

GENETIC VARIABILITY AND ASSOCIATION OF YIELD ATTRIBUTING TRAITS WITH GRAIN YIELD IN UPLAND RICE

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A study was undertaken to find out the genetic variability and correlation between yield and other yield attributing characters of rice genotypes in upland ecology. The experiment was conducted with twenty two upland genotypes grown during Wet season under direct seeded condition in a randomized block design. Analysis of variance shows significance in all the traits indicating the presence of considerable amount of genetic variation among the genotypes. The traits like plant height, ear bearing tiller and yield has high genotypic coefficient of variance, phenotypic coefficient of variance and genetic advance. Plant height, ear bearing tiller, panicle length, panicle weight and length were positively and significantly correlated with yield. Plant height and grain per panicle, 50% flowering, thousand grain weight and ear bearing tiller has high direct effect on yield. Therefore, selection based on plant height, 50% flowering, thousand grain weight and ear bearing tiller could be more effective in upland rice.

Key words: correlation, direct effect, genetic advance, heritability, path analysis, rice

INTRODUCTION

Rice (*Oryza sativa* L.) is the staple food for a large proportion of the world's population (ZHANG, 2007). In India, rain fed upland rice accounts for 6.00 million hectares, which is 13.5% of the total rice area in the country where farmers mostly used traditional early rice varieties and contributing low productivity i.e. 0.6 to 1.5 t ha⁻¹. Development of high yielding genotypes under such conditions requires a thorough knowledge of existing genetic variation and extent of association of yield contributing characters. Yield revolution witnessed in irrigated areas following the introduction of plant type based high yielding varieties in mid sixties bypassed the eastern region, as the varietal technology hardly suited its highly diverse rainfed environment. The success of any breeding program depends on understanding the genetic nature of the character of interest, creation and prediction of genetic variability in subsequent generations and their inter relation ship

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with other characters. Yield is a complex character and is influenced by various other characters therefore it is essential to understand the association of other characters with yield in addition to the information on genetic variability. Yield contributing traits are interrelated and highly influenced by the environments (CHANDRA *et al.*, 2007; NAYAK *et al.*, 2008; PRASAD *et al.*, 2001; ESWARA REDDY *et al.*, 2013) and partitioned into direct and indirect effect for yield (MOHSIN *et al.*, 2009). Efficiency of indirect selection depends on the magnitude of correlations between yield and target yield components (TOKER and CAGIRGAN, 2004; BOSE *et al.*, 2007; IDRIS *et al.*, 2012; DHANWANI *et al.*, 2013; PRATAP *et al.*, 2014). The path analysis has been used by plant breeders to support in identifying traits that are promising as selection criteria to improve crop yield and to detect the amount of direct and indirect effect of the causal components on the effect component (BOSE *et al.*, 2005; INDU RANI *et al.*, 2008; TOGAY *et al.*, 2008; ALI *et al.*, 2009; CHANDRA *et al.*, 2009; AKHATAR *et al.*, 2011; CYPRIAN and KUMAR, 2011). Breeding for upland rice is a challenging task because all these information is meagre under stress situations. However, there are several reports on genetic variability and correlation studies on different characters in rice under normal conditions. Keeping in view this urgent need, this investigation was undertaken to understand the genetic variability and correlation between yield and other yield attributing characters under this ecology

MATERIALS AND METHODS

The material for the present investigation consists of 22 upland genotypes. These were grown in a randomized complete block design with three replications during wet season 2011 at Central Rice Research Institute research farm, Cuttack, India. The entries were direct seeded with six rows per entry having 30 hills per row with 20 × 15 cm spacing and care was taken to maintain 1-2 seedlings per hill. Observations on quantitative traits like days to 50% flowering (DFF), plant height, total tiller (TT), ear bearing tiller (EBT), panicle length (PL), panicle weight (PW), grain per panicle (GPP), test grain weight, yield, spikelet length and spikelet breadth. EBT/ m² and seed test weight were recorded on five randomly selected plants excluding the border rows from each entry while days to 50% flowering and plot yield were recorded on plot basis. The genotypic and phenotypic co-efficient of variations were computed through Burton's method (BURTON, 1952). Heritability and genetic advance were worked out as per the method of HANSON *et al.* (1955). Phenotypic correlation co-efficient was calculated according to the procedure suggested by ALJIBOUNI *et al.* (1958) and path analysis was worked out following DEWEY and LU (1959). The statistical analysis was done using SAS 9.2 software.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) shows that among the genotypes all traits were significant indicates the presence of considerable amount of genetic variation among the genotypes (Table 1). The magnitude of variations between genotypes was revealed by high values of mean and range for traits of the genotypes (Table 2). High genetic variability for different traits in rice was earlier reported (KHAN *et al.*, 2009; UMADEVI *et al.*, 2009; AKINWALE *et al.*, 2011; ULLAH *et al.*, 2011). The Estimates of mean, range, coefficient of variance (CV), genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability and genetic advance of studied traits are presented in Table 2. It is observed that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) indicating environmental effect on the expression of

