



Multivariate Analysis in Rice (*Oryza sativa* L.)

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ABSTRACT

Thirty five genotypes of rice were evaluated for 18 characters to study genetic divergence by using Mahalanobis' D^2 statistic, cluster analysis and principal component analysis. On the basis of these three clustering methods six clusters were obtained for D^2 statistic and cluster analysis for each method. Absolute growth rate showed maximum contribution towards genetic divergence in D^2 statistics. PCA identified six components with eigen value more than one which contributed 79.526 per cent of cumulative variance. Highest inter - cluster distance was observed between cluster IV viz., IR 8 and VI viz., MTU 1061 followed by clusters V viz., CSR 4 and VI viz., MTU 1061 and clusters IV viz., IR 8 and V viz., CSR 4. Whereas cluster I viz., MTU 1075, TELLA HAMSA, MTU 1061, ACC. No. 11081 and cluster VI viz., KAVYA, IR 8 And PR 109 etc followed by cluster IV viz., NLR 28523 and NLR 145 and clusters V viz., MTU 1002, WGL 186 and CSR 4 and cluster II viz., PR 106, BPT 5204, BPT 2270 and NLR 3041 etc and cluster V viz., MTU 1002, WGL 186 and CSR 4 showed maximum inter cluster distance in hierarchical cluster analyses. For varietal improvement strains from these clusters were important on the basis of their genetic distance and highest cluster means. Divergence studies indicated that selection for hybridization should be more based on genetic diversity rather than the geographic diversity.

Key words : Cluster analysis, D^2 analysis, Principal component analysis, Rice.

Rice (*Oryza sativa* L.) is the most important food crop in South and South East Asian countries particularly in developing countries like India and it is the third important staple food crop after maize and wheat of the world in particular. Most of the people in Asia, particularly in developing countries like India, meet their major calorific requirement through rice. Rice offers a great wealth of material for genetic studies because of its wide ecological distribution and enormous variation for various morphological and physiological characters.

In the hybridization programme, diversity of parents was very much important, because the crosses between the genotypes with maximum genetic divergence would be responsible for obtaining desirable improvement as they are likely to yield desirable recombinants in the progenies.

The present study was carried out with different methods of clustering based on D^2 analysis, hierarchical cluster analysis and principal component analysis. Therefore, the present investigation is an attempt to study genetic divergence in 35 genotypes of rice via multivariate analysis.

MATERIAL AND METHODS

Thirty five rice genotypes were raised in a randomized complete block design with three

replications during *kharif* 2009-10 at Agricultural College Farm, Bapatla. The inter and intra-row spacing adapted was 20cm x 15cm. Each plot consisted of ten rows of 5m length and observations were recorded on ten randomly selected plants from each population per replication for characters viz., plant height (cm), days to 50% flowering, absolute growth rate (AGR), No. of ear bearing tillers m^{-2} , panicle length (cm), No. of filled grains panicle $^{-1}$, test weight (g), grain yield (kg plot $^{-1}$), harvest index (%), grain length (mm), grain breadth (mm), kernel length (mm), kernel breadth (mm), volume expansion ratio on cooking, head rice recovery, milling (%), hulling (%) and protein content of the grain (%).

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among 35 genotypes for all the characters under study in rice indicating substantial genetic variability for all the characters. On the basis of D^2 values and cluster analysis the thirty five genotypes were grouped into six clusters for each (Table 1). Based on D^2 values, clustering pattern comprised six clusters, out of which cluster I was the biggest cluster with 21 genotypes followed by clusters III which consisted of ten genotypes while the remaining clusters i.e. cluster II, cluster IV

Table 1. Clustering pattern of 35 genotypes of rice by Tocher's method.

| Cluster No. | No. of genotypes | Name of the genotype |
|-------------|------------------|---|
| I | 21 | MTU 3626, IR 70, NAVEEN, HANSRAJ, MTU 1010, IR 64, MTU 1031, MTU 1064, BPT 2231, BPT 5204, MTU 1001, WGL 186, MTU 1075, PR 109, JGL 11727, MTU 1002, MTU 7029, BPT 1768, PLA 838, BPT 3291, KAVYA |
| II | 1 | TELLA HAMSA |
| III | 10 | BPT 2270, NLR 3041, NLR 33892, PR 106, ACC. No. 10948, NLR 33358, NLR 34449, NLR 28523, NLR 145, ACC. No. 11071 |
| IV | 1 | IR 8 |
| V | 1 | CSR 4 |
| VI | 1 | MTU 1061 |

