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## **Association Analysis for Yield and Quality Attributes in *Indica* Rice and Screening of Hybrids Against Blast Disease (*Magnaporthe grisea* Barr.)**

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### **ABSTRACT**

Rice is mostly grown in the Asian subcontinent and known by its good cooking qualities. Its production is, however, often constrained by several biotic factors. The present study may be useful for the development of resistant lines against the blast disease possess high yielding capacity. Thirty nine *Indica* rice genotypes were used to study the extent of genetic parameter and association analysis for quantitative and qualitative traits. These genotypes were screened against blast disease of rice by artificial inoculation in field. All quantitative and qualitative traits exhibited highly significant difference ( $p < 0.01$ ) among treatments, it indicates the adequate genetic variability among the genotypes under study. Estimates of genotypic and phenotypic coefficient of variation were high for filled grains per plant, total grains per plant, panicle initiation and Grain Yield per Plant (GYPP). Heritability was high ( $> 80\%$ ) for all the characters except head rice recovery, hulling percentage and kernel breadth; indicates the roles of additive gene action and a good scope of selection using their phenotypic performance. GYPP showed strong positive association with yield contributing traits while non-significant association with rest of the traits. In blast screening, none of the varieties and  $F_1$  hybrids found highly resistant. Among the parental lines, Anjali was resistant, HUR3022, Vandana, HUR105 and BPT5204 were moderately resistant and six lines were moderately to highly susceptible. Among the hybrids, only two hybrids (Anjali  $\times$  BPT 5204 and Annada  $\times$  BPT 5204) were found resistant to rice blast disease.

**Key words:** Moderately resistant, blast disease, heritability, path analysis, *Indica* rice

### **INTRODUCTION**

Rice is one of the most important staple food crop of the world and over half of the global population depends on it for their feed (Sasaki, 2005). Presently more than 114 countries cultivated rice over an area of 161.4 m ha in a wide range of ecosystems under varying temperature and water regimes with annual production of 466.7 m t (on milled basis) (FAO, 2011). It is cultivated in both tropical and subtropical regions. In India, the total area under rice production is about 45 m ha (22% of cropped area), an annual production of 104.3 m t with productivity of 23.7 q ha and contributes 25% to total agricultural GDP (FAO, 2011; Rice Profile, 2013). The world population will grow up to 8.5 billion till 2030 and 9 billion in 2050 for that to feed this growing population about 40% more rice will be required.

Agricultural scientists and plant breeders are facing great challenges in crop improvement due to climate change. Factors such as water insufficiency, decrease in cultivated land, new emerging pathogen and pest dynamics are greatly influenced. Several ways like amendment of soil conditions, adequate irrigation facility, cultural techniques and breeding of high yielding varieties can be employed for enhancing the yield of rice. Rice ranks second amongst cereal cultivation around the globe, but unfortunately, its production is constrained by considerable number diseases caused by various pathogens which include bacteria, fungi, viruses and nematodes. The fungus *Pyricularia oryzae* Cavara [synonym *Pyricularia grisea* Sacc. the anamorph of *Magnaporthe grisea* (Herbert) Yaegashi and Udagawa] causes blast disease of rice, is one of the most destructive and wide spread disease (Jia *et al.*, 2000). Blast disease produces significant yield loss in many rice growing countries and upto 75 and 50% losses have been reported from India and Philippines, respectively. Studies on crop loss assessment have revealed that this disease reduces grain yield to varying levels and it depends on several factors like stage of the crop, degree of cultivar susceptibility and environmental conditions favouring disease incidence (Gnanamanickam *et al.*, 1999). Application of fungicides, resistant cultivars, agronomic practices and biotechnological methods have proved useful in managing the diseases (Ribot *et al.*, 2008). Basic knowledge on genetic variability, heritability, its association, direct and indirect effect of yield contributing traits are of prime importance in order to make any necessary genetic improvement of grain yield in rice by employing methods of conventional breeding. Selection criteria can be formulated using these informations (Allard, 1999).

The estimates of heritability together with genetic advance and correlation for quantitative and qualitative traits can be achieved by selection of better parents and crosses of high yielding varieties (Burton, 1952; Johnson *et al.*, 1955). Some of the rice traits to be improved through breeding programmes include reduced plant height, effective tillers per hill, increased kernel number per panicle, increased 1000 grain weight and higher yield (Paterson *et al.*, 2005; Ullah *et al.*, 2011). The method of path coefficient analysis partitions the genetic correlation between yield attributes and quality traits into direct and indirect effects and hence has been effectively employed in identifying useful traits as selection criteria to improve grain yield in rice and other crops (Kole *et al.*, 2008; Singh, 2012). The management of rice blast disease by the use of resistant cultivars which has proved to be most economical and environment friendly (Castano *et al.*, 1990; Haq *et al.*, 2002; Chandrashekara *et al.*, 2008). But, with the appearance of new virulent races of the pathogen, this resistant can break down/over-come.

In this experiment, we studied the genetic variability, heritability, genetic advance, correlation and path coefficient analysis for yield and quality traits. Screening against blast disease resistance among *indica* rice (cultivars and hybrids) was done to develop multiple disease resistant varieties which combine high yield potential and possess quality characters. This study also reports the screening/evaluation of cultivar and hybrids for identifying sources of resistance against blast disease.

