant, panicle length, grain yield per plant, kernel breadth, amylose content indicating nearly symmetrical distribution of positive and negative alleles at loci showing dominance for the traits. Likewise, ratios, KD/KR and $h^2/H_2$ revealed presence of dominant genes/group of genes for different traits. Heritability in narrow sense ($h^2n$), more than 50% for Plant Height, Seed per panicle, Kernel length and Kernel Length After cooking indicated major part of additive gene action in phenotypic variability and selection should be effective for improvement of these characters in rice.

***Key words* :** Basmati Rice, Hayman's analysis, Over Dominance, Heritability.

## Introduction

Rice (*Oryza sativa* L., 2n : 2X = 24) is a major cereal and staple food crop for half of the world's population providing 23% of the global human per capita energy and 16% of the per capita protein ( IRRI, 1997). The area under rice cultivation in India was 43.5 million hectares with a production of 103 million tonnes during 2015-2016 (USDA Grain Report, 2016). Among them, Basmati rice is the leading aromatic fine quality rice indigenous to the Indian sub-continent and endowed with unique quality traits are palatal delights of the rice connoisseurs' world over. According to the Agricultural and Processed Food Products Export Development Authority (APEDA), basmati acreage was about 2.3 million hectares and produced over 6.05 million tons in 2014-15. Nearly 75% of the country's annual basmati produce, which was 4.6 million tons in 2014-15, is exported to countries, mainly in West Asia, Europe and North America. In value terms, the export of basmati rice stood at Rs.30000 crores in 2014-15. Physical appearance, cooking and eating qualities of Basmati rices are important to the rice eaters (Zhou *et al*., 2002). Acclaimed for delightful fragrance, characteristic grain length and fine texture, Basmati rice fetches premium price in domestic and international markets (Sood *et al*., 1978). Aroma is due to certain chemical present in the endosperm identified as '2-acetyl- 1-pyrroline' (Itani *et al*., 2004).

Most of the traits of interest to breeder in order to

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improve any crop are complex and result of the interaction of a number of components (Sarawagi *et al.*, 1997). Yield related traits like number of spikelet per panicle and 1000 grain weight, are also inherited quantitatively, but they have comparatively higher heritability (Xing *et al.*, 2001). As rice (*Oryza sativa* L.) is a staple food around the globe, therefore to meet the food growing demands, it is necessary to improve rice grain yield (Liu *et al.*, 2013). Diallel design provide good evaluation of parents and full-sib families that have been used extensively for the genetic analysis of quantitative characters (Sabouri *et al.,* 2013). The practical application of diallel method was carried out for the improvements of almost all the crop plants such as rice (Verma and Srivastava, 2004) and maize (Crosbie *et al.*, 1978). Knowledge of heritability and genetic advance of the character indicates the scope for the improvement through selection. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et al.,* 1955). Keeping in view the above mentioned facts, the present investigation was done with the following objectives:

1. To find the nature of gene actions for yield and quality traits in six parent lines of Basmati rice by employing graphical analysis of diallel.
2. To estimate the components of genetic variation and their proportions in order to study the inheritance of various traits.

## Materials and Methods

The present study was conducted at the Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh during *Kharif* 2014 and *Kharif* 2015. The experimental material comprised of six parents and 15 crosses. Six parental lines selected for the experiments were HUBR 10-9, HUBR-16, Type 3, Basmati 370, Taraori basmati, and Sonowal Basmati. The hybrids used in the experiments were obtained by crossing the parents in diallel fashion without reciprocals during *Kharif* 2014.

21 days old seedlings of the 15 hybrids and six parents were planted in Randomised Block Design (RBD) with three replications during *Kharif* 2015. Single seedling per hill was planted with a spacing of 20 × 20 cm and recommended agronomic package of practices were followed to raise a healthy crop. Observations were recorded on ten competitive plants both in parents and hybrids in each replication for the following eleven traits *viz.,* days to 50 per cent flowering, days to maturity, plant height, number of effective tillers per plant, panicle length, number of grains or seeds per panicle, 100 grain weight, grain yield per plant, kernel length, kernel breadth, kernel Length after cooking, kernel breadth after cooking, Alkali Spread Value, amylose content.

### Statistical analyses

#### Diallel cross

In this design (Method 2, Model I), all possible mating of selected set of fixed genotypes i.e. six parents were made, excluding reciprocals, and this yielded a total of 15 hybrids.