cluster V and cluster VI consisted of single genotype each as shown in Table 1. The lack of correspondence between genetic diversity and geographical origin was observed in the present study as also reported by Shiv Datt and Mani (2003) and Prasad *et al.*, (2009) it could possibly be due to genetic drift, selection pressure and environment which might have resulted in greater diversity than geographic isolation. The intra-cluster average distance ranged from 0.00 to 153.977. The inter-cluster distance ranged from 126.212 (between cluster II and VI) to 484.439 (between cluster IV and VI) suggesting that the genotypes from these clusters could be used as donors in hybridization programme for obtaining a wide spectrum of variation among the segregants. Absolute growth rate at 65-80 DAT (35.63%) showed maximum contribution towards genetic divergence followed by absolute growth rate at 50-65 DAT (24.54%), test weight (g) (14.62%), days to 50% flowering (8.40%), grain yield (kg plot⁻¹) (4.71%), kernel length (mm) (3.87%) and volume expansion ratio on cooking (3.03%). The relative importance of contribution of yield components towards divergence can be judged by comparing the group means of 18 characters. The highest mean values for plant height (121.667cm), No. of ear bearing tillers m⁻² (341.000), no. of filled grains panicle⁻¹ (191.033) and absolute growth rate at 50-65 DAT (2.733) were depicted by cluster V (CSR 4). Test weight (25.377g), grain breadth

(2.740mm), kernel breadth (2.287mm), volume expansion ratio (7.323) and protein content of grain (8.070) were depicted by cluster IV (IR8). harvest index (49.35%), grain length (9.270 mm), hulling (%) (79.483) and head rice recovery (68.977 %) were depicted by cluster VI (MTU 1061).

Based on Ward minimum variance dendrogram, the hierarchical cluster analysis resulted in four genotypes in cluster I, nine in cluster II, nine in cluster III, two in cluster IV, three in cluster V and eight in cluster VI as shown in Table 1 and dendrogram. The intra-cluster average distance ranged from 157.985 to 315.672 during *kharif* 2009. The inter-cluster distances ranged from 333.795 (between III and IV) to 803.080 (between I and VI). The highest mean values for plant height (109.281cm), No. of ear bearing tillers m⁻² (316.166), panicle length (23.521cm), harvest index (56.014 %), kernel breadth (2.103mm), hulling (%) (78.631) and absolute growth rate at 50-65 DAT (2.310) were depicted by cluster V.

The principal component analysis identified seven principal components in rice genotypes. The contribution by the first PC was maximum in the groups. Absolute growth rate 65-80 DAT, absolute growth rate 50-65 DAT, test weight (g), days to 50% flowering, grain yield (kg plot⁻¹), kernel length (mm) and volume expansion ratio contributed more towards divergence in rice genotypes. Principal components showing values less than one were considered non-

Table 2. Average intra-and inter-cluster D² values among six clusters in 35 rice (*Oryza sativa* L.) genotypes.

| Cluster No | I | II | III | IV | V | VI |
|------------|---------------|--------------|----------------|--------------|--------------|--------------|
| I | 95.998 | 132.721 | 152.419 | 132.071 | 219.919 | 329.089 |
| II | | 0.000 | 138.999 | 250.615 | 162.603 | 126.212 |
| III | | | 153.977 | 227.662 | 328.612 | 233.536 |
| IV | | | | 0.000 | 359.254 | 484.439 |
| V | | | | | 0.000 | 482.370 |
| VI | | | | | | 0.000 |

Table 3. Contribution of different characters towards genetic divergence among 35 genotypes of rice.

| Character | % Contribution towards divergence |
|--|-----------------------------------|
| Days to 50% flowering | 8.40 |
| No. of ear bearing tillers m ⁻² | 0.34 |
| No. of filled grains panicle ⁻¹ | 1.51 |
| Test weight (g) | 14.62 |
| Grain yield (kg Plot ⁻¹) | 4.71 |
| Harvest index (%) | 0.34 |
| Grain breadth (mm) | 0.50 |
| Kernel length(mm) | 3.87 |
| Kernel breadth (mm) | 0.17 |
| Milling (%) | 0.84 |
| Volume expansion ratio | 3.03 |
| Protein content of grain | 1.51 |
| Absolute growth rate 50-65 DAT | 24.54 |
| Absolute growth rate 65-80 DAT | 35.63 |

significant (Legendre and Legendre, 1984). These results are in accordance with the reports of Altaher and Singh (2003). The PCA scores for 35 rice genotypes were plotted in graph to get the 2D and 3D scattered diagram. These graphs showed wide divergence between the MTU 1001, MTU 1002, NLR 28523, MTU 1010 and MTU 7029 along PCA I axis and the genotypes PR106, ACC .No. 10948, NLR 33358, BPT 2270, KAVYA along PCA II axis showed wide distance and signifying their usefulness in rice breeding.