## MATERIALS AND METHODS

**Experimental sites and material (genotypes):** The present experiment was carried out at Agriculture Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (UP), India. The experimental site situated at 17.5°N latitude, 78.27°E longitude and altitude of 545 m above to mean sea level. The experimental material of rice (Table 1) staggered sown at ten

Table 1: Parental description of *Indica* rice cultivar, its pedigree and features

| Name of cultivars | Parentage and year of release | Specific features of <i>Indica</i> rice cultivars   |
|-------------------|-------------------------------|---|
| Anjali            | RR-19-2x RR-149-1129 (2001)   | Semi dwarf, 90-95 days to maturity, grains-short bold, white; tolerant to drought, resistant to BS, resistant to blast and sheath blight; yield: 30-35 q ha <sup>-1</sup>                             |
| HUR 3022          | IR 36xHR 137 (2005)           | Semi dwarf (100 cm); 105 days to maturing, grains-long slender, fine, tolerant to bacterial leaf blight, sheath blight, resistant to leaf and neck blast; yield: 48-50 q ha <sup>-1</sup>             |
| Vandana           | C-22xKalakeri (1992)          | Tall (95-155 cm), early maturing, grains-long bold, white, moderately resistance to termite and sheath blight, blast and bacterial leaf blight; yield: 30-35 q ha <sup>-1</sup>                       |
| Govind            | IR 20xIR 2 (1983)             | Dwarf, early maturing, long slender grain, flowering in 75 days, yield: 35-40   |
| Annada            | MTU-15xYaikaku Nantoku (1988) | 110-112 days to maturing, short statured grains, moderately resistant to blast and stem borer, susceptible to bacterial leaf blight, gall midth, brown plant hopper; yield: 45- 50 q ha <sup>-1</sup> |
| NDR 97            | Nagina 22xRatna (1992)        | Medium, early maturing, medium slender, flowering in 70 days, yield: 40- 45 q ha <sup>-1</sup>  |
| Shanthi           | RatnaxIR-36 (2002)            | Semi dwarf, 120-130 days to maturity, grains-long slender, resistant to blast, moderately resistant to sheath rot, brown spot and, white brown plant hopper; yield : 50 q ha <sup>-1</sup>            |
| HUR 4-3           | Mutant of Lanjhi (2009)       | Semi dwarf 90-100 cm, 135-140 days to maturity, grains-long slender, resistant to leaf roller and brown plant hopper, moderately resistant to bacterial leaf blight; yield: 52-54 q ha <sup>-1</sup>  |
| HUR 105           | Mutant of MPR 7-2 (2009)      | Semi dwarf (100-102 cm), 130-135 days to maturity, grains-long slender, tolerant to leaf and neck blast, sheath blast, sheath blight, yield: 58-60 q ha <sup>-1</sup>                                 |
| MTU 7029          | VasistaxMashuri (1982)        | Dwarf, 140 days to maturity, medium slender grain shape, resistant to bacterial leaf blight and tolerant to many diseases, yield: 55-60 q ha <sup>-1</sup>  |
| BPT 5204          | GEB24xTN-1+Mahsuri (1986)     | Dwarf, 140-150 days to maturity, low grain, medium grain length, fine and medium slender decorticated grain shape, yield: 55-65 q ha <sup>-1</sup>  |

days interval in nursery bed during 5th, 15th and 25th June, 2009. Twenty one days old seedling was transplanted in crossing block (Kharif, 2009). The crosses were made between the parents in linextester mating design to produce 28 F<sub>1</sub> hybrids. Thereafter, 11 parents and 28 crosses (39 genotypes) of *indica* rice were again sown to generate the seedlings in June, 2010 and it transplant in well paddled field during Kharif, 2010 (July, 2010) under Randomized Block Design with three replications.

**Cultural practices and fertilizer application:** Each entry was transplanted in three row of 3 m length spaced at 20 cm apart and the distance between plant to plant (15 cm) was maintained. The experimental field was kept free from weeds by adopting manual weeding. The fertilizers were applied at the rate of 120 kg nitrogen (N), 60 kg phosphorus (P<sub>2</sub>O<sub>5</sub>) and 60 kg potash (K<sub>2</sub>O) through Urea (46%), Single super phosphate (18%) and murate of potash (60%) ha<sup>-1</sup> under well irrigated condition. Half of N and full dose of P<sub>2</sub>O<sub>5</sub> and K<sub>2</sub>O used as basal dose before transplanting in irrigated field. Remaining half of nitrogen was applied at a time of tillering. All the recommended cultural practices and plant protection measures (except blast disease control measure) were followed for raising the vigorous crop.

Table 2: Standard screening scale (0-9 grade for disease rating) was used for blast disease of *Indica* rice (Source-IRRI, 1996; Ghazanfar *et al.*, 2009)

| Grade | Disease severity  | Host response               |
|-------|---|-----------------------------|
| 0     | Lesion are not present  | Highly resistant (HR)       |
| 1     | Small brown specks of pin point size on lower leaves  | Resistant (R)               |
| 2     | Small roundish to slightly elongated, necrotic gray spots, about 1-2 mm in diameter, with a distinct brown margin. Lesions are mostly found on the lower leaves | Moderately resistant (MR)   |
| 3     | Lesion type same as in 2, but significant number of lesions on the upper leaves   | Moderately resistant (MR)   |
| 4     | Typical susceptible blast lesions, 3 mm or longer infecting less than 4% of leaf area   | Moderately susceptible (MS) |
| 5     | Typical susceptible blast lesions of 3 mm or longer infecting 4-10% of the leaf area  | Moderately susceptible (MS) |
| 6     | Typical susceptible blast lesions of 3 mm or longer infecting 11-25% of the leaf area   | Susceptible (S)             |
| 7     | Typical susceptible blast lesions of 3 mm or longer infecting 26-50% of the leaf area   | Susceptible (S)             |
| 8     | Typical susceptible blast lesions of 3 mm or longer infecting 51-75% of the leaf area many leaves are dead  | Highly susceptible (HS)     |
| 9     | Typical susceptible blast lesions of 3 mm or longer infecting more than 75% leaf area affected  | Highly susceptible (HS)     |

**Disease scoring and screening techniques:** After germination, the crop was regularly watched for appearance of major diseases. The pathogen may infect all the aboveground parts of a rice plant at different growth stages: Leaf, collar, node, internodes, base, or neck and other parts of the panicle and sometimes the leaf sheath. A typical blast lesion on a rice leaf is gray at the center, has a dark border and is spindle-shaped. The observations on disease appearance were recorded on the basis of ten randomly selected plants from each genotype at maximum disease occurrence. The data recorded on disease appearance and disease scoring scored on the basis of disease severity following 0-9 scale as given and suggested by IRRI (1996) and Ghazanfar *et al.* (2009) which is stated below and mention in Table 2.