the characters. Maximum coefficient of variation was observed in TT, EBT and yield (Table 1.) This indicates that there is scope for further improvement of these characters through selection. High GCV values were observed in plant height followed by EBT and yield. This indicates that these characters can be manipulated for breeding high yielding varieties through hybridization and selection in subsequent generations in rice improvement programme under rainfed upland situation. High PCV values were observed in EBT followed by TT, plant height and yield (Table 2). The heritability of all the traits is greater than 89% except TT, EBT and yield (Table 2). The genetic advance values ranges from 19.56% (breadth) to 45.59% (plant height). Moderate to high degree of heritability estimates indicate the presence of additive genetic effects hence selection based on phenotypic performance of these character will be effective.

Table 1: Analysis of Variance for different traits

| Source | df | DFF | MS | | | | | | | | | |
|-------------|----|----------|-----------|---------|---------|---------|--------|-----------|---------|---------|----------|--------|
| | | | PLHT | TT | EBT | PL | PW | GRAINPP | TGWT | SLENGTH | SBREADTH | YIELD |
| Replication | 2 | 0.136 | 15.107 | 9.365 | 3.767 | 0.856 | 0.139 | 345.905 | 0.071 | 0.035 | 0.019 | 0.781* |
| Genotype | 21 | 469.986* | 1244.271* | 30.592* | 25.949* | 29.289* | 1.001* | 2084.942* | 23.217* | 2.246* | 0.199* | 0.814* |
| Error | 42 | 1.105 | 6.742 | 6.430 | 3.291 | 0.940 | 0.039 | 64.304 | 0.100 | 0.019 | 0.005 | 0.081 |
| CV | | 1.582 | 2.852 | 15.353 | 13.451 | 4.137 | 6.503 | 4.455 | 1.309 | 1.630 | 2.616 | 11.225 |

*- significant at 1%

DFF: days to 50% flowering; PLHT: plant height; TT: total tiller; EBT: ear bearing tiller; PL: panicle length; PW: panicle weight; GRAINPP: grains per panicle; TGWT: test grain weight; SLENGTH: spikelet length; SBREADTH: spikelet breadth

Table 2: Estimates of different parameters of variability of different traits

| Trait | Mean | Range | Phenotypic variance | Genotypic variance | Variability | | Heritability (%) | Genetic advance (% of Mean) |
|----------|---------|-----------|---------------------|--------------------|-------------|--------|------------------|-----------------------------|
| | | | | | GCV | PCV | | |
| DFF | 66.455 | 42-92 | 157.398 | 156.294 | 18.812 | 18.879 | 0.993 | 38.617 |
| PLHT | 91.028 | 53-140 | 419.252 | 412.510 | 22.312 | 22.494 | 0.984 | 45.592 |
| TT | 16.516 | 8-25.4 | 14.484 | 8.430 | 17.183 | 23.043 | 0.556 | 26.396 |
| EBT | 13.487 | 7.6-23 | 10.844 | 7.552 | 20.377 | 24.416 | 0.696 | 35.032 |
| PL | 23.441 | 15.2-29 | 10.390 | 9.450 | 13.114 | 13.751 | 0.910 | 25.763 |
| PW | 3.034 | 1.9-4.2 | 0.360 | 0.321 | 18.661 | 19.762 | 0.892 | 36.301 |
| GRAINPP | 179.988 | 118-235 | 737.850 | 673.546 | 14.419 | 15.092 | 0.913 | 28.380 |
| TGWT | 24.168 | 18-30 | 7.806 | 7.706 | 11.486 | 11.560 | 0.987 | 23.508 |
| YIELD | 2.541 | 1.5-3.8 | 0.325 | 0.244 | 19.444 | 22.452 | 0.750 | 34.690 |
| SLENGTH | 8.467 | 6.8-10.06 | 0.761 | 0.742 | 10.176 | 10.306 | 0.975 | 20.699 |
| SBREADTH | 2.588 | 2-3.1 | 0.069 | 0.065 | 9.827 | 10.169 | 0.934 | 19.563 |

