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RESEARCH ARTICLE

# Assessment of Genetic Variability and Pollen Viability in Rice (*Oryza sativa* L.) Germplasm for Low Temperature Tolerance at Reproductive Stage

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A panel of rice genotypes consisting of the mini core, lowland and upland genotypes were evaluated for their ability to withstand cold stress to assess their genetic variability and pollen viability. The analysis of variance revealed highly significant differences among the genotypes for all the traits studied in ENV 1. Days to 50% flowering, plant height and spikelet fertility showed highest genotypic and phenotypic variance in all the three environments. Overall correlation analysis showed that spikelet fertility and biological yield were highly correlated with grain yield. Pollen viability test under cold stress condition relative to timely sown were studied and genotypes performing well were BAM 5889, BAM 5179, and BAM 4408. Among the mini core rice accessions studied, genotypes performing well under both timely and late sown environment were BAM 4115, UR 100, BAM 5179, BAM 3808, LR 11, BAM 4483 and UR 3.

**Key Words: Cold Stress, Genetic variability, Rice, Reproductive Stage.**

## Introduction

Rice occupies a pivotal place in Indian agriculture as it provides 43% calorie requirement for more than 70% of population. In India, it is cultivated in an area of 43.94 million hectares which is the largest among all rice growing countries with, annual production of about 104.8 million tonnes and productivity of 2.3 tonnes $ha^{-1}$ in 2014-15 (GoI, 2016). To feed the increasing population, it is projected that yields of rice, must increase by at least 70% before 2050 (Furbank and Tester, 2011). Cold stress causes various injuries to rice in low-temperature and high-altitude areas affecting rice production stage pollen sterility can be induced by cold, decreasing the final number of grains which will ultimately leads to drastic reduction in grain yield. Low temperature stress is manifested at different growth stages such as germination, seedling, vegetative, reproductive, and grain maturity (Andaya and Mackill, 2003). Cold temperature during the reproductive phase leads to seed sterility, which reduces yield and grain quality. Low temperature at the booting stage has also been reported to cause degeneration of young microspores, hypertrophy, dissolution of tapetal cells and interrupting or decreasing the supply of nutrients from the anther walls to the pollens (Satake, 1989). Hence, from above fact it is well understood that cold stress is one of the threats to rice production. Hence, there is a need to breed cold tolerant rice varieties, for which exploitation of variability followed by selection is an important criteria. A concept of core and mini-core collection where the germplasm is representative of diverse genotype will be an excellent material to screen for cold tolerance. To improve the yield it is important to understand correlation between yield and its component traits. Keeping this in view, the present investigation is taken up to assess genetic variability, heritability and correlation among traits under low temperature stress.

## Materials and Methods

### *Plant Material*

The present study was conducted at CPGS (College of post graduate studies), Umiam, Meghalaya, situated at latitude of 25º41´ and longitude of 91º54´ and an elevation of 950 m above mean sea level in *Kharib* 2014-15. A panel of rice genotypes consisting of 85 mini core (Tiwari *et al*., 2015), 21 lowland rice genotypes and 11 upland and three checks were screened for their ability to withstand cold stress at reproductive stage. These genotypes were staggered planted at three different dates – timely sown (ENV 1), medium sown (ENV 2) and late sown (ENV 3) in an augmented field design with three

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blocks for each environment maintaining a spacing of 18 cm and 22 cm between plants and rows, respectively. Check varieties were randomly allotted in each block in each environment. Observations were recorded on ten randomly selected plants of each genotype per replication for ten traits *viz*. days to 50% flowering, flag leaf area, panicle exertion, panicle length, plant height, panicle number, spikelet fertility, test weight, spikelet per panicle, biological yield and grain yield per plant.

### *Statistical Analysis*

Analysis of variance was carried out for the above mentioned characters separately for three environments, by using online augmented analysis software (Rathore *et al.*, 2004) available at http://www.iasri.res.in/SpadWeb/. The ANOVA table generated from augmented design was used to estimate genotypic and phenotypic components of variance and heritability. The genotypic and phenotypic components of variation were calculated by the formula given by (Burton and Devane 1953) and heritability by (Allard, 1960). Genotypic and phenotypic correlation coefficients for all possible comparisons were made as per the formulae suggested by (Miller *et al.,* 1958). To test the significant of correlation coefficients, the estimated values were compared with the table value at n-2 degrees of freedom at 5% and 1% level of significance. The partitioning of genotypic correlation coefficient of the character in study into direct and indirect effects was carried out by using the procedure of (Dewey and Lu, 1959).