**Observation recorded and data collection:** The observations were recorded from randomly selected plants in parents and F<sub>1</sub> hybrids in each replication for all eighteen quantitative and qualitative traits studied. Plant height (PH-cm), effective tillers per plant (ET/P), filled grains per plant (FG/P), total grains per plant (TG/P) and spikelet fertility (SF-%) were measured before physiological maturity from randomly selected 10 (parents) and 20 (F<sub>1</sub> hybrids) sample plants in each plot. At maturity, Grain Yield per Plant (GY/P-g) was taken from the middle row and yield was adjusted at 13% moisture level. Test Weight (TW-g) or thousand grain weight was determined from bulked grains collected from middle rows of each plot and recorded on 12% seed moisture basis. After threshing, hulling percentage (HP-%), milling percentage (MP-%), head rice recovery (HRR-%), kernel length (KL-mm), kernel width (KB-mm) and kernel length breadth ratio (KL/B R-%) were taken from bulked seed sample collected from middle row of replication. Data on panicle initiation (PI-days), 50% panicle emergence (FPE-days), days to 50% flowering (DFF-days) and days to maturity (DM-days) were also collected on the plot basis.

**Statistical analysis:** The collected data for studied traits were pooled for statistical analysis. The genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability ( $h^2_{bs}$ ) broad sense, genetic advance and correlation coefficients were analyzed by standard statistical procedure (Singh and Chaudhary, 1995) and statistical software Windostat ver. 8.3. The path coefficient analysis was done by Dewey and Lu (1959). The disease scoring data were generated based on the standard Evaluation System for rice (IRRI, 1996) for disease screening on ten randomly selected plants. Average disease severity (ASC) and percent disease intensity (PDI) were recorded with the help of following equation which are given below (IRRI, 1996):

$$ASC = \frac{(N-1 \times 0) + (N-2 \times 1) + (N-3 \times 3) + (N-4 \times 5) + (N-5 \times 7) + (N-6 \times 9)}{\text{No. of leaf samples}} \times 100$$

$$PDI = \frac{(N-1 \times 0) + (N-2 \times 1) + (N-3 \times 3) + (N-4 \times 5) + (N-5 \times 7) + (N-6 \times 9)}{\text{No. of leaf samples} \times 9} \times 100$$

where, N-1 to N-6 represents frequency of leaves in the respective score.

## RESULTS AND DISCUSSION

The analysis of variance (ANOVA) shown in Table 3. On the basis of ANOVA examination of the pooled data, it appears that all quantitative and qualitative traits exhibited highly significant difference ( $p < 0.01$ ) among the treatments. However, 50% panicle emergence and kernel breadth

Table 3: Analysis of variance (ANOVA) and estimates on genetic parameters for different yield and quality characters in *Indica* rice cultivars

| Characters             | df | PI        | FPE       | DF        | DM        | PH        | PL        | ET/P    | FG/P       | TG/P       |
|------------------------|----|-----------|-----------|-----------|-----------|-----------|-----------|---------|------------|------------|
| Replication            | 2  | 0.171     | 4.223*    | 0.529     | 0.380     | 0.003     | 0.0080    | 0.255   | 14.417     | 3.536      |
| Treatments             | 41 | 817.648** | 801.152** | 771.405** | 778.678** | 995.222** | 21.4410** | 8.717** | 5007.110** | 6579.730** |
| Error                  | 82 | 1.109     | 1.171     | 1.278     | 1.231     | 1.793     | 1.0400    | 0.524   | 4.858      | 11.499     |
| GCV                    |    | 18.890    | 16.770    | 15.740    | 12.360    | 16.480    | 10.4100   | 16.130  | 27.250     | 26.950     |
| PCV                    |    | 18.930    | 16.810    | 15.780    | 12.390    | 16.530    | 11.1700   | 17.610  | 27.290     | 27.020     |
| ECV                    |    | 1.210     | 1.120     | 1.110     | 0.850     | 1.220     | 4.0700    | 7.060   | 1.470      | 1.950      |
| Heritability ( $h^2$ ) |    | 99.600    | 99.660    | 99.500    | 99.510    | 99.510    | 86.7200   | 83.900  | 99.710     | 99.500     |
| Genetic advance        |    | 33.920    | 33.570    | 32.930    | 33.080    | 37.390    | 5.0100    | 3.120   | 83.990     | 96.140     |
| GA as % of mean        |    | 38.830    | 34.470    | 32.350    | 25.390    | 33.860    | 19.9600   | 30.440  | 56.050     | 55.380     |
| Range                  | L  | 58.430    | 68.160    | 73.270    | 101.990   | 81.590    | 19.7800   | 6.780   | 91.350     | 100.850    |
|                        | H  | 114.830   | 123.510   | 127.610   | 155.180   | 146.020   | 30.4000   | 13.780  | 220.780    | 246.980    |
| Mean                   |    | 87.350    | 97.370    | 101.790   | 130.260   | 110.410   | 25.0700   | 10.250  | 149.870    | 173.620    |
| SE                     |    | 0.610     | 0.630     | 0.650     | 0.640     | 0.770     | 0.5900    | 0.420   | 1.270      | 1.960      |
| CD at 5%               |    | 1.710     | 1.760     | 1.840     | 1.810     | 2.180     | 1.6600    | 1.180   | 3.580      | 5.510      |
| Characters             | df | SF (%)    | TW        | H (%)     | M (%)     | HRR (%)   | KL        | KB      | KL/BR      | GY/P       |
| Replication            | 2  | 1.118     | 2.253     | 0.013     | 2.481     | 8.233     | 0.052     | 0.024*  | 0.025      | 0.119      |
| Treatments             | 41 | 112.678** | 13.611**  | 40.302**  | 47.557**  | 30.514**  | 0.818**   | 0.075** | 0.456**    | 78.681**   |
| Error                  | 82 | 1.508     | 0.966     | 3.275     | 3.028     | 4.170     | 0.039     | 0.008   | 0.011      | 1.442      |
| GCV                    |    | 7.230     | 9.360     | 4.690     | 6.090     | 5.140     | 8.720     | 7.270   | 13.430     | 18.490     |
| PCV                    |    | 7.370     | 10.380    | 5.270     | 6.690     | 6.240     | 9.360     | 8.410   | 13.930     | 18.990     |
| ECV                    |    | 1.460     | 4.480     | 2.410     | 2.750     | 3.540     | 3.400     | 4.220   | 3.720      | 4.380      |
| Heritability ( $h^2$ ) |    | 96.110    | 81.320    | 79.030    | 83.110    | 67.800    | 86.800    | 74.800  | 92.910     | 94.710     |
| Genetic advance        |    | 12.290    | 3.820     | 6.440     | 7.230     | 5.030     | 0.980     | 0.270   | 0.760      | 10.170     |
| GA as % of mean        |    | 14.590    | 17.390    | 8.580     | 11.440    | 8.720     | 16.740    | 12.960  | 26.650     | 37.060     |
| Range                  | L  | 69.340    | 18.250    | 65.950    | 54.010    | 50.400    | 5.160     | 1.810   | 2.060      | 17.630     |
|                        | H  | 93.520    | 27.710    | 85.750    | 71.620    | 64.070    | 7.120     | 2.590   | 3.620      | 35.720     |
| Mean                   |    | 84.280    | 21.930    | 74.980    | 63.210    | 57.670    | 5.840     | 2.060   | 2.870      | 27.450     |
| SE                     |    | 0.710     | 0.570     | 1.050     | 1.010     | 1.180     | 0.120     | 0.050   | 0.060      | 0.690      |
| CD at 5%               |    | 1.990     | 1.590     | 2.940     | 2.830     | 3.320     | 0.330     | 0.140   | 0.170      | 1.950      |