DFF: days to 50% flowering; PLHT: plant height; TT: total tiller; EBT: ear bearing tiller; PL: panicle length; PW: panicle weight; GRAINPP: grains per panicle; TGWT: test grain weight; SLENGTH: spikelet length; SBREADTH: spikelet breadth

Table 3: Simple correlation of traits

| | PLHT | TT | EBT | PL | PW | GRAINPP | TGWT | SLENGTH | SBREADTH | YIELD |
|----------|-------|--------|--------|----------|--------|---------|--------|---------|----------|---------|
| DFE | 0.034 | 0.093 | 0.110 | -0.077 | -0.008 | 0.134 | 0.087 | -0.211 | -0.258** | 0.116 |
| PLHT | | -0.104 | 0.164 | 0.596* | 0.119 | 0.090 | 0.483* | 0.459* | -0.028 | 0.417* |
| TT | | | 0.852* | -0.300** | -0.091 | -0.022 | -0.077 | -0.206 | 0.064 | 0.070 |
| EBT | | | | -0.135 | -0.061 | 0.003 | 0.172 | -0.026 | 0.022 | 0.292** |
| PL | | | | | 0.591* | 0.510* | 0.333* | 0.566* | -0.102 | 0.506* |
| PW | | | | | | 0.755* | -0.028 | 0.583* | -0.317* | 0.323* |
| GRAINPP | | | | | | | -0.194 | 0.421* | -0.408* | 0.267** |
| TGWT | | | | | | | | 0.236 | 0.239 | 0.217 |
| SLENGTH | | | | | | | | | -0.429* | 0.294** |
| SBREADTH | | | | | | | | | | -0.141 |

*- significant at 1%, ** - significant at 5%

DFE: days to 50% flowering; PLHT: plant height; TT: total tiller; EBT: ear bearing tiller; PL: panicle length; PW: panicle weight; GRAINPP: grains per panicle; TGWT: test grain weight; SLENGTH: spikelet length; SBREADTH: spikelet breadth

Table 4: Genotypic and phenotypic correlation of traits

| | | PLHT | TT | EBT | PL | PW | GRAINPP | TGWT | SLENGTH | SBREADTH | YIELD |
|----------|---|-------|--------|---------|-----------|---------|---------|---------|---------|-----------|----------|
| DFE | G | 0.034 | 0.132 | 0.130 | -0.073 | -0.004 | 0.145 | 0.089 | -0.215 | -0.269 ** | 0.134 |
| | P | 0.034 | 0.095 | 0.111 | -0.077 | -0.008 | 0.134 | 0.087 | -0.211 | -0.259 ** | 0.119 |
| PLHT | G | | -0.152 | 0.208 | 0.624 | 0.128 | 0.092 | 0.494 * | 0.474 * | -0.030 | 0.482 * |
| | P | | -0.103 | 0.167 | 0.596 * | 0.116 | 0.087 | 0.484 * | 0.460 * | -0.025 | 0.425 * |
| TT | G | | | 0.895 * | -0.404 * | -0.182 | -0.002 | -0.107 | -0.263 | 0.099 | 0.171 |
| | P | | | 0.850 * | -0.303 ** | -0.083 | -0.009 | -0.076 | -0.207 | 0.062 | 0.102 |
| EBT | G | | | | -0.109 | -0.091 | 0.044 | 0.197 | -0.028 | 0.030 | 0.459 * |
| | P | | | | -0.135 | -0.055 | 0.013 | 0.175 | -0.026 | 0.021 | 0.325 * |
| PL | G | | | | | 0.662 * | 0.541 * | 0.351 * | 0.611 * | -0.112 | 0.641 * |
| | P | | | | | 0.590 * | 0.510 * | 0.333 * | 0.570 * | -0.098 | 0.514 * |
| PW | G | | | | | | 0.798 * | -0.036 | 0.631 | -0.337 * | 0.391 * |
| | P | | | | | | 0.752 * | -0.029 | 0.590 * | -0.311 ** | 0.307 ** |
| GRAINPP | G | | | | | | | -0.200 | 0.449 * | -0.450 * | 0.303 ** |
| | P | | | | | | | -0.197 | 0.427 * | -0.404 * | 0.246 ** |
| TGWT | G | | | | | | | | 0.239 | 0.256 | 0.256 |
| | P | | | | | | | | 0.236 | 0.240 | 0.223 |
| SLENGTH | G | | | | | | | | | -0.461 * | 0.375 * |
| | P | | | | | | | | | -0.435 * | 0.312 ** |
| SBREADTH | G | | | | | | | | | | -0.082 |
| | P | | | | | | | | | | -0.126 |