### *Principal Component Analysis (PCA)*

Data reduction method of PCA was used to distribute the genotypes along two major principal components that were derived on the basis of correlation coefficient of six characters that showed highest correlation with grain yield under ENV 3 and relative values of these characters with respect to ENV 1, expressed as the ratio of values in ENV 3 and values in ENV 1. Scatter plot was made using MS-EXCEL on the basis of principle component scores obtained by using SPAR 2.0 software developed by ICAR Indian Agricultural Statistics Research Institute, New Delhi. Outliers having high principal component values were identified as superior performers.

### *Pollen Viability Test*

Spikelet and pollen fertility is an appropriate index to evaluate cold tolerance at the booting stage and it was estimated under controlled environmental conditions in contrasting genotypes shortlisted from the field experiment. Pollen with round shape and dark blue colour were considered to be fertile; otherwise they were recorded as sterile. Panicles, which had exserted more than two-thirds out of flag leaf sheath were chosen early in the morning just before anthesis around 07:00 – 09:000 AM and the spikelets were selected from the second or third branch from top on the primary rachis. Third or fourth spikelets on the branch were used to estimate pollen viability. From each genotype, florets from three plants were collected and again from each plant, three spikelets were used for pollen viability test. Soon after collection, anthers from each spikelet were excised with a needle on the glass slide. The six anthers from each spikelet were crushed and stained with 10 µl of 1% (v/v) of $I_2$ (iodine) in 3% (v/v) KI (potassium iodide) solution. And from this, 1 µl was sampled and observed under light microscope at 10x magnification and digital images were taken and evaluated number of viable pollen. Afterwards, the numbers of pollen grains stained with $I_2$-KI as well as unstained pollen grains were counted. Pollen viability was estimated as the ratio of no. of stained pollen to the total no. of pollen grains and expressed as percentage i.e. Pollen viability = (No. of stained pollen/ Total no. of pollen grains) × 100.

## Results and Discussion

### *Analysis of Variance*

The analysis of variance revealed highly significant differences within the genotypes for all the traits studied in ENV 1 (Table 1). This indicated that the genotypes were possessing inherent genetic variation among themselves with respect to the traits studied. These findings are in accordance with the findings of (Rashmi *et al.,* 2017; Singh *et al.,* 2015; Singh *et al*., 2007). In ENV 3, panicle exsertion and spikelet per panicle were highly significant. Proportion of total variance due to genotypes was studied and variance components were further used to compute heritability estimates for each trait. Days to 50% flowering, Plant height and Spikelet fertility showed highest genotypic and phenotypic variance in all the three environments. Heritability in broad sense plays a predictive role in selection procedures and gives an idea of the total variation ascribable to genotypic effects, which are exploitable portion of variation (Sanghera *et al.,* 2013). Among all the traits, heritability of plant height (1.00, 0.98) in ENV 1 and ENV 2 was found to be highest whereas in ENV 3, spikelet per panicle (0.86) shown highest heritability. This finding was in close agreement with (Abebe *et al.,* 2017).