\*,\*\*Significant at 5 and 1% level of probability, respectively; df: Degree of freedom, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, ECV: Environmental coefficient of variation, GA: Genetic advance, SE: Standard error, CD: Critical difference, PI: Panicle initiation (days), FPE: 50% panicle emergence (days), DF: Days to 50% flowering (days), DM: Days to maturity (days), PH: Plant height (cm), ET/P: Effective tillers per plant, FG/P: Filled grain per plant, TG/P: Total grains per plant, SF: Spikelet fertility, TW: Test weight, H: Hulling (%), M: Milling (%), HRR: Head rice recovery, KL: Kernel length, KB: Kernel width, K L/B R: Kernel length width ratio, GY/P: Grain yield per plant

showed significant ( $p < 0.05$ ) variation among replication. The critical differences for all the qualitative and yield traits in *indica* rice were ranged from 0.14 (kernel breadth) to 5.51 (total grains panicle<sup>-1</sup>). This indicates the adequate genetic variability among the genotypes under study. It exhibits that selection had considerable effect on the mean performance of the studied traits. These results are in good agreement of Garg *et al.* (2011) and Ullah *et al.* (2011).

### **Genetic parameters**

**Genotypic and phenotypic coefficient of variation:** Generally, estimates of Phenotypic Coefficient of Variation (PCV) were slightly greater than Genotypic Coefficient of Variation (GCV) for the entire quantitative and qualitative traits (except some quality traits). The extent of environmental (influence due to environment) coefficient of variation (ECV) is explained by the amount of the difference between GCV and PCV and it ranged from 1.11 (days to 50% flowering) to 7.06 (effective tillers per panicle). However, the estimates of GCV (ranged from 4.69 to 27.25) and PCV (ranged from 5.27 to 27.29) were high for filled grains per plant, total grains per plant, panicle initiation and grains yield per plant (Table 3) and environmental coefficient of variability was found very low to moderate direction, it indicates the genotypes are least influence by the environments. These results were in conformity with the findings of Ahmadikhah (2010). Other characters showed low to moderate estimates of coefficient of variability; it is suggested that hybridization involving diverse genotypes may lead to an overall increase in spectrum of variability in rice (Seyoum *et al.*, 2012).

**Heritability and genetic advance:** Heritability broad sense ( $h^2_{b_s}$ ) estimates were found high (>85%) for all the characters except effective tillers per plant, test weight, head rice recovery, hulling percentage and kernel breadth which ranged from 67.80-99.70%. Genetic Advance (GA) for different characters ranged from 0.27% (kernel breadth) to 96.14% (total grains panicle<sup>-1</sup>) and were high for total grains per plant, filled grains per plant, plant height, panicle initiation, 50% panicle emergence, days to maturity and days to 50% flowering. However, GA as percent of mean varied from 8.58 (hulling%) to 56.05 (filled grains per panicle). It was high for filled grains per plant, panicle initiation, total grains per plant, grain yield per plant, 50% panicle emergence, plant height, days to 50% flowering and effective tillers per plant. High heritability (broad sense) associated with high genetic advance revealed the control of traits by additive gene effects and selection may be effective for those characters and there is considerable potential for developing high yielding varieties through selection of desirable plants in succeeding generations. The results are in line of various reports in this area of research (Ahmadikhah, 2010; Garg *et al.*, 2011; Singh, 2012).

**Correlation coefficient analysis:** The genetic architecture of grain yield in rice is based on the balance or overall net effect produced by various yield components interactive with one another. Therefore, selection would not be effective as such unless accompanied by the selection for various component traits responsible for conditioning it. Thus, identification of important yield components and information about their interrelationship with yield and also each other will be very useful in developing high yielding variety (Johnson *et al.*, 1955; Singh, 2012). The correlation coefficient provides the degree of association between two variables or characters. The nature and magnitude of association among yield and quality traits are important for the breeder to make an effective selection.

The genotypic and phenotypic correlation coefficients between yield and quality attributes are presented in Table 4. A very strong positive association of grain yield per plant was observed with total grains per panicle (0.459 and 0.447), fertile grains per panicle (0.533 and 0.517), effective tillers per panicle (0.388 and 0.347), days to maturity (0.682 and 0.662), days to 50% flowering (0.678 and 0.661), 50% panicle emergence (0.671 and 0.654) and panicle initiation (0.670 and 0.652); a non-significant positive association was formed with panicle length (0.152 and 0.145), plant height (0.167 and 0.160), head rice recovery (0.241 and 0.208), kernel breadth (0.273 and 0.223) while negative but significant association was observed with kernel length/breadth ratio (-0.495 and -0.457) and kernel length (-0.505 and -0.454) at both genotypic as well as phenotypic levels. Generally, genotypic association is greater than phenotypic association. Thus, these characters emerged as most important associates for grain yield plant in rice. The available literatures also identified the above traits as important associates of grain yield in rice (Krishnaveni and Rani, 2006; Sharma and Sharma, 2007; Yogameenakshi and Vivekanandan, 2010).