#### Hayman's approach

This approach utilises the graphical approach as well as genetic component analysis to ascertain the role of additive and non-additive type of gene action in the expression of the trait. Based on parental array variance (Vr) and parent-offspring co-variance (Wr) relationships in diallel cross progenies, a two-way representation or distribution of parental arrays along a regression line of Wr on Vr was first suggested by Jinks and Hayman (1953), and later refined by Hayman (1954a). This two-directional depiction is widely known as Vr-Wr graph and the analysis as 'graphical approach'. This approach includes certain inbuilt tests for the presence of epistasis. After testing the validity of hypothesis and presence/ absence of epistasis, graphic analysis is followed by determination of components of genetic variance (*viz.* additive and dominance variance) together with related genetic parameters. Estimation of variances and co-variances, testing the validity of the hypothesis, test of significance of 'b', estimation of different components and their proportion in genetic variation, proportion of dominant and recessive genes in the parents and heritability in narrow sense were worked out by using graphical and component analyses.

Adequacy of the additive dominance model was tested with the help of '$t^2$' test as proposed by Hayman (1954a) as follows:

$$t^2 = \frac{(n-2)}{4}\left[\frac{\{V_{ar}(V_r)-V_{ar}(W_r)\}^2}{V_{ar}(V_r)V_{ar}(W_r)-C_{ov^2}(V_r,W_r)}\right]$$

Which is an 'F' test with 4 and (n – 2) degrees of freedom and n=Number of parents.

## Results and Discussion

### Vr-Wr analysis

The two directional depictions made based on the parent offspring co-variance (Wr) and parental variance (Vr) are presented under the topic. Hayman Graphical

**Table 1:** Estimates of "$t^2$" and "b" for 6 x 6 diallel analysis for yield and quality traits

| Traits | "$t^2$" | b(Slope) + SE(b) | H : b = 0 | H : b =1 |
|---|---|---|---|---|
| Days to 50% flowering | 2.483 | 1.263±.4743 | NS | NS |
| Days to maturity | 1.765 | 0.730±0.809 | NS | NS |
| Plant height (cm) | 1.860 | 0.694±0.155 | ** | NS |
| Effective tillers/ plant | 8.741* | 0.095±0.152 | NS | ** |
| Panicle length (cm) | 1.269 | 0.320±0.269 | NS | NS |
| Seeds/panicle | 19.129** | 0.178±0.106 | NS | ** |
| 100 grain weight | 0.535 | 0.687±0.224 | * | NS |
| Grain yield/ plant | 3.480 | 0.093±0.216 | NS | * |
| Kernel length | 0.176 | 0.104±0.403 | NS | NS |
| Kernel breadth | 2.437 | 0.176±0.238 | NS | * |
| Kernel length after cooking | 0.022 | 0.734±0.305 | NS | NS |
| Kernel breadth after cooking | 4.435 | 0.189±0.193 | NS | * |
| Alkali spread value | 2.323 | 0.996±0.764 | NS | NS |
| Amylose content | 3.148 | 0.192±0.218 | NS | * |

* and ** significant at 0.05 and 0.01 probability level.

approach to Diallel analysis is based on monogenic additive model. Hence, testing the adequacy of the model is important to detect the presence or absence of epistasis. Different assumptions underlying the diallel cross analysis were tested by $t^2$ (test of homogeneity of Wr-Vr variances) and b (test of deviation of regression slope from zero and unity).

The non-significant '$t^2$' values (table 1) for all the traits except Effective tillers/plant and seeds per panicle indicated the uniformity of Vr-Wr, which confirms the validity of the hypothesis and fulfilment of all the assumptions of diallel. Traits exhibiting significant '$t^2$' values suggested the lack of fulfilment of at least one of the assumptions. Iftekharuddaula *et al*., (2009) in a similar finding reported non-significant estimates of '$t^2$- test' for primary branch length, secondary branch length, primary branch/panicle, unfilled grains/primary branch, filled grains/secondary branch and unfilled grains/secondary branch in rice while significant for secondary branch/ panicle and filled grains/primary branch possibly because of presence of epistasis estimates.

Non-significant deviation of regression coefficient 'b' from zero suggested the absence of linear relationship between variances and co-variances for most of the traits like days to 50% flowering, days to maturity, effective tiller per plant, panicle length, seeds per panicle, grain yield per plant, kernel length, kernel breadth, kernel length and kernel breadth after cooking, alkali spread value, amylose content. Traits like plant height and 100 seed weight, which are significantly deviating from zero indicate the fulfilment of assumptions/validity of Vr-Wr graph. Traits such as days to 50% flowering, days to maturity, plant height, panicle length, 100 seed weight, kernel length, kernel length after cooking, alkali spread value, showed non-significant deviation of 'b' from unity, which indicated absence of epistasis or inter-allelic interactions. Moreover, significant deviation from the unity suggests the presence of epistasis for the traits like Effective tillers/plant, seeds per panicle, grain yield per plant, kernel breadth, kernel breadth after cooking, and amylose content.

