# Genetic analysis of yield and quality traits in Basmati rice

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## ABSTRACT

*Genetic components of variance for yield and yield contributing traits were carried out by using 8 x 8 diallel mating design excluding reciprocals. Results revealed that both additive and non-additive gene effects were important for the inheritance of characters studied with preponderance of later for all traits, except 1000-grain weight, kernel breath, kernel L/B ratio, content of amylose and alkali spreading value. The significance of gene distribution indicated the presence of gene asymmetry except for panicle length. High-narrow sense heritability further supported the importance of additive gene effects for 1000-grain weight, kernel breath, kernel L/B ratio, content of amylose and alkali spreading value. Since non-additive/dominance components were higher than the additive for most of the characters in F1 generation, therefore, biparental mating and/or reciprocal recurrent selection could be used for genetic improvement of these characters.*

*Key words: diallel mating, additive and non-additive gene effects, heritability, dominance*

Crop breeding for economic traits had received attention since long and this factor has been fully exploited in rice. Among different methods to assess the nature of gene action in the parents, the diallel cross technique (Hayman, 1954a) is a systematic method. Now the yield level of Basmati rice has almost reached a plateau, further breakthrough in yield level may be obtained by exploiting certain traits related to yield. Yield components of HYV's vary with different levels of interactions depending on the genetic constitution of the parents. The information on genetic nature of yield contributing traits is, therefore, important for developing potential genotypes for targeted ecosystem by manipulating these traits. With this view, the present study was undertaken to understand the genetics of sixteen traits in progenies in order to select suitable parent for different eco-geographical situations of rice cultivation.

The material comprised of eight basmati rice varieties namely, Pant Sugandh Dhan 15, Basmati 370, Type 3, Pant Sugandh Dhan 17, Pusa Basmati 1, Pusa sugandh 4, UPR 2845-6-3-1, UPR 3003-11-1-1. The 36 entries (28 crosses and 8 parents) were grown in a randomised block design with two replications at the

G. B. Pant University of Agriculture and Technology, Pantnagar (Uttarakhand). Single seedling per hill was transplanted with a spacing of 20 x 15 cm. The $F_1$s and parents were planted in a two row plot of 2 meter length. Data were recorded on 5 random but competitive plants, leaving border plant on each side of each genotype (Dhaliwal and Sharma, 1990). Observations were recorded on 16 characters *viz.* days to 50% flowering (DF), plant height (PH), flag leaf length (FL), flag leaf breath (FB), panicle length (PL), panicles plant$^{-1}$ (PN), grain number panicle$^{-1}$ (GP), 1000-grain weight (TW), grain yield plant$^{-1}$ (GY), biological yield plant$^{-1}$ (BY), harvest index (HI), kernel length (KL), kernel breath (KB), kernel L/B ratio (LBR), amylose content (AC) and alkali spreading value (AS). The statistical procedures of Hayman (1954b) for genetic component analysis, Allard (1960) for broad sense heritability, Hayman (1954) and Griffing (1956) for narrow sense heritability, Allard (1960) for estimation of genetic advance in $F_1$ were followed.

The genetic components and relative proportion of various components are given in table 1, and an overview of components of variance is given in table

2. The variance analysis revealed the preponderance of non-additive genetic variance for all the characters except 1000-grain weight, kernel breath, kernel L/B ratio, amylose content and alkali spreading value. The estimates of dominant components were higher than additive components suggesting that dominance variances were more important. The importance of dominance variances has also been reported earlier in rice by Mishra and Singh (1998) for plant height, biological yield, harvest index and grain yield. The estimate of $H_2$ component was smaller than $H_1$ for most of the traits reflecting unequal proportion of positive and negative alleles at loci governing these traits in parents. The value of $H_2/4H_1$ also indicate that the dominant genes having increasing and decreasing effects on various yield contributing traits are irregularly distributed in parents (Sharma, 1995) except for Panicle length, which indicated almost equal proportion of positive and negative alleles. Estimates of degree of dominance indicated overdominance for all the characters except 1000-grain weight, kernel breath, kernel L/B ratio, amylose content and alkali spreading value for which partial dominance was observed. The ratio of dominant and recessive alleles (KD/KR) indicated the presence of dominant alleles in excess for most of the traits except, days to 50% flowering, grain number panicle$^{-1}$ and harvest index. The non-significant estimate of E for plant height, panicles per plant, grain number panicle$^{-1}$, grain yield plant$^{-1}$, biological yield plant$^{-1}$, and harvest index indicated that the expression of these traits were least influenced by environment (Verma, 2003).