Panicle initiations, 50% panicle emergence, days to 50% flowering and days to maturity exhibited highly significant positive association to most of the traits except plant height (0.047 and 0.049), spikelet fertility (-0.211 and -0.210) and with few quality traits. Similarly, panicle length confirmed positive significant association with maturing traits and plant height (0.377 and 0.337) and non-significant association with grain yield per plant (0.152 and 0.145), effective tillers per plant (0.273 and 0.182), fertile grains per plant (0.233 and 0.223), total grains per plant (0.233 and 0.209), test weight (0.269 and 0.169) and with some quality traits. However, spikelet fertility, milling percentage, kernel length and kernel length/breadth ratio were exhibited negative association with most of the yield traits. The characters, total grains per panicle, fertile grains per panicle, effective tillers per panicle, days to maturity, days to 50% flowering, panicle length and spikelet fertility were most important yield influencing traits. The occurrence of positive association at significant level of grain yield with most of its component traits and positive association between most of the yield components reveals less complex inter relationship between yield and yield components. Such situation is favourable from breeding point of view because selection for one trait may bring correlated response for improvement of other traits which are positively associated with it. These findings are broadly in agreement with some of the earlier reports of Sharma and Sharma (2007), Yogameenakshi and Vivekanandan (2010) and Seyoum *et al.* (2012).

**Path coefficient analysis:** Path coefficient analysis measures the direct influence of one variable (independent variable i.e., yield) upon the other variable (dependent variable i.e., yield and quality traits) and permits separation of correlation coefficients into components of direct and indirect effects. The actual information on contributing characters was provided by portioning of correlation into direct and indirect effects. Path analysis has emerged as a powerful and widely used technique for understanding the direct and indirect contribution of different characters to economic yield in crop plants so that relative importance of various yield contributing traits may be estimated (Kole *et al.*, 2008; Singh, 2012).

Path coefficient analysis was carried out by using simple correlation coefficient among 17 traits (Table 5). The high positive direct contribution towards grain yield per plant was exhibited by days to maturity (0.770) followed by panicle initiation (0.734), days to 50% flowering (0.532), fertile grains per panicle (0.296), effective tillers per plant (0.117) and spikelet fertility (0.031) in quantitative traits and, kernel length (0.543) and milling percentage (0.023) in qualitative traits.





Table 5. Genotypic and phenotypic direct and indirect effects of different yield and quality traits in parental and hybrids lines of *Indica* rice