Vr-Wr graphs were plotted only for those traits which exhibited significant deviation of regression coefficient 'b' from zero and for those which showed non-significant deviation of regression coefficient 'b' from unity. For the trait plant height (Fig. 3), the regression coefficient 'b' is highly significant and showed deviation from zero, thus, valid predictions can be made through the graph. The regression line cuts the Wr axis below the origin point suggesting over dominance gene action. HUBR-16 was farthest from origin exhibiting higher proportion of recessive genes, whereas Type 3 was closest to origin as it had highest proportion of dominant genes. The other two parents, Taraori basmati and Sonowal basmati possess more proportion of additive genes than recessive genes as they fell near to the origin. Basmati 370 and HUBR 10-9 were near the farthest HUBR-16 so they would also have more number of recessive genes. Similarly, intersection of regression line below the origin on Vr-Wr axis clearly indicated the presence of over dominance for 100 grain weight (Fig. 5). Simultaneously, the value of regression coefficient 'b' was significantly deviating from zero proving valid explanation through the graph from diallel analysis. Parent Sonowal basmati was farthest from origin and thus possess higher proportion of recessive genes, whereas parents Taraori basmati, Basmati 370, Type 3 and HUBR-16 possess equal

**Table 2:** Hayman's genetic parameters

| **Estimate** | **Days to 50% flowering** | **Days to maturity** | **Plant height cm** | **Effective tillers/ plant** | **Panicle length (cm)** | **Seeds/ panicle** | **100 grain weight** | **Grain yield/ plant** |
|---|---|---|---|---|---|---|---|---|
| D | 40.085**<br>(± 6.585) | 35.006**<br>(±11.158) | 398.714**<br>(±42.266) | 4.502<br>(±21.116) | 7.893**<br>(±2.802) | 576.159<br>(±542.099) | 0.114**<br>(±0.013) | 41.584<br>(±132.059) |
| F | 64.440**<br>(±16.088) | 65.322*<br>(±27.259) | 132.142<br>(±103.255) | -2.072<br>(±51.586) | 6.010<br>(±6.845) | -390.096<br>(±1324.37) | 0.120**<br>(±0.031) | -5.489<br>(±322.621) |
| $H_1$ | 72.898**<br>(±16.717) | 97.637**<br>(±28.325) | 415.264**<br>(±107.296) | 112.522*<br>(±53.605) | 30.740**<br>(±7.113) | 3442.037*<br>(±1376.16) | 0.172**<br>(±0.032) | 1227.855**<br>(±335.245) |
| $H_2$ | 44.677**<br>(±14.934) | 66.187**<br>(±25.304) | 334.805**<br>(±95.850) | 100.451*<br>(±47.886) | 27.355**<br>(±6.354) | 2756.302*<br>(±1229.36) | 0.107**<br>(±0.029) | 1059.579**<br>(±299.483) |
| $h^2$ | 9.420<br>(±10.052) | 15.239<br>(±17.031) | 132.441*<br>(±64.513) | 126.410**<br>(±32.231) | 3.309<br>(±4.277) | 913.141<br>(±827.44) | 0.088**<br>(±0.019) | 958.248**<br>(±201.572) |
| E | 0.259<br>(±2.4890) | 0.312<br>(±4.217) | 4.875<br>(±15.975) | 1.266<br>(±7.981) | 0.731<br>(±1.059) | 87.055<br>(±204.89) | 0.005<br>(±0.005) | 13.416<br>(±49.914) |
| Proportion of component | | | | | | | | |
| $(H_1/D)^{0.5}$ | 1.349 | 1.670 | 1.021 | 4.999 | 1.973 | 2.444 | 1.231 | 5.434 |
| $H_2/4H_1$ | 0.153 | 0.169 | 0.202 | 0.223 | 0.222 | 0.200 | 0.156 | 0.216 |
| KD/KR | 0.3951 | 3.532 | 1.388 | 0.912 | 1.478 | 0.757 | 2.504 | 0.976 |
| $h^2 / H_2$ (No. of Gene Groups) | 0.211 | 0.230 | 0.396 | 1.258 | 0.121 | 0.331 | 0.817 | 0.904 |
| $h^2n$ (Heritability in Narrow Sense) | 0.145<br>(±14.271) | 0.033<br>(±84.473) | 0.662<br>(±0.367) | 0.261<br>(±11.368) | 0.258<br>(±2.259) | 0.516<br>(±1.932) | 0.477<br>(±2.820) | 0.279<br>(±3.593) |