*- significant at 1%, ** - significant at 5%

DFE: days to 50% flowering; PLHT: plant height; TT: total tiller; EBT: ear bearing tiller; PL: panicle length; PW: panicle weight; GRAINPP: grains per panicle; TGWT: test grain weight; SLENGTH: spikelet length; SBREADTH: spikelet breadth

Table 3 gives the simple linear correlation coefficient between all the pairs of studied traits. It shows that yield is positively and significantly correlated with the traits plant height, EBT, PL, PW, grain per panicle and length. The genotypic and phenotypic correlation coefficient among all the studied traits is given in Table 4, which revealed that the genotypic and phenotypic correlation of yield is positive and significant with plant height, EBT, PL, PW, grain per panicle and length; whereas other traits were not significantly correlated. The genotypic correlation coefficients were partitioned using path analysis to find out the direct and indirect effects of yield contributing traits towards grain yield and number in parenthesis are the direct on yield (Table 5 and Figure 1) which reveals that plant height (0.239) has highest direct effect on yield followed by grain per panicle (0.112), DFF, thousand grain weight and EBT. This suggests that these traits can be manoeuvred successfully for breeding high yielding varieties for this dynamic ecology.

Table 5: Path coefficient showing direct and indirect effects of trait on grain yield

| Trait | DFE | PLHT | TT | EBT | PL | PW | GRAINPP | TGWT | SLENGTH | SBREADTH | Total correlation with yield |
|----------|---------|----------|-----------|----------|-----------|-----------|----------|----------|-----------|-----------|------------------------------|
| DFE | (0.062) | 0.0013 | -0.0041 | 0.0041 | -0.0182 | -0.0098 | -0.0105 | -0.0113 | 0.0015 | 0.0013 | 0.0163 |
| PLHT | 0.005 | (0.2396) | 0.0261 | -0.0182 | 0.0339 | -0.0211 | -0.0052 | -0.0464 | -0.047 | 0.0244 | 0.1911 |
| TT | 0.0056 | -0.0092 | (-0.0843) | -0.0674 | 0.0065 | -0.0174 | 0.0032 | -0.004 | 0.0111 | 0.0044 | -0.1515 |
| EBT | 0.0015 | -0.0018 | 0.0185 | (0.0232) | -0.0068 | 0.0021 | -0.0032 | 0.0045 | -0.0007 | -0.0006 | 0.0367 |
| PL | 0.0337 | -0.0163 | 0.0089 | 0.0335 | (-0.1149) | 0.0069 | -0.0219 | -0.001 | 0.0134 | -0.0089 | -0.0666 |
| PW | 0.0152 | 0.0084 | -0.0198 | -0.0088 | 0.0058 | (-0.0959) | -0.0318 | -0.0119 | -0.0033 | 0.0033 | -0.1388 |
| GRAINPP | -0.019 | -0.0024 | -0.0043 | -0.0153 | 0.0214 | 0.0373 | (0.1125) | -0.0226 | 0.0067 | 0.0161 | 0.1304 |
| TGWT | -0.0083 | -0.0089 | 0.0022 | 0.0089 | 0.0004 | 0.0057 | -0.0092 | (0.0459) | 0.0048 | -0.0096 | 0.0319 |
| SLENGTH | -0.001 | 0.0086 | 0.0058 | 0.0014 | 0.0051 | -0.0015 | -0.0026 | -0.0046 | (-0.0439) | -0.0051 | -0.0378 |
| SBREADTH | -0.0099 | -0.0474 | 0.0244 | 0.0126 | -0.0359 | 0.0162 | -0.0668 | 0.0976 | -0.0537 | (-0.4658) | -0.5287 |

*- significant at 1%, ** - significant at 5%

DFE: days to 50% flowering; PLHT: plant height; TT: total tiller; EBT: ear bearing tiller; PL: panicle length; PW: panicle weight; GRAINPP: grains per panicle; TGWT: test grain weight; SLENGTH: spikelet length; SBREADTH: spikelet breadth