| Character | PI | FPE     | DF      | DM      | PH     | PL      | ET/P    | FG/P    | TG/P    | SF (%)  | TW     | H (%)   | M (%)  | HRR (%) | KL      | KB     | KL/B R  | GY/P   |
|-----------|----|---------|---------|---------|--------|---------|---------|---------|---------|---------|--------|---------|--------|---------|---------|--------|---------|--------|
| PI        | G  | 71.515  | 71.138  | 70.918  | 3.388  | 23.945  | 23.110  | 40.932  | 43.732  | -15.071 | -9.114 | 8.838   | -8.174 | 17.506  | -30.806 | 7.064  | -25.695 | 0.670  |
|           | P  | 0.734   | 0.729   | 0.726   | 0.036  | 0.225   | 0.216   | 0.418   | 0.448   | -0.154  | -0.088 | 0.084   | -0.075 | 0.140   | -0.294  | 0.066  | -0.256  | 0.652  |
| FPE       | G  | -86.843 | -86.581 | -86.358 | -5.347 | -29.014 | -28.395 | -50.528 | -53.798 | 18.004  | 9.899  | -12.202 | 8.574  | -22.057 | 37.925  | -9.907 | 32.212  | 0.671  |
|           | P  | -1.492  | -1.497  | -1.489  | -0.092 | -0.465  | -0.443  | -0.867  | -0.922  | 0.305   | 0.156  | -0.182  | 0.136  | -0.303  | 0.605   | -0.153 | 0.536   | 0.654  |
| DF        | G  | -0.171  | -0.172  | -0.172  | -0.008 | -0.056  | -0.058  | -0.097  | -0.104  | 0.038   | 0.019  | -0.027  | 0.016  | -0.045  | 0.075   | -0.019 | 0.064   | 0.678  |
|           | P  | 0.528   | 0.529   | 0.530   | 0.026  | 0.158   | 0.162   | 0.298   | 0.321   | -0.117  | -0.054 | 0.075   | -0.045 | 0.112   | -0.217  | 0.052  | -0.191  | 0.661  |
| DM        | G  | 15.725  | 15.759  | 15.833  | 15.858 | 4.798   | 5.332   | 8.971   | 9.668   | -3.524  | -1.805 | 2.342   | -1.621 | 4.070   | -6.793  | 1.536  | -5.669  | 0.682  |
|           | P  | 0.761   | 0.763   | 0.767   | 0.026  | 0.214   | 0.232   | 0.433   | 0.468   | -0.168  | -0.077 | 0.102   | -0.068 | 0.157   | -0.305  | 0.066  | -0.265  | 0.662  |
| PH        | G  | 0.089   | 0.116   | 0.089   | 0.062  | 1.885   | 0.711   | 0.468   | -0.104  | -0.224  | -0.368 | 0.813   | 0.269  | 0.152   | -0.194  | 1.100  | -0.674  | 0.167  |
|           | P  | 0.007   | 0.009   | 0.007   | 0.005  | 0.139   | 0.047   | 0.031   | -0.008  | -0.016  | -0.027 | 0.054   | 0.019  | 0.049   | -0.014  | 0.070  | -0.048  | 0.160  |
| PL        | G  | -0.259  | -0.258  | -0.251  | -0.234 | -0.292  | -0.211  | -0.180  | -0.181  | 0.174   | -0.208 | -0.169  | 0.068  | -0.013  | 0.208   | -0.187 | 0.247   | 0.152  |
|           | P  | -0.041  | -0.042  | -0.040  | -0.037 | -0.045  | -0.134  | -0.030  | -0.028  | 0.022   | -0.023 | -0.018  | 0.015  | 0.000   | 0.028   | -0.025 | 0.036   | 0.145  |
| ET/P      | G  | -0.022  | -0.022  | -0.023  | -0.017 | -0.019  | -0.068  | -0.022  | -0.033  | 0.023   | -0.001 | 0.001   | 0.011  | -0.025  | 0.017   | -0.017 | 0.021   | 0.388  |
|           | P  | 0.034   | 0.035   | 0.036   | 0.035  | 0.026   | 0.117   | 0.035   | 0.051   | -0.037  | 0.007  | -0.006  | -0.019 | 0.034   | -0.024  | 0.017  | -0.028  | 0.347  |
| FG/P      | G  | 0.446   | 0.453   | 0.439   | 0.441  | -0.043  | 0.181   | 0.248   | 0.779   | 0.123   | -0.154 | 0.118   | 0.027  | 0.122   | -0.448  | 0.089  | -0.359  | 0.533  |
|           | P  | 0.169   | 0.172   | 0.166   | 0.167  | -0.017  | 0.066   | 0.087   | 0.296   | 0.047   | -0.051 | 0.037   | 0.008  | 0.039   | -0.157  | 0.029  | -0.130  | 0.517  |
| TG/P      | G  | 0.417   | 0.422   | 0.412   | 0.415  | -0.081  | 0.159   | 0.330   | 0.579   | 0.681   | -0.062 | 0.149   | 0.015  | 0.095   | -0.297  | 0.041  | -0.233  | 0.459  |
|           | P  | -0.106  | -0.106  | -0.104  | -0.105 | 0.020   | -0.036  | -0.075  | -0.146  | -0.173  | 0.017  | 0.020   | -0.037 | -0.005  | 0.071   | -0.009 | 0.057   | 0.447  |
| SF (%)    | G  | -0.075  | -0.074  | -0.079  | -0.079 | -0.070  | -0.080  | -0.123  | -0.033  | 0.357   | -0.040 | 0.012   | 0.111  | 0.021   | -0.008  | -0.014 | 0.006   | -0.090 |
|           | P  | -0.007  | -0.006  | -0.007  | -0.007 | -0.006  | -0.005  | -0.010  | -0.003  | 0.031   | -0.003 | 0.000   | 0.008  | 0.001   | 0.000   | -0.001 | 0.001   | -0.088 |
| TW (%)    | G  | -0.055  | -0.049  | -0.047  | -0.049 | 0.186   | 0.116   | 0.005   | -0.053  | -0.049  | 0.432  | 0.057   | -0.008 | 0.000   | 0.047   | 0.209  | -0.069  | -0.046 |
|           | P  | 0.001   | 0.001   | 0.001   | 0.001  | -0.003  | -0.001  | 0.000   | 0.001   | 0.001   | -0.007 | -0.001  | 0.000  | 0.000   | 0.000   | -0.003 | 0.001   | -0.053 |
| H (%)     | G  | -0.022  | -0.025  | -0.027  | -0.026 | -0.025  | -0.038  | -0.027  | -0.039  | -0.006  | -0.023 | -0.176  | -0.128 | -0.064  | 0.004   | -0.055 | 0.030   | -0.014 |
|           | P  | -0.014  | -0.014  | -0.017  | -0.016 | -0.017  | -0.016  | -0.015  | -0.026  | -0.001  | -0.011 | -0.119  | -0.078 | -0.037  | 0.007   | -0.030 | 0.020   | -0.012 |
| M (%)     | G  | -0.149  | -0.129  | -0.124  | -0.134 | 0.105   | -0.214  | 0.045   | 0.029   | 0.405   | -0.024 | 0.949   | 1.307  | 0.511   | 0.253   | 0.240  | 0.072   | -0.090 |
|           | P  | -0.002  | -0.002  | -0.002  | -0.002 | -0.003  | -0.004  | 0.001   | 0.001   | 0.006   | 0.000  | 0.015   | 0.023  | 0.007   | 0.003   | 0.003  | 0.001   | -0.112 |
| HRR (%)   | G  | -0.255  | -0.254  | -0.275  | -0.257 | -0.451  | -0.379  | -0.163  | -0.146  | -0.062  | 0.002  | -0.378  | -0.407 | -1.042  | 0.198   | -0.541 | 0.388   | 0.241  |
|           | P  | -0.005  | -0.005  | -0.006  | -0.005 | -0.009  | -0.008  | -0.003  | -0.003  | -0.001  | 0.000  | -0.008  | -0.008 | -0.026  | 0.004   | -0.010 | 0.008   | 0.208  |
| KL        | G  | -1.288  | -1.305  | -1.311  | -1.281 | -0.307  | -0.802  | -1.721  | -1.303  | -0.063  | 0.323  | -0.066  | 0.579  | -0.568  | 2.991   | -1.422 | 2.716   | -0.505 |
|           | P  | -0.217  | -0.219  | -0.221  | -0.215 | -0.055  | -0.114  | -0.288  | -0.222  | -0.001  | 0.036  | -0.030  | 0.082  | -0.092  | 0.543   | -0.165 | 0.463   | -0.454 |
| KB        | G  | -0.181  | -0.208  | -0.201  | -0.177 | -1.067  | -0.442  | -0.209  | -0.109  | 0.072   | -0.884 | -0.569  | -0.335 | -0.949  | 0.869   | -1.828 | 1.455   | 0.273  |
|           | P  | -0.037  | -0.042  | -0.040  | -0.035 | -0.208  | -0.076  | -0.040  | -0.022  | 0.015   | -0.142 | -0.103  | -0.063 | -0.156  | 0.126   | -0.412 | 0.309   | 0.223  |
| KL/B R    | G  | 1.798   | 1.855   | 1.856   | 1.789  | 1.791   | 1.599   | 1.525   | 2.307   | 1.708   | -0.080 | 0.802   | -0.277 | 1.863   | -4.546  | 3.984  | -5.005  | -0.495 |
|           | P  | 0.338   | 0.348   | 0.348   | 0.334  | 0.338   | 0.234   | 0.428   | 0.323   | -0.026  | 0.129  | 0.160   | -0.035 | 0.302   | -0.829  | 0.728  | -0.971  | -0.457 |