Therefore, selection of parents for hybrid breeding programme is of prime importance in the partial utilization of heterosis. For obtaining hybrids with high level of heterosis a question generally arises regarding the ideal distance (degree of divergence) at phenotypic level. Hence, selection of varieties should be more dependent on genetic diversity than the geographical diversity.

Table 4. Mean values of six clusters by Tocher's method for 35 genotypes of rice (*Oryza sativa* L.).

| | Plant height (cm) | Days to 50% flowering | No. of ear bearing tillers m ⁻² | Panicle length (cm) | No. of filled grains panicle ⁻¹ | Test weight (g) | Grain yield (*kg Plot ⁻¹) | Harvest index (%) |
|-------------|-------------------|-----------------------|--|---------------------|--|-----------------|---------------------------------------|-------------------|
| Cluster I | 82.639 | 99.048 | 284.350 | 21.138 | 150.008 | 20.501 | 6.014 | 48.810 |
| Cluster II | 106.267 | 95.000 | 282.410 | 24.133 | 147.333 | 18.673 | 4.637 | 41.960 |
| Cluster III | 83.251 | 104.067 | 271.412 | 19.697 | 144.766 | 17.844 | 4.824 | 42.872 |
| Cluster IV | 61.333 | 96.667 | 255.183 | 18.800 | 86.533 | 25.377 | 4.857 | 34.850 |
| Cluster V | 121.667 | 76.000 | 341.000 | 22.563 | 191.033 | 19.817 | 5.370 | 43.793 |
| Cluster VI | 107.933 | 92.000 | 308.187 | 22.600 | 100.467 | 14.893 | 5.950 | 49.350 |

Table 4 cont.....

| Grain length (mm) | Grain breadth (mm) | Kernel length (mm) | Kernel breadth (mm) | Hulling (%) | Milling (%) | Head rice recovery (%) | Volume expansion Ratio | Protein content of grain (%) | Absolute growth rate 50-65 DAT | Absolute growth rate 65-80 DAT |
|-------------------|--------------------|--------------------|---------------------|---------------|---------------|------------------------|------------------------|------------------------------|--------------------------------|--------------------------------|
| 8.353 | 2.340 | 5.992 | 1.993 | 76.167 | 87.021 | 62.859 | 3.950 | 6.898 | 1.289 | 0.877 |
| 8.943 | 2.167 | 7.080 | 1.960 | 78.327 | 92.740 | 66.647 | 3.750 | 6.757 | 1.490 | 1.897 |
| 7.947 | 2.286 | 5.495 | 1.945 | 73.733 | 85.699 | 59.758 | 3.948 | 6.518 | 1.036 | 1.295 |
| 9.010 | 2.740 | 6.000 | 2.287 | 78.313 | 85.503 | 52.357 | 7.323 | 8.070 | 1.120 | 0.223 |
| 8.267 | 2.243 | 6.453 | 1.953 | 77.360 | 83.150 | 52.727 | 3.200 | 6.543 | 2.733 | 1.013 |
| 9.270 | 2.250 | 6.500 | 1.953 | 79.483 | 89.223 | 68.977 | 3.600 | 6.767 | 0.300 | 2.897 |

Table 5. Clustering pattern of 35 genotypes of rice by Ward's minimum variance method.

| Cluster No. | No. of genotypes | Name of the genotypes |
|-------------|------------------|--|
| I | 4 | MTU 1075, TELLA HAMSA, MTU 1061, ACC. No. 11081 |
| II | 9 | PR 106, BPT 5204, BPT 2270, NLR 3041, NLR 33892, BPT 3291, BPT 1768, PLA 838, ACC. No. 10948 |
| III | 9 | IR 64, MTU 1031, MTU 1064, MTU 1010, MTU 1001, MTU 7029, MTU 3626, IR 70, NAVEEN |
| IV | 2 | NLR 28523, NLR 145 |
| V | 3 | MTU 1002, WGL 186, CSR 4 |
| VI | 8 | HANSRAJ, NLR 33358, KAVYA, NLR 34449, PR 109, BPT 2231, JGL 11727, IR 8 |