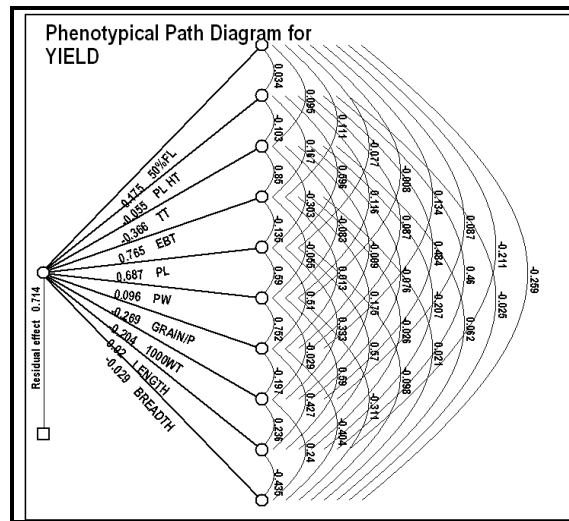


Figure 1. Phenotypical path diagram for yield

CONCLUSION

The results of the present study show that there is adequate genetic variability in the studied material. TT, EBT and yield has high coefficient of variation. The traits plant height, EBT and yield has high GCV, PCV and genetic advance. The traits plant height, EBT, PL, PW and length were positively and significantly genetically and phenotypically correlated with yield. Plant height and grain per panicle, 50% flowering, thousand grain weight and EBT has high direct effect on yield. Therefore, for increasing rice grain yield, a genotype with traits like high plant height, EBT, grain per panicle, thousand grain weight and 50% flowering should be considered for upland ecology.

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REFERENCES

- AKHATAR, N., M.F. NAZIR, A. RABNAWAZ, T. MAHMOOD, M.E. SAFDAR, M. ASIF, A. REHMAN (2011): Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza sativa* L.). The Journal of Animal & Plant Sciences 21(4):660-664.
- AKINWALE, M.G., GREGORIO, G., NWILENE, F., AKINYELE, B.O., OGUNBAYO, S.A., ODIYI, A.C. (2011): Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). African Journal of Plant Science 5: 207-212.
- ALI, M.A., NAWAD, N.N., ABBAS, A., ZULKIFFAL, M., SAJJAD, M. (2009): Evaluation of selection criteria in *Cicer arietinum* L. using correlation coefficients and path analysis. Australian Journal of Crop Science 3(2): 65-70.
- ALJIBOURI, H.A., P.A. MILLER, H.F. ROBINSON (1958): Genotypic and environmental variances and covariances in an upland cotton cross of inter-specific origin. Agronomy Journal 50: 633-637.
- BOSE, L.K., S.K. PRADHAN, A. MOHANTY, M. NAGARAJU (2005): Genetic variability and association of yield attributing characters with grain yield in deepwater rice. Korean Journal of Crop Science 50(4): 262-264.