Residual effect = 0.241; \*Bold figure indicate the direct effects, PI= panicle initiation (days), FPE = 50% panicle emergence (days), DF = Days to 50% flowering (days), DM = Days to maturity (days), PH = Plant height (cm), ET/P = Effective tillers per plant, FG/P = Filled grain per plant, TG/P = Total grains per plant, SF = Spikelet fertility, TW = Test weight, H = Hulling (%), M = milling (%), HRR = head rice recovery (%), KL = kernel length, KB = kernel width, K L/B R = kernel length width ratio, GY/P = grain yield per plant

These characters have also been identified as major direct contributors towards grain yield in rice by earlier workers Krishnaveni and Rani (2006) and Seyoum *et al.* (2012). However, 50% panicle emergence (-1.497), total grains per plant (-0.173), panicle length (-0.134), kernel length/breadth ratio (-0.971) and hulling percentage (-0.119) were the traits having substantial negative direct effect on grain yield per plant.

The quantitative traits, total grains per panicle (0.468), fertile grains per panicle (0.433), panicle initiation (0.761), 50% panicle emergence (0.763) and days to 50% flowering (0.767) exerted substantial positive indirect effect on grain yield per plant via days to maturity. Among qualitative traits, kernel length (0.463) and kernel breadth (0.309) was important indirect contributors to grain yield via kernel length/breadth ratio. This suggest that traits, total grains per panicle, effective tillers per plant, fertile grains per panicle, days to 50% flowering, kernel breadth and kernel length were the most important indirect contributor to grain yield. Some of the earlier reports have also identified such characters as important indirect contributors towards expression of grain yield in rice (Krishnaveni and Rani, 2006; Kole *et al.*, 2008; Ullah *et al.*, 2011).

**Disease screening of *indica* rice genotypes (parents and F<sub>1</sub> hybrids):** Blast caused by fungus *Magnaporthe grisea* Barr (*Pyricularia oryzae*) is responsible for spotting and blasting of the foliage and for blighting of the panicles. The sequential apparent infection rate between observation periods were better correlated with disease progress than total apparent infection rate between the first and last observations. The disease appearance is rapidly increases and more destructive, when the rainfall and atmospheric humidity both are high under field condition. Hence, the use of resistant varieties is considered to be the best method of controlling the disease and few reports are available on the screening of entries against the blast disease. Therefore, the present study was carried out to find out the sources of resistance against blast disease of rice. A total of 39 genotypes of *Indica* rice were screened under field conditions during Kharif 2009 and 2010 and the results obtained for variable reaction on the basis of Percent Disease Intensity (PDI) to the blast disease are presented in Table 6.

Table 6: Responses of *Indica* rice genotypes on the basis of screening and percent disease intensity (PDI) results to blast disease caused by *Magnaporthe grisea* Barr. (*Pyricularia oryzae*)

| Genotypes | Resistant                                    | Moderately resistant   | Moderately susceptible  | Susceptible   | Highly susceptible                     |
|-----------|--|--|---|---|--|
| Parents   | Anjali                                       | HUR 3022, Vandana,<br>HUR 105 and BPT 5204   | Govind and Annada   | NDR 97, Shanthi<br>and HUR 4-3  | MTU 7029                               |
| Crosses   | Anjali×BPT<br>5204 and<br>Annada×BPT<br>5204 | Anjali×HUR 4-3,<br>HUR Anjali×MTU 7029,<br>HUR 3022×HUR 4-3,<br>HUR 3022×HUR 105,<br>HUR 3022×MTU 7029,<br>3022×BPT 5204,<br>Vandana×HUR 4-3,<br>Vandana×HUR 105,<br>Govind×HUR 105,<br>Annada×HUR 4-3,<br>Annada×HUR 105,<br>Shanthi×HUR 4-3<br>and Shanthi×HUR 105 | Anjali×HUR 105,<br>Govind×BPT 5204<br>and Vandana×BPT<br>5204 | Vandana×MTU 7029,<br>Govind×HUR 4-3,<br>Govind×MTU 7029,<br>Annada×MTU 7029,<br>NDR 97×MTU 7029,<br>NDR 97×HUR 105,<br>NDR 97×BPT 5204,<br>and Shanthi×BPT 5204 | Shanthi×MTU 7029<br>and NDR 97×HUR 4-3 |

Out of the 39 genotypes of *indica* rice were screened on the basis of PDI against blast disease of rice, none of the parents showed highly resistant reaction. Cultivar Anjali was found to be resistant and 4 cultivars HUR 3022, Vandana, HUR 105 and BPT 5204 were moderately resistant. However, cultivar Govind and Annada were found moderately susceptible and 3 cultivars NDR 97, Shanthi and HUR 4-3 showed susceptible reaction. Only one cultivar MTU 7029 was found to be highly susceptible to the blast disease. Similar results were also in accordance of the reports by Haq *et al.* (2002) in screening of 25 rice germplasm lines and found that two lines KSK-282 and IRRI-6 were highly resistant. Similarly, Arshad *et al.* (2008) screened 40 entries/varieties in the field against the blast disease; it revealed that only three entries from different places showed resistant reaction against blast disease.