High heritability was recorded for the characters grain yield per plant, biological yield per plant, harvest index, panicles plant$^{-1}$, grain number panicle$^{-1}$, plant height, it was moderate for days to 50% flowering and amylose content however traits like panicle length, kernel length, flag leaf length, flag leaf breath, alkali spreading value, 1000-grain weight, kernel L/B ratio and kernel breath show low heritability. Highest magnitude of genetic advance was observed for biological yield plant$^{-1}$, followed by grain number panicle$^{-1}$, plant height, grain yield plant$^{-1}$ and harvest index. The high value of genetic advance as percent of mean coupled with high heritability was observed for characters like grain yield plant$^{-1}$, biological yield plant$^{-1}$, panicles plant$^{-1}$, harvest index and plant height suggested that genotypic variance in parent material

**Table 1.** Estimates of genetic components of variance for different characters in basmati rice

| Component | DF | PH (cm) | FL (cm) | FB (cm) | PL (cm) | PN | GP | GY(g) | TW (g) | BY(g) | HI (%) | KL (mm) | KB (mm) | LBR (mm) | AC | AS |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| D | 19.85 ±13.72 | 410.30* ±132.82 | 29.31** ±6.45 | 0.01 ±0.009 | 0.699 ±0.972 | 2.215 ±9.75 | 195.14 ±248.77 | 26.58 ±43.63 | 6.18** ±1.08 | 96.67 ±287.15 | 11.63 ±8.06 | 0.32** ±0.08 | 0.010** ±0.004 | 0.11** ±0.028 | 1.81** ±0.231 | 0.1878** ±0.049 |
| $H_1$ | 84.68* ±31.53 | 942.29* ±305.35 | 43.17* ±14.83 | 0.025 ±0.021 | 3.44 ±2.24 | 152.23** ±22.41 | 2215.10** ±571.892 | 729.14** ±100.3 | -2.477 ±2.49 | 4079.04** ±660.11 | 130.50** ±18.52 | 0.48* ±0.18 | 0.007 ±0.009 | 0.038 ±0.064 | 1.79** ±0.532 | -0.011 ±0.113 |
| $H_2$ | 73.56** ±27.43 | 874.35** ±265.65 | 20.17 ±12.90 | 0.023 ±0.018 | 3.404 ±1.945 | 140.26** ±19.49 | 1785.79** ±497.55 | 589.37** ±87.26 | -4.66* ±2.16 | 3506.64** ±574.29 | 105.81** ±16.11 | 0.31* ±0.15 | 0.0047 ±0.008 | 0.046 ±0.056 | 0.89 ±0.46 | -0.027 ±0.98 |
| $h^2$ | 4.36 ±18.40 | 535.10* ±178.16 | 18.37* ±8.65 | 0.0053 ±0.012 | 21.77** ±1.30 | 236.526** ±13.07 | 1047.28* ±333.68 | 1148.73** ±58.52 | -1.62 ±1.45 | 7839.42** ±385.14 | 37.53** ±10.81 | 0.08 ±0.10 | 0.013* ±0.54 | -0.037 ±0.0373 | -0.014 ±0.31 | 0.315** ±0.661 |
| F | -17.1 ±32.41 | 62.76 ±313.85 | 51.63** ±15.24 | 0.012 ±0.021 | 0.4 ±2.298 | 7.88 ±23.03 | -61.06 ±587.83 | 5.99 ±103.1 | 5.05* ±2.56 | 139.69 ±678.5 | -0.88 ±19.04 | 0.48* ±0.18 | 0.015 ±0.0095 | 0.096 ±0.066 | 2.39** ±0.55 | 0.123 ±0.116 |
| E | 11.68* ±4.57 | 39.94 ±44.28 | 16.22** ±2.15 | 0.014** ±0.0029 | 1.61** ±0.32 | 3.13 ±3.25 | 60.93 ±82.93 | 1.57 ±14.54 | 4.48* ±0.36 | 13.97 ±95.71 | 1.97 ±2.68 | 0.14** ±0.026 | 0.010** ±0.133 | 0.13** ±0.0093 | 0.29** ±0.077 | 0.157** ±0.016 |
| $(H_1/D)^{0.5}$ | 2.066 | 1.52 | 1.22 | 1.39 | 2.22 | 8.29 | 3.37 | 5.24 | 0.63 | 6.49 | 3.35 | 1.24 | 0.82 | 0.59 | 0.994 | 0.25 |
| $(H_2/4H_1)$ | 0.22 | 0.23 | 0.12 | 0.234 | 0.247 | 0.23 | 0.2 | 0.2 | 0.47 | 0.21 | 0.2 | 0.61 | 0.17 | 0.3 | 0.125 | 0.6 |
| $(KD/KR)$ | 0.65 | 1.1 | 6.29 | 2.01 | 1.298 | 1.55 | 0.911 | 1.04 | 4.64 | 1.25 | 0.98 | 3.4 | 18.36 | 6.75 | 4.93 | -7.02 |