**Table 1. Analysis of variance for characters under study**

| ANOVA | | DTF | FLA | PE | PL | PH | PN | SF | TW | SPP | BY | GY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ENV 1 | 76.04** | 28.94 | 2.73* | 5.82** | 134.83** | 1.25 | 0.97 | 0.02** | 207.15 | 25.42* | 8.53 |
| Block(adj) | ENV 2 | 14.78 | 14.81 | 0.99 | 1.34 | 26.94* | 1.29 | 5.08 | 0.02 | 428.40 | 196.76** | 53.64* |
| | ENV 3 | 4.00 | 0.25 | 0.81 | 0.49 | 45.27 | 2.32 | 164.89 | 0.01 | 16.33 | 33.59* | 7.70 |
| | ENV 1 | 209.92** | 135.86** | 5.56** | 7.72** | 318.42** | 11.33* | 346.90** | 0.37** | 2013.2* | 528.38** | 215.59** |
| Treatment | ENV 2 | 166.30** | 82.36** | 4.35** | 9.89 | 293.86** | 11.29* | 499.70* | 0.26* | 730.65* | 162.84** | 42.88* |
| | ENV 3 | 132.86* | 14.92 | 5.64** | 5.68 | 172.91* | 3.33 | 492.10* | 0.27 | 302.03** | 15.64* | 2.98 |
| | ENV 1 | 1.41 | 8.57 | 0.33 | 5.82 | 0.12 | 1.33 | 3.02 | 0.00 | 292.82 | 2.09 | 13.59 |
| Error | ENV 2 | 10.28 | 4.40 | 0.24 | 6.33 | 2.31 | 1.94 | 65.52 | 0.03 | 110.17 | 1.59 | 4.22 |
| | ENV 3 | 12.83 | 5.07 | 0.44 | 0.49 | 27.52 | 2.15 | 58.51 | 0.23 | 15.69 | 2.15 | 1.72 |
| | ENV 1 | 86.11 | 31.41 | 3.91 | 22.03 | 97.28 | 8.44 | 61.73 | 2.44 | 94.05 | 42.01 | 22.99 |
| Mean | ENV 2 | 83.32 | 22.36 | 3.26 | 19.71 | 86.58 | 8.73 | 60.84 | 2.35 | 53.69 | 23.37 | 8.52 |
| | ENV 3 | 82.42 | 17.29 | 0.07 | 16.35 | 72.51 | 4.91 | 40.31 | 2.30 | 43.52 | 8.93 | 2.41 |
| | ENV 1 | 1.38 | 9.32 | 14.76 | 0.33 | 0.36 | 13.68 | 2.81 | 1.34 | 18.19 | 3.44 | 16.04 |
| CV | ENV 2 | 3.85 | 9.38 | 14.87 | 12.76 | 1.76 | 15.97 | 13.30 | 7.56 | 19.55 | 5.40 | 24.11 |
| | ENV 3 | 4.35 | 13.02 | 1015.44 | 8.71 | 7.23 | 29.92 | 18.97 | 20.95 | 9.10 | 16.44 | 54.38 |
| | ENV 1 | 69.50 | 42.43 | 1.74 | 0.63 | 106.10 | 3.33 | 114.63 | 0.12 | 573.49 | 175.43 | 67.33 |
| $V_g$ | ENV 2 | 52.01 | 25.99 | 1.37 | 1.19 | 97.18 | 3.11 | 144.73 | 0.08 | 206.83 | 53.75 | 12.89 |
| | ENV 3 | 40.01 | 3.29 | 1.73 | 1.73 | 48.47 | 0.39 | 144.53 | 0.01 | 95.45 | 4.50 | 0.42 |
| | ENV 1 | 70.91 | 51.00 | 2.08 | 6.45 | 106.22 | 4.67 | 117.64 | 0.12 | 866.31 | 177.52 | 80.92 |
| $V_p$ | ENV 2 | 62.28 | 30.38 | 1.61 | 7.51 | 99.49 | 5.06 | 210.25 | 0.11 | 317.00 | 55.34 | 17.11 |
| | ENV 3 | 52.84 | 8.35 | 2.17 | 2.22 | 75.98 | 2.54 | 203.04 | 0.25 | 111.14 | 6.65 | 2.14 |
| | ENV 1 | 0.98 | 0.83 | 0.84 | 0.10 | 1.00 | 0.71 | 0.97 | 0.99 | 0.66 | 0.99 | 0.83 |
| H | ENV 2 | 0.83 | 0.86 | 0.85 | 0.16 | 0.98 | 0.62 | 0.69 | 0.71 | 0.65 | 0.97 | 0.75 |
| | ENV3 | 0.76 | 0.39 | 0.80 | 0.78 | 0.64 | 0.15 | 0.71 | 0.05 | 0.86 | 0.68 | 0.20 |

DTF – Days to Flowering, FLA – Flag Leaf Area, PE- Panicle Exsertion, PL – Panicle Length, PH – Plant Height, PN – Panicle Number, SF – Spikelet Fertility, TW – Test Weight, SPP – Spikelet Per Panicle, BY – Biological Yield and GY – Grain Yield, CV – Coefficient of varience, Vg – Genotypic varience, Vp – Phenotypic varience, H – Heritability, ENV – Environment.

## Identifications of Important Traits

### *Correlation Coefficient Analysis*

Traits such as yield, which are of interest to breeders are complex and are the result of the interaction among number of components. Knowing the relationship between grain yield and its components is of paramount importance for making the best use of these relationships in selection (Sarawagi *et al*., 1997). The correlation coefficient study on grain yield based on yield contributing traits recorded for ten characters was done for three different environments (Table 2). For timely sown environment (ENV 1), overall correlation analysis showed that days to 50% flowering (r = 0.368), flag leaf area (r = 0.421), panicle length (r = 0.436), spikelet fertility (r = 0.588), spikelet per panicle (r = 0.643), biological yield (r = 0.493) were highly significant and correlated with grain yield. The study of correlation coefficient from medium sowing (ENV 2) revealed spikelet fertility (r = 0.491), spikelet per panicle (r = 0.520) and biological yield (r = 0.448) were significantly correlated to grain yield. In case of late sown environment (ENV 3), panicle exsertion (r = 0.253), panicle number (r = 0.490), spikelet fertility (r = 0.389), biological yield (r = 0.651) were positively correlated to grain yield. Overall correlation analysis showed that spikelet fertility and biological yield were highly and correlated with grain yield in all the three environments.

### *Path Coefficient Analysis*

Path coefficient analysis developed by Sewall Wright (1918) determines the significance of correlations between yield components and assigns relative importance to yield relations. The correlation coefficients generated by path analysis measure the direct and the indirect influence of a variable upon another (Nakawuka and