In F<sub>1</sub> hybrids, two hybrids (Anjali×BPT 5204 and Annada×BPT 5204) were found resistant by regarding 1 grade to the blast disease. However, 13 crosses showed moderately resistant reaction to the blast disease. The three F<sub>1</sub> hybrids (Anjali×HUR 105, Vandana×BPT 5204 and Govind×BPT 5204) showed moderately susceptible reactions and the other remaining eight F<sub>1</sub> hybrids were susceptible by regarding 6 and 7 grade to the blast disease. The only two F<sub>1</sub> hybrids (Shanthi×MTU 7029 and NDR 97×HUR 4-3) exhibited highly susceptible reaction by regarding 8 grade to the blast disease. These results are in good agreement with the result of Ghazanfar *et al.* (2009). Chandrashekara *et al.* (2008) screened 265 germplasm of rice and reported that eight genotypes showed resistant to blast and 138 genotypes exhibited moderately resistant reaction as observed in the present study.

## CONCLUSION

The screening of rice genotypes against the blast disease and its association study for quality traits were also carried out in other countries. In this study, it was concluded that genotypes/lines having blast resistance coupled with good yield and quality traits are selected. These genotypes/lines can be used in future breeding programmes for the development of high yielding multiple disease resistant hybrids.

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## REFERENCES

- Ahmadikhah, A., 2010. Study on selection effect, genetic advance and genetic parameters in rice. *Annal. Biol. Res.*, 1: 45-51.
- Allard, R.W., 1999. Principles of Plant Breeding. John Wiley and Sons Inc., New York, USA., ISBN-13: 9780471023098, Pages: 254.
- Arshad, H.M.I., J.A. Khan and F.F. Jamil, 2008. Screening of rice germplasm against blast and brown spot disease. *Pak. J. Phytopathol.*, 20: 52-57.
- Burton, G.W., 1952. Quantitative inheritance in grasses. Proceedings of the 6th International Grassland Congress, August 17-23, 1952, Pennsylvania State College, USA., pp: 277-283.
- Castano, J.B., B. Amril, D. Syahril and Z. Zaini, 1990. Upland rice genotypes resistant to blast (B1) disease in West Sumatra. *Int. Rice Res. Newslett.*, 15: 11-12.
- Chandrashekara, M.V., G. Sunkad, M.K. Naik and P. Nagaraju, 2008. Screening of rice genotypes against blast caused by *Pyricularia oryzae* cavara. *Karnataka J. Agric. Sci.*, 21: 305-305.
- Dewey, D.R. and K.H. Lu, 1959. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agron. J.*, 51: 515-518.

- FAO, 2011. GIEWS country briefs. Food and Agriculture Organization of the United Nation, Rome, Italy. <http://www.fao.org/giews/countrybrief/>
- Garg, P., D.P. Pandey and D. Singh, 2011. Genetic variability for yield and quality traits in rice (*Oryza sativa* L.). *Res. Crops*, 12: 182-184.
- Ghazanfar, M.U., A. Habib and S.T. Sahi, 2009. Screening of rice germplasm against *Pyricularia oryzae* the cause of rice blast disease. *Pak. J. Phytopathol.*, 21: 41-44.
- Gnanamanickam, S.S., V.B. Priyadarisini, N.N. Narayanan, P. Vasudevan and S. Kavitha, 1999. An overview of bacterial blight disease of rice and strategies for its management. *Curr. Sci.*, 77: 1435-1444.
- Haq, I.M., M. Fadnan, F.F. Jamil and A. Rehman, 2002. Screening of rice germplasm against *Pyricularia oryzae* and evaluation of various fungi toxicants for control of disease. *Pak. J. Phytopathol.*, 14: 32-35.
- IRRI, 1996. Standard Evaluation System for Rice. 4th Edn., International Rice Research Institute (IRRI), Los Banos, Philippines, Pages: 52.
- Jia, Y., S.A. McAdams, G.T. Bryan, H.P. Hershey and B. Valent, 2000. Direct interaction of resistance gene and avirulence gene products confers rice blast resistance. *EMBO J.*, 19: 4004-4014.
- Johnson, H.W., H.F. Robinson and R.E. Comstock, 1955. Estimates of genetic and environmental variability in soybean. *Agron. J.*, 47: 314-318.
- Kole, P.C., N.R. Chakraborty and J.S. Bhat, 2008. Analysis of variability, correlation and path coefficients in induced mutants of aromatic non-basmati rice. *Trop. Agric. Res. Exten.*, 113: 60-64.
- Krishnaveni, B. and N.S. Rani, 2006. Association of grain yield with quality characteristics and other yield components in rice. *Oryza*, 43: 320-322.
- Paterson, A.H., M. Freeling and T. Sasaki, 2005. Grains of knowledge: Genomics of model cereals. *Genome Res.*, 15: 1643-1650.
- Ribot, C., J. Hirsch, S. Balzergue, D. Tharreau, J.L. Notteghem, M.H. Lebrun and J.B. Morel, 2008. Susceptibility of rice to the blast fungus, *Magnaporthe grisea*. *J. Plant Physiol.*, 165: 114-124.
- Rice Profile, 2013. Rice profile, production, productivity and export. <http://agricoop.nic.in/imagedefault/trade/Rice%20profile.pdf>
- Sasaki, T., 2005. The map-based sequence of the rice genome. *Nature*, 436: 793-800.
- Seyoum, M., S. Alamerew and K. Bantte, 2012. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). *J. Plant Sci.*, 7: 13-22.
- Sharma, A.K and R.N. Sharma, 2007. Genetic variability and character association in early maturing rice. *ORYZA-Int. J. Rice*, 44: 300-303.
- Singh, R.K. and B.D. Chaudhary, 1995. *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publisher, Ludhiana, New Delhi, ISBN: 978-3-659-247897, pp: 342.
- Singh, P., 2012. *Genetic Analysis in Lentil: Genetic Analysis and Breeding Tools for Improvement of Lentil*. Lambert Academic Publishers, Saarbrücken, Germany, ISBN: 8176633070, Pages: 117.
- Ullah, M.Z., M.K. Bashir, M.S.R. Bhuiyan, M. Khalequzzaman and M.J. Hasan, 2011. Interrelationship and cause-effect analysis among morpho-physiological traits in birain rice of Bangladesh. *Int. J. Plant Breed. Genet.*, 5: 246-254.
- Yogameenakshi, P. and P. Vivekanandan, 2010. Association analysis in F1 and F2 generations of rice under reproductive stage drought stress. *Electron. J. Plant Breed.*, 1: 890-898.