*, ** = Significant at 5% and 1% Probability levels, respectively. D = Additive gene effect, $H_1$ = dominance effect, $H_1$ = dominance effect, F = Relative frequency of dominant to recessive allele, $(H_1/D)^{0.5}$ = Degree of dominance, $(H_2/4H_1)$ = Ratio of positive and negative alleles, $(KD/KR)$ = Ratio of dominant and recessive genes

**Table 2.** Components of variance and various ratios for different characters.

| Characters | Variance component fraction | | | | Ratio | | |
|---|---|---|---|---|---|---|---|
| | D | $H_1$ | $H_2$ | $h^2$ | $(H_2/D)^{0.5}$ | $(H_2/4H_1)$ | KD/KR |
| Days to 50% flowering | ns | s | s | ns | Over dominance | Unequal | Recessive genes |
| Plant height (cm) | s | s | s | s | Over dominance | Unequal | Dominant genes |
| Flag leaf length (cm) | s | s | ns | s | Over dominance | Unequal | Dominant genes |
| Flag leaf breath (cm) | ns | ns | ns | ns | Over dominance | Unequal | Dominant genes |
| Panicle length (cm) | ns | ns | ns | s | Over dominance | Nearly equal | Dominant genes |
| Panicles per plant (Number) | ns | s | s | s | Over dominance | Unequal | Dominant genes |
| Grain number panicle$^{-1}$ | ns | s | s | s | Over dominance | Unequal | Recessive genes |
| 1000-grain weight (gm) | s | ns | s | ns | Partial dominance | Unequal | Dominant genes |
| Grain yield Plant$^{-1}$ (g) | ns | s | s | s | Over dominance | Unequal | Dominant genes |
| Biological yield plant$^{-1}$ (g) | ns | s | s | s | Over dominance | Unequal | Dominant genes |
| Harvest index (HI) (%) | ns | s | s | s | Over dominance | Unequal | Recessive genes |
| Kernel length (mm) | s | s | s | ns | Over dominance | Unequal | Dominant genes |
| Kernel breath (mm) | s | ns | ns | s | Partial dominance | Unequal | Dominant genes |
| Kkernel L/B ratio (mm) | s | ns | ns | ns | Partial dominance | Unequal | Dominant genes |
| Amylose content | s | s | ns | ns | Partial dominance | Unequal | Dominant genes |
| Alkali spreading | s | ns | ns | s | Partial dominance | Unequal | Dominant genes |

D = Additive gene effect, $H_1$ = dominance effect, F = Relative frequency of dominant to recessive allele, $(H_1/D)^{0.5}$ = Degree of dominance, $(H_2/4H_1)$ = Ratio of positive and negative alleles, (KD/KR) = Ratio of dominant and recessive genes

for these characters might be due to appreciably high additive genetic components and selection for the improvement of these traits will be rewarding.