*Contd…*

| **Est ate** | **Kernel length** | **Kernel breadth** | **Kernel length after cooking** | **Kernel breadth after cooking** | **Alkali spread value** | **Amylose content** |
|---|---|---|---|---|---|---|
| D | 0.525**<br>(±0.167) | 0.012*<br>(±0.005) | 3.206**<br>(±0.431) | 0.002<br>(±0.006) | 0.977**<br>(±0.246) | 1.966<br>(±1.822) |
| F | 0.260<br>(±0.409) | 0.005<br>(±0.013) | 2.345*<br>(±1.054) | 0.002<br>(±0.014) | 1.202*<br>(±0.600) | 2.436<br>(±4.452) |
| $H_1$ | 0.970*<br>(±0.425) | 0.036**<br>(±0.013) | 4.067**<br>(±1.095) | 0.059**<br>(±0.014) | 2.450**<br>(±0.623) | 16.073**<br>(±4.626) |
| $H_2$ | 0.737<br>(±0.379) | 0.033**<br>(±0.012) | 3.198**<br>(±0.978) | 0.047**<br>(±0.013) | 1.666**<br>(±0.557) | 15.033**<br>(±4.132) |
| $h^2$ | 0.151<br>(±0.255) | 0.072**<br>(±0.008) | 0.978<br>(±0.658) | 0.000<br>(±0.009) | 0.083<br>(±0.375) | 0.852<br>(±2.781) |
| E | 0.020<br>(±0.063) | 0.003<br>(±0.002) | 0.019<br>(±0.163) | 0.002<br>(±0.002) | 0.053<br>(±0.093) | 0.028<br>(±0.689) |
| $(H_2/D)^{0.5}$ | 1.360 | 1.720 | 1.126 | 5.115 | 1.584 | 2.860 |
| $H_2/4H_1$ | 0.190 | 0.230 | 0.197 | 0.197 | 0.170 | 0.234 |
| KD/KR | 1.446 | 1.289 | 1.962 | 1.162 | 2.271 | 1.553 |
| $h^2 / H_2$ (No. of Gene Groups) | 0.205 | 2.163 | 0.306 | 0.008 | 0.050 | 0.057 |
| $h^2n$ (Heritability in Narrow Sense) | 0.549<br>(±2.363) | 0.297<br>(±16.932) | 0.514<br>(±1.212) | 0.318<br>(±11.298) | 0.373<br>(±2.527) | 0.070<br>(±25.034) |

* and ** significant at 0.05 and 0.01 probability level.

number of dominant and recessive genes as they are lying between the parents HUBR 10-9 and Sonowal basmati. Parent HUBR 10-9 was closest to origin and thus it revealed more proportion of dominant genes. It also falls below the origin showing influence of epistasis.