Table 6. Average intra- and inter-cluster Euclidian² values among six clusters in 35 genotypes of rice.

| | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI |
|-------------|----------------|----------------|----------------|---------------|----------------|----------------|
| Cluster I | 315.672 | 440.415 | 579.105 | 562.195 | 655.148 | 803.080 |
| Cluster II | | 247.876 | 376.914 | 433.293 | 721.03 | 464.145 |
| Cluster III | | | 157.985 | 333.795 | 387.912 | 335.889 |
| Cluster IV | | | | 294.34 | 721.575 | 694.139 |
| Cluster V | | | | | 267.448 | 596.992 |
| Cluster VI | | | | | | 286.167 |

Table 7. Mean values of six clusters estimated by Ward's minimum variance method from 35 genotypes of rice.

| | Plant height cm | Days to 50% flowering | No. of ear bearing tillers m ⁻² | Panicle length (cm) | No. of filled grains panicle ⁻¹ | Test weight (g) | Grain yield (*kg Plot ⁻¹) | Harvest index (%) |
|-------------|-----------------|-----------------------|--|---------------------|--|-----------------|---------------------------------------|-------------------|
| Cluster I | 104.473 | 92.000 | 282.969 | 23.092 | 132.943 | 18.456 | 5.395 | 48.332 |
| Cluster II | 82.044 | 107.333 | 282.727 | 19.350 | 151.826 | 16.415 | 5.228 | 38.696 |
| Cluster III | 82.808 | 100.815 | 278.511 | 21.850 | 149.348 | 22.197 | 6.599 | 52.339 |
| Cluster IV | 82.683 | 111.833 | 267.168 | 19.283 | 199.292 | 25.580 | 5.262 | 47.857 |
| Cluster V | 109.281 | 87.667 | 316.166 | 23.521 | 148.700 | 22.026 | 5.651 | 56.014 |
| Cluster VI | 71.295 | 94.042 | 275.798 | 19.583 | 129.522 | 18.645 | 4.983 | 43.412 |

Table 7 cont.....

| Grain length (mm) | Grain breadth (mm) | Kernel length (mm) | Kernel breadth (mm) | Hulling (%) | Milling (%) | Head rice recovery (%) | Volume expansion Ratio | Protein content of grain (%) | Absolute growth rate 50-65 DAT | Absolute growth rate 65-80 DAT |
|-------------------|--------------------|--------------------|---------------------|---------------|---------------|------------------------|------------------------|------------------------------|--------------------------------|--------------------------------|
| 8.799 | 2.356 | 6.561 | 2.074 | 73.011 | 88.258 | 64.007 | 3.783 | 6.437 | 1.016 | 2.213 |
| 7.813 | 2.301 | 5.530 | 1.913 | 75.298 | 88.016 | 62.576 | 4.005 | 6.677 | 0.988 | 1.296 |
| 8.050 | 2.444 | 5.823 | 2.090 | 77.748 | 86.356 | 63.843 | 3.746 | 6.811 | 1.287 | 0.935 |
| 7.328 | 2.075 | 5.010 | 2.063 | 77.690 | 88.582 | 62.318 | 3.918 | 5.990 | 0.815 | 1.613 |
| 8.696 | 2.400 | 6.530 | 2.103 | 78.631 | 86.780 | 60.977 | 3.877 | 6.536 | 2.310 | 1.131 |
| 8.957 | 2.241 | 6.099 | 1.838 | 73.698 | 84.396 | 57.120 | 4.494 | 7.431 | 1.247 | 0.230 |