- BOSE, L.K., S. DAS, S. K. PRADHAN, H.N. SUBUDHI, S. SINGH, O.N. SINGH (2007). Genetic variability of quality characters and grain yield in lowland rice genotypes of Eastern India. *Korean Journal of Breeding Science* 39(1): 1-6.
- BURTON, G.W. (1952). Quantitative inheritance in grasses. *Proc 6th Int Grassid Cong, 1*: 277-281.
- CHANDRA, R., S.K. PRADHAN, S. SINGH, L.K. BOSE, O.N. SINGH (2007): Multivariate analysis in upland genotypes. *World Journal of Agricultural Sciences* 3(3): 295-300.
- CHANDRA. B.S., T.D. REDDY, N.A. ANSARI, S.S. KUMAR (2009): Correlation and path analysis for yield and yield components in rice (*Oryza sativa* L.). *Agricultural Science Digest* 29(1):45-47.
- CYPRIAN, M., V.KUMAR (2011): Correlation and path coefficient analysis of rice cultivars data. *Journal of Reliability and Statistical Studies* 4(2):119-131.
- DEWEY, D.R., K.H. LU (1959). A correlation and path co-efficient analysis of components of crested wheat grass seed production. *Agronomy Journal* 51: 515-518.
- DHANWANI, R.K., A.K. SARAWGI, A. SOLANKI, J.K. TIWARI (2013): Genetic variability analysis for various yield attributing and quality traits in rice (*O. sativa* L.). *The Bioscan* 8(4): 1403-1407.
- ESWARA REDDY, G., B.G. SURESH, T. SRAVAN, P.ASHOK REDDY (2013): Interrelationship and cause-effect analysis of rice genotypes in north east plain zone. *The Bioscan* 8(4): 1141-1144.
- HANSON, C.H., H.F. ROBINSON, R.E. COMSTOCK (1955): Biometrical studies of yield in segregating population of Korean lespechea. *Agronomy Journal* 48: 262-272.
- IDRIS, A.E., F.J. JUSTIN, Y.M.I. DAGASH, A.I. ABDULI (2012): Genetic variability and inter relationship between yield and yield components in some rice genotypes. *American Journal of Experimental Agriculture* 2(2):233-239.
- INDU RANI, C., D. VEERARAGATHANTHAM, S.SANJUTHA (2008): Studies on correlation and path coefficient analysis on yield attributes in Root Knot Nematode Resistant F1 hybrids of tomato. *J Appl Sci Res* 4(3): 287-295.
- KHAN, A.S., M. IMRAN, M.ASHFAQ (2009): Estimation of genetic variability and correlation for grain yield components in rice (*Oryza sativa* L.). *American-Eurasian Journal of Agricultural & Environmental Sciences* 6: 585-590.
- MOHSIN, T., N. KHAN, F.N. NAQVI (2009): Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. *Journal of Food Agriculture & Environment* 7: 278-282.
- NAYAK, D., L.K. BOSE, U.D. SINGH, S. SINGH, P.NAYAK (2008): Measurement of genetic diversity of virulence in populations of *Xanthomonas oryzae* pv. *oryzae* in India. *Communications in Biometry and Crop Science* 3(1): 16-28.
- PRASAD, B., A.K. PATWARY, P.S. BISWAS (2001): Genetic variability and selection criteria in fine rice (*Oryza sativa* L.). *Pakistan Journal of Biological Sciences* 4: 1188-1190.
- PRATAP, N., P.K. SINGH, R. SHEKHAR, S.K. SONI, A.K. MALL (2014): Genetic variability, character association and diversity analyses for economic traits in rice (*Oryza sativa* L.) SAARC *Journal of Agriculture* 10(2): 83-94.
- SAS INSTITUTE (2010): SAS/STAT Version 9.2. SAS Institute, Cary, North Carolina USA.
- TOGAY, N., Y. TOGAY, B. YILDIRIN, Y.DOGAN (2008): Relationships between yield and some yield components in pea (*Pisum sativum* ssp. *arvense* L.) genotypes by using correlation and path analysis. *African Journal of Biotechnology* 7(23): 4285-4287.
- TOKER, C., M.I. CAGIRGAN (2004): The use of phenotypic correlations and factor analysis in determining characters for grain yield selection in chickpea (*Cicer arietinum* L.). *Hereditas* 140: 226-228.
- ULLAH, M.Z., M.K. BASHAR, M.S.R. BHUIYAN, M. KHALEQUZZAMAN, M.J. HASAN (2011): Interrelationship and cause-effect analysis among morpho-physiological traits in birain rice of Bangladesh. *International Journal of Plant Breeding and Genetics* 5: 246-254.
- UMADEVI, M., P. VEERABADHIRAN, S.MANONMANI (2009): Genetic variability, heritability, genetic advance and correlation for morphological traits in rice genotypes. *Madras Agricultural Journal* 96: 316-318.
- ZHANG, Q. (2007): Strategies for developing green super rice. *Proceeding of the National Academy of Sciences USA* 104: 16402-16409.

GENETIČKA VARIJABILNOST PRINOSA I OSOBINA POVEZANIH SA PRINOSOM KOD BRDSKOG PIRINČA

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Izvod

U ovom radu je proučavana genetička varijabilnost i korelacije prinosa i drugih osobina povezanih sa prinosom kod genotipova pirinča u brdskom području. Eksperiment je izveden sa 22 genotipa brdskog pirinča, gajenih tokom vlažne sezone direktnom setvom u randomiziranom blok dizajnu. Analiza varijanse je pokazala značajnost za sva ispitivana svojstva, ukazujući na prisustvo značajne genetičke varijabilnosti između genotipova. Svojstva kao što su visina biljke, stable sa klasom i prinos imala su visok koeficijent genotipske i fenotipske varijanse i genetičko poboljšanje. Visina biljke zrna po klasu, 50% cvetalih biljaka, masa 1000 zrna i broj stabala sa klasom imaju visok direktan uticaj na prinos. Zbog toga bi selekcija zasnovana na ovim svojstvima trebalo da bude mnogo efikasnija kod brdskog pirinča.

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