Now, considering traits showing non-significant

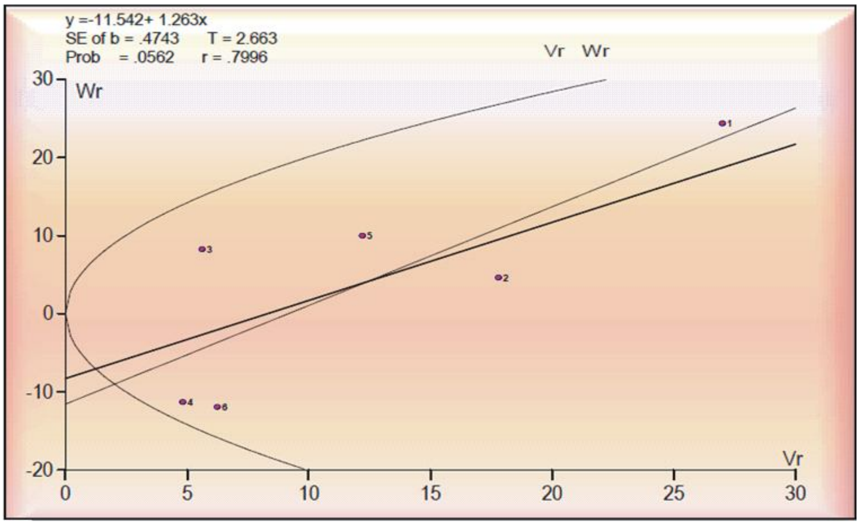


**Fig. 1:** Vr-Wr graph for Days to 50% flowering

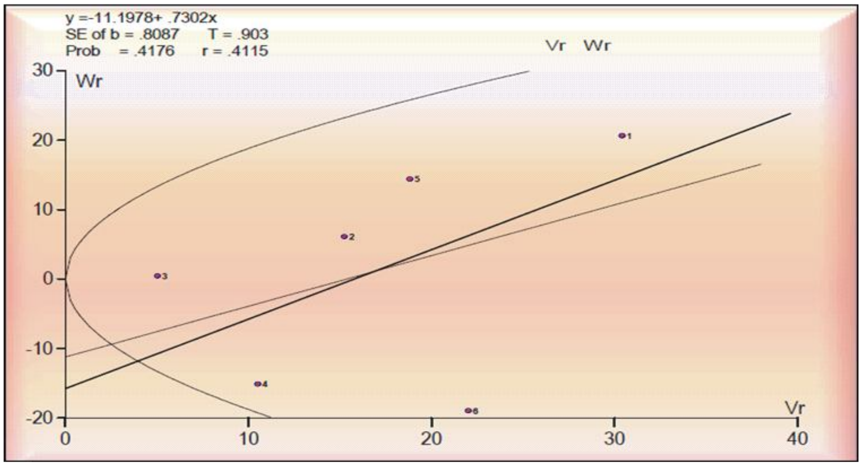


**Fig. 2 :** Vr-Wr graph for Days to maturity

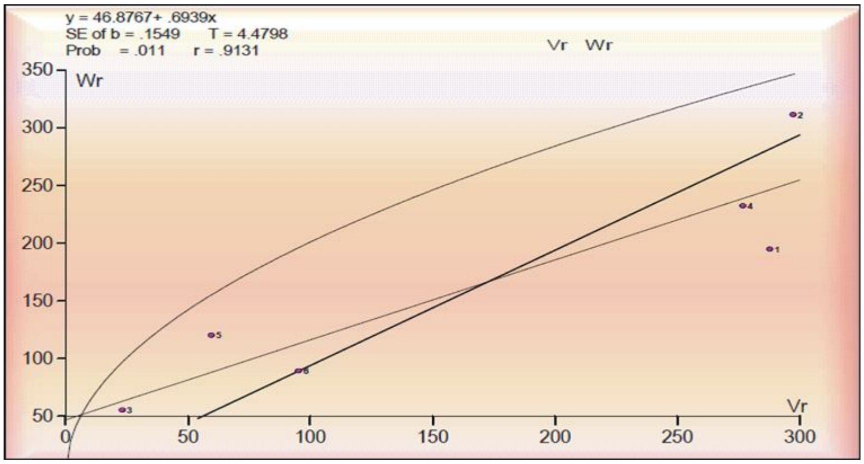


**Fig. 3 :** Vr-Wr graph for Plant height cm

deviation from unity, as in case of days to 50% flowering and days to maturity (Fig.1 and 2). The regression line intersected the Wr-axis below the origin which revealed over-dominance. Parental line HUBR 10-9 exhibited greater proportion of recessive alleles whereas Type 3 exhibited greater proportion of dominant alleles for the trait. The remaining HUBR-16 and Taraori Basmati possess nearly equal proportion of dominance and recessive genes as they fell nearly in the middle of the regression lines. Parents Basmati 370 and Sonowal Basmati were closer and below the origin and thus they were under the influence of epistasis.

Likewise, in case of panicle length (Fig. 4), the scattered points over the regression line revealed diversity among parents. Occurrence of parental points away from the origin indicated high influence of G × E interaction. Parental lines Taraori Basmati and Type 3 exhibited higher proportion of recessive alleles for the trait whereas Sanowal basmati exhibited greater proportion of dominant alleles for the trait. HUBR 10-9, Basmati 370 and HUBR-16 possess almost equal proportion of dominant and recessive genes The regression line cuts the Wr axis below the origin point suggesting over dominance gene action. Similarly, over dominance gene action gene action was found for kernel length before and after cooking traits (fig. 6 and 7). Parents Type 3 and Basmati 370 possessed higher proportion of recessive alleles, whereas parents HUBR 10-9, Taraori basmati, HUBR-16, and Sonowal basmati revealed more proportion of dominant alleles for kernel length before cooking. However, for kernel length after cooking, Parent Taraori basmati, Sonowal basmati, Type 3 and HUBR 10-9 are found to having higher proportion of dominant alleles while, Parents Basmati 370 and HUBR-16 were having higher proportion of recessive alleles. With over dominance kind of gene action for Alkali Spread Value (Fig. 8), Parent Sonowal basmati was farthest from origin and thus revealed highest proportion of recessive alleles, whereas parents HUBR-16, Basmati 370, Taraori basmati and Type 3 showed almost equal proportion of dominant and recessive alleles. Parent HUBR 10-9 found closest to origin and thus it has highest proportion of dominant genes.

Over dominance of days to 50% flowering, plant height, panicle length, and grain yield per plant in rice

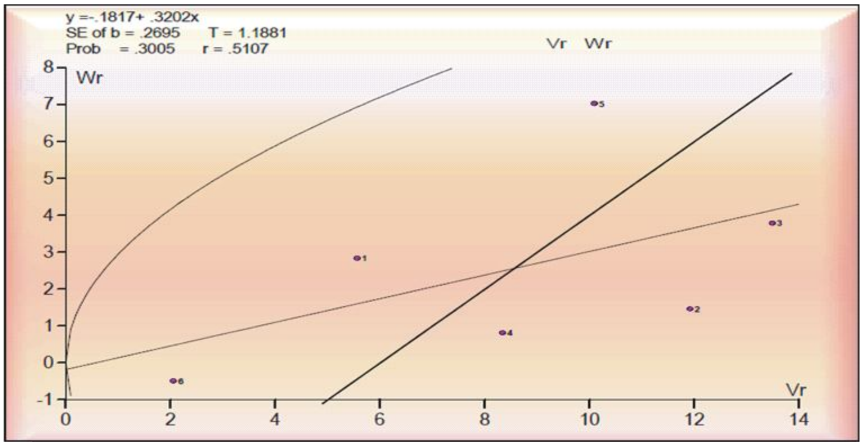


**Fig. 4 :** Vr-Wr graph for Panicle length cm

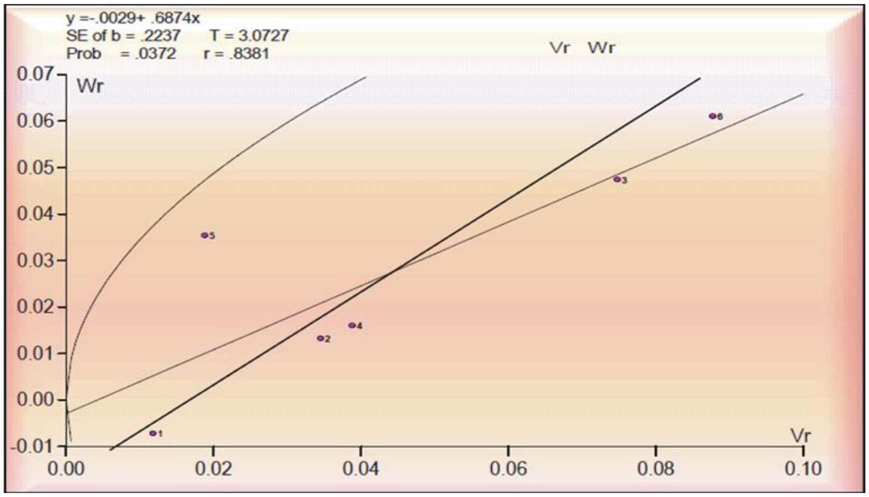


**Fig. 5** : Vr-Wr graph for 100-Grain weight

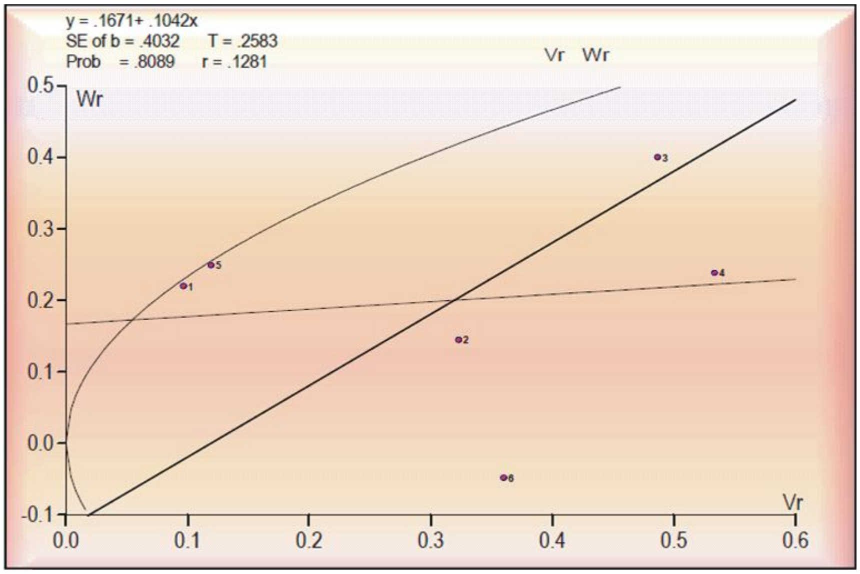


**Fig. 6 :** Vr-Wr graph for Kernel length

was also reported by Chaturvedi *et al.,* (2015) which are in agreement with present finding. Raju *et al.,* (2011) in a similar kind of study found over dominance for plant height, and panicle length. He also reported that for ear bearing tillers per plant, the deviations of regression coefficient from zero were not significant. Hence, Vr-Wr graph were not plotted. This is similar to present finding. In further studies, Xu and Shen (1991) reported both partial dominance and over dominance for inheritance of tillers per plant in rice. Ilieva *et al*., (2013) also reported over-dominance for grain yield per plant in rice.

## Component analysis

Estimates of components of genetic variations and the various ratios from them are presented in table 2. The component D which reflect the additive genetic variance was significant for all the characters studied except for effective tillers per plant, seeds per panicle, grain yield per plant, kernel breadth after