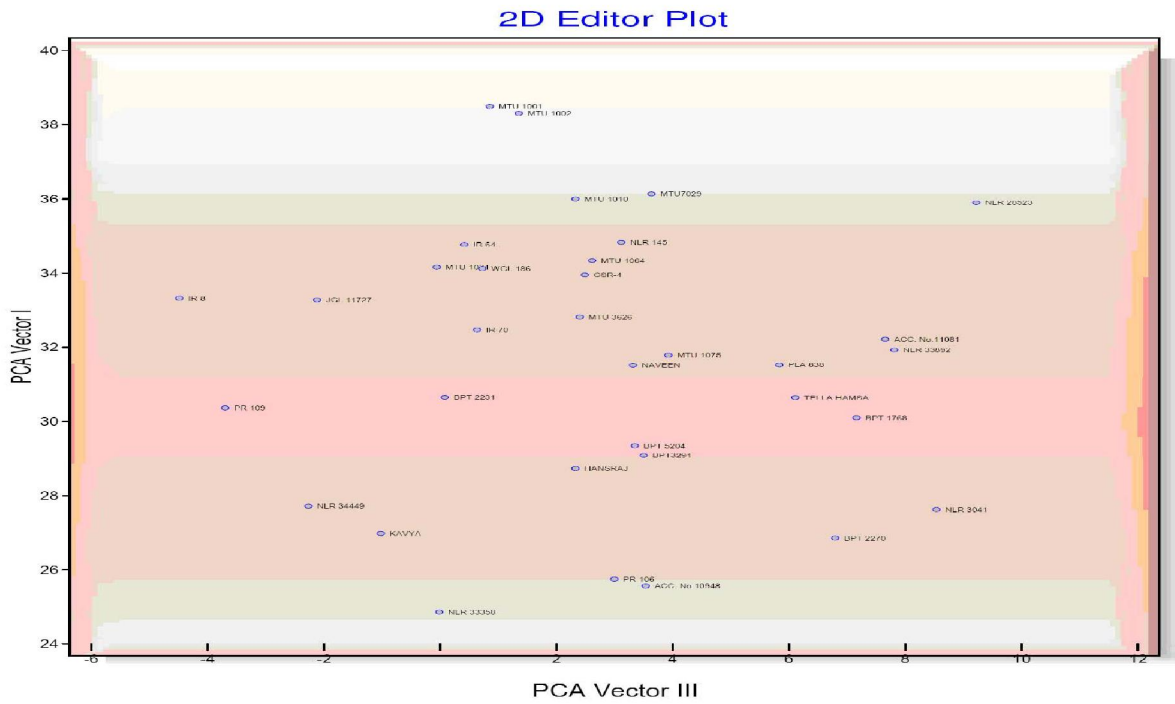


Fig. 1. 2D plot showing scattering in 35 genotypes of rice based on PCA scores.