However, relatively higher magnitude of difference between PCV and GCV values for flag leaf length, flag leaf breath, panicle length, 1000-grain weight, kernel length, kernel breath, kernel L/B ratio, amylose content and alkali spreading value indicated more environmental influence in its expression which is also supported by values of heritability and genetic advance as percent of mean because high value of heritability is associated with low value of genetic advance. The high heritability is being exhibited due to favourable influence of environment rather than genotype so selection for these traits will not be rewarding.

**Table 3.** Estimates of heritability and genetic advance for various characters in rice

| Character | Range | Mean | SEm ± | GCV | PCV | Heritability (%) | Expected Genetic Advance | GA as % of mean |
|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | 98.5-123.0 | 109.30 | 2.42 | 5.92 | 6.69 | 78.18 | 11.78 | 10.77 |
| Plant height (cm) | 98.9-172.0 | 143.04 | 4.47 | 14.25 | 14.92 | 91.23 | 40.11 | 28.04 |
| Flag leaf length (cm) | 22.2-45.0 | 36.62 | 2.85 | 10.85 | 15.45 | 49.33 | 5.74 | 15.67 |
| Flag leaf breath (cm) | 1.07-1.70 | 1.38 | 0.084 | 8.53 | 12.08 | 49.90 | 0.17 | 12.31 |
| Panicle length (cm) | 27.5-33.8 | 31.63 | 0.898 | 4.73 | 6.20 | 58.15 | 2.35 | 7.42 |
| Panicles plant$^{-1}$ (Number) | 13.2-36.5 | 23.12 | 1.25 | 26.79 | 27.86 | 92.47 | 12.26 | 53.02 |
| Grain number panicle$^{-1}$ | 26.46-128.9 | 68.46 | 5.52 | 38.86 | 40.50 | 92.07 | 52.59 | 76.81 |
| 1000-grain weight (gm) | 16.25-29.08 | 21.53 | 1.50 | 8.31 | 12.87 | 41.68 | 2.38 | 11.05 |
| Grain yield Plant$^{-1}$ (g) | 13.75-64.5 | 33.44 | 0.887 | 43.80 | 43.96 | 99.27 | 30.06 | 89.89 |
| Biological yield plant$^{-1}$ (g) | 47.5-157.5 | 100.68 | 2.64 | 33.37 | 33.57 | 98.78 | 68.78 | 68.31 |
| Harvest index (HI) (%) | 19.82-42.34 | 32.35 | 0.993 | 19.33 | 19.81 | 95.20 | 12.57 | 38.85 |
| Dehulled kernel length (mm) | 5.9-7.8 | 6.86 | 0.268 | 6.38 | 8.44 | 57.24 | 0.68 | 9.91 |
| Dehulled kernel breath (mm) | 1.45-1.9 | 1.74 | 0.071 | 4.57 | 7.37 | 38.57 | 0.10 | 5.74 |
| Dehulled kernel L/B ratio (mm) | 3.17-4.68 | 3.95 | 0.252 | 7.39 | 11.67 | 40.05 | 0.38 | 9.62 |
| Endosperm content of amylose | 20.25-24.72 | 23.15 | 0.38 | 3.43 | 4.14 | 68.52 | 1.35 | 5.83 |
| Gelatinization temperature | 5.33-7.00 | 6.34 | 0.28 | 5.74 | 8.49 | 45.70 | 0.50 | 7.88 |

It is apparent from the present study that both non-additive and additive genetic effects are important with preponderance of previous one in the inheritance of most of the characters which may be utilized through selection in the early segregating generation exploiting the fixable effects. To utilize both types of genetic effect breeding method like modified recurrent selection i.e. alternating pedigree and recurrent selection cycles (Khadr and Frey, 1965); diallel selective mating (Jensen, 1970), multiple crossing and early generation selection followed by intermating among $F_2/F_3$ generation of selected plants (Redden and Jensen, 1974) is proposed for further improvement in the crop.

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