cooking and amylose content indicating the importance of additive gene effects in their inheritance. The sign of component F indicates the relative frequencies of dominant and recessive alleles in the parents. In the present study, the values for most of the characters except for effective tillers per plant, seeds per panicle and grain yield per plant, were positive and greater than zero, expressing preponderance of dominant alleles over recessive alleles. The component $H_1$, which measures the dominance variation, was significant for all the characters indicating the importance of dominance gene effects in controlling them. Likewise, the component $H_2$ was significant for all the traits except for kernel length, indicating dominance with asymmetry of positive and negative effects. Environmental estimate, E was positive for all the characters indicating the definite influence of environment in the expression of the characters. Asymmetrical distribution of dominant and recessive alleles in parents was corroborated by the direction of F. The significant and positive F value indicated the prevalence of dominant alleles in parents for most of the characters except for effective tillers per plant, seeds per panicle and grain yield per plant.

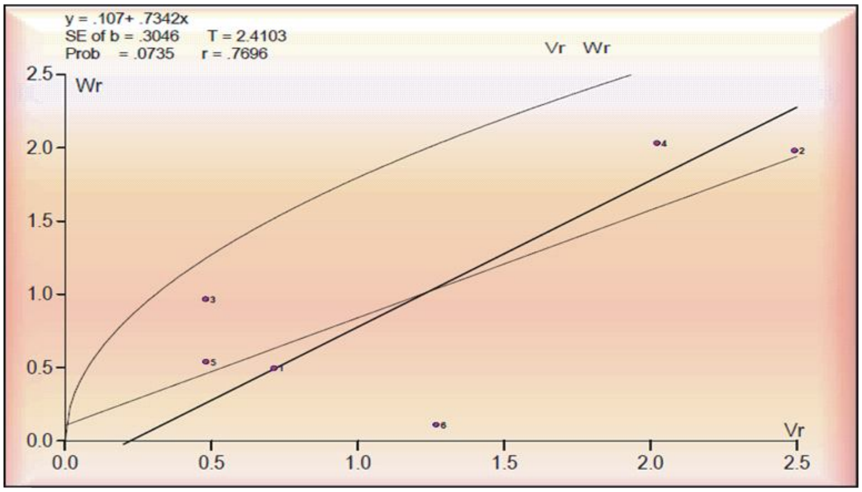
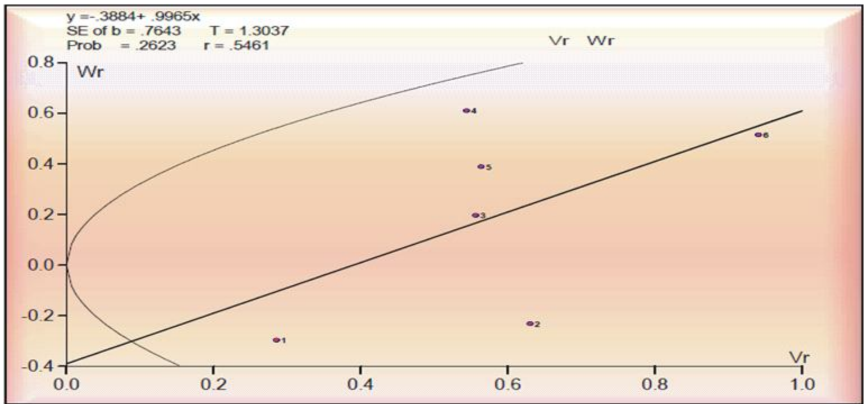