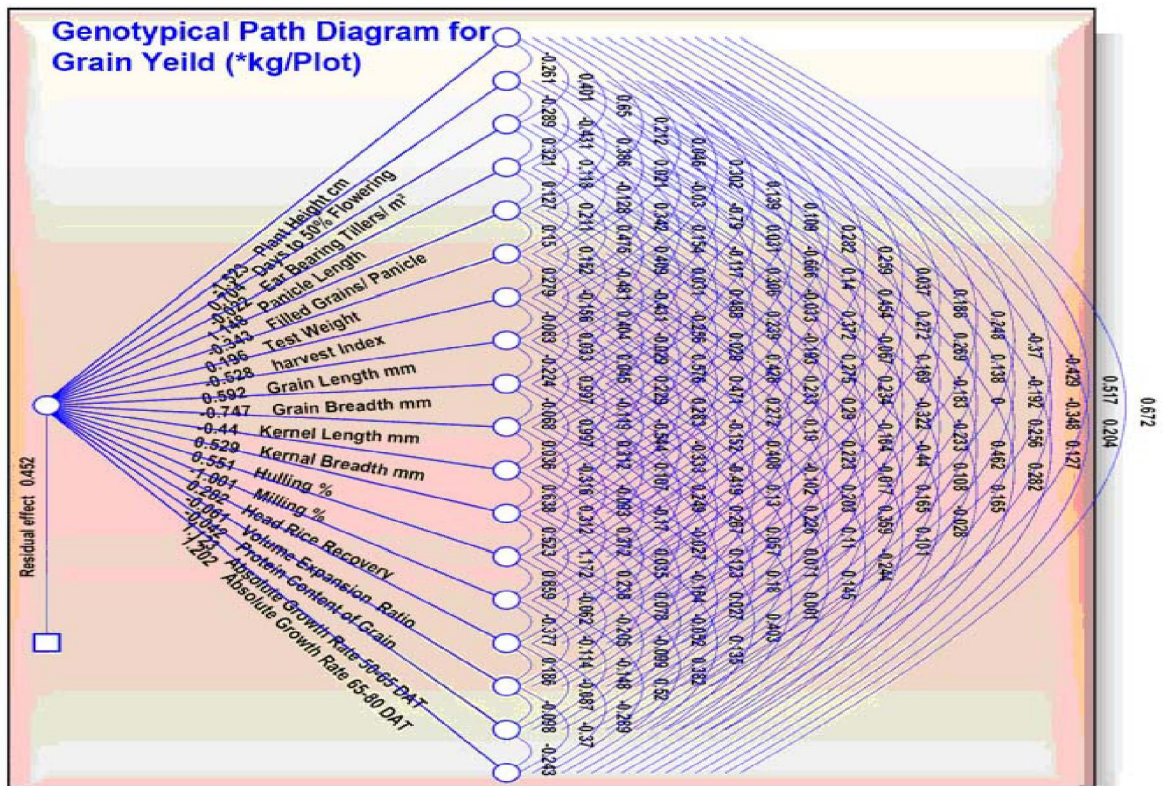


Fig. 2. Genotypic path diagram showing cause-effect relationship in rice.

Table 8. Eigen values, proportion of the total variance represented by first seven principal components, cumulative per cent variance and component loading of different characters in rice.

| | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 |
|--|--------|--------|--------|--------|--------|--------|--------|
| Eigene value (Root) | 4.925 | 3.363 | 2.433 | 1.812 | 1.539 | 1.039 | 0.926 |
| Expression of percentage variance | 25.919 | 17.700 | 12.805 | 9.535 | 8.101 | 5.466 | 4.876 |
| Expression of cumulative variance | 25.919 | 43.619 | 56.424 | 65.959 | 74.060 | 79.526 | 84.401 |
| Plant height (cm) | 0.130 | 0.336 | 0.321 | 0.092 | 0.305 | 0.127 | 0.082 |
| Days to 50% flowering | 0.052 | -0.395 | 0.284 | -0.087 | -0.266 | -0.002 | 0.041 |
| No. of ear bearing tillers m ⁻² | 0.044 | 0.258 | 0.036 | -0.438 | -0.119 | 0.499 | 0.085 |
| Panicle length (cm) | 0.235 | -0.039 | 0.065 | 0.045 | -0.130 | -0.544 | 0.521 |
| No. of filled grains panicle ⁻¹ | 0.155 | 0.169 | 0.267 | 0.124 | -0.514 | 0.017 | -0.191 |
| Test weight (g) | 0.387 | -0.072 | -0.121 | 0.065 | 0.161 | -0.013 | -0.299 |
| Grain yield (*kg Plot ⁻¹) | 0.368 | 0.020 | 0.012 | -0.097 | -0.118 | -0.138 | -0.023 |
| Harvest index (%) | 0.314 | 0.121 | -0.183 | 0.024 | 0.071 | 0.185 | 0.481 |
| Grain length (mm) | -0.405 | 0.094 | 0.015 | -0.043 | 0.011 | -0.273 | 0.050 |
| Grain breadth (mm) | 0.045 | -0.353 | -0.092 | -0.016 | 0.528 | 0.007 | -0.202 |
| Kernel length(mm) | -0.023 | 0.366 | 0.023 | -0.402 | 0.072 | -0.324 | -0.134 |
| Kernel breadth (mm) | 0.239 | -0.081 | 0.240 | -0.460 | 0.080 | 0.013 | 0.026 |
| Hulling (%) | -0.193 | -0.327 | 0.243 | -0.248 | -0.154 | 0.216 | -0.026 |
| Milling (%) | 0.311 | -0.189 | 0.153 | -0.248 | 0.094 | -0.136 | -0.142 |
| Head rice recovery | -0.336 | 0.183 | 0.126 | -0.177 | 0.136 | -0.030 | 0.122 |
| Volume expansion ratio | -0.010 | 0.146 | -0.319 | -0.369 | -0.054 | -0.291 | -0.259 |
| Protein content of grain | -0.026 | -0.199 | -0.415 | -0.278 | 0.020 | 0.141 | 0.384 |
| Absolute growth rate 50-65 DAT | 0.212 | 0.317 | -0.118 | 0.134 | 0.026 | 0.175 | -0.121 |
| Absolute growth rate 65-80 DAT | -0.018 | 0.059 | 0.488 | 0.021 | 0.388 | -0.053 | 0.167 |

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