**Fig. 7 :** Vr-Wr graph for Kernel length after cooking



1. HUBR 10-9, 2. HUBR-16, 3. Type 3, 4. Basmati 370, 5. Taraori Basmati, 6. Sonowal Basmati

**Fig. 8** : Vr-Wr graph for Alkali spread value

Further, the ratio $(H_1/D)^{0.5}$ which measured the mean degrees of dominance over all loci was more than one indicating over dominance for all the characters. This was also confirmed by the negative Y intercept in the Vr-Wr graph for the same trait. The ratio, $H_2/4H_1$ was close to 0.25 for characters effective tillers per plant, panicle length, grain yield per plant, kernel breadth, amylose content indicating nearly symmetrical distribution of positive and negative alleles at loci showing dominance for the traits. Ratio of dominant to recessive genes *i.e.* KD/KR was more than one for all characters except days to 50% flowering and seeds per panicle showing presence of excess of dominant genes in parental inbreds, while it was close to unity for grain yield per plant and effective tillers per plant showing equal proportion of dominant and recessive genes among parents. Ratio $h^2/H_2$ ranged from 0.008 for kernel breadth after cooking to 2.163 for kernel breadth revealing that at least one to two genes or group of genes showing dominance were present for these traits. The heritability in narrow sense ($h^2n$) was more than 50% for Plant Height, Seed per panicle, Kernel length and Kernel Length After cooking indicated major part of additive gene action in phenotypic variability in nature and selection should be effective for improvement of these characters in rice.

Torres and Geraldi, (2006) found the predominant direction of dominance effects was negative for days to 50% flowering, and positive for all the other characters in rice. Petchiammal and Kumar, (2007) in a similar study in rice found a significant role of additive gene action for days to 50% flowering, plant height, panicle length, grains per panicle, yield per plant, spikelet fertility, 1000-grain weight and harvest index. Ashfaq *et al.,* (2012) based on the genetic component analysis in rice, found that both additive and non-additive components appeared to be important in the inheritance of most of the traits. Morphological traits *viz.*, plant height, productive tillers per plant and 1000 seed weight showed over dominance type of gene action in both environments (control and drought environments), while seeds per panicle and seed length width ratio showed this type of gene action only in drought conditions. The seeds per panicle and length width ratio showed additive type of gene action with partial dominance only in normal irrigation conditions. Adilakshmi and Upendra, (2014**)** found that the characters *viz.*, L/B ratio, volume expansion ratio, amylose, iron and zinc contents are predominantly governed by non-additive gene action. However, the role of additive component of gene action appeared to be considerable along with non-additive effect for head rice recovery, L/B ratio and elongation ratio. Aditya & Bhartiya, (2015) found preponderance of dominant gene action for plant height, days to 50% flowering, days to maturity, grains per panicle, fertile grains per panicle, 1000 grain weight, kernel length, kernel width, L/B ratio and grain yield per plant in their study.

## Conclusion

On the basis of significant deviation of 'b' from zero and non significant deviation of 'b' from unity, valid graphical analysis were done for the traits like plant height, 100 seed weight, days to 50% flowering, days to maturity, kernel length before and after cooking, panicle length and alkali spread value. The regression line intersected the Wr axis below the origin point suggesting over dominance gene action in all the characters studied through graphical analysis thus, it would be worth while to examine these in the development of hybrids. Similarly, component D, which reflects the additive genetic variance, was also found significant for the characters studied like days to 50% flowering, days to maturity, kernel length before and after cooking, panicle length, plant height, 100 seed weight and alkali spread value, indicating the importance of additive gene effects in their inheritance and selection would be rewarding for these traits. Moreover estimates like $H_1$, $H_2$, and proportion of components like $(H_1/D)^{0.5}$, $H_2/4H_1$ KD/KR and $h^2/H_2$ for different traits revealed further information regarding dominance and recessive alleles involved in their inheritance. Likewise, heritability in narrow sense ($h^2n$) was more than 50% for Plant Height, Seed per panicle, Kernel length and Kernel Length After cooking indicated major part of additive gene action in phenotypic variability and selection should be effective for improvement of these characters in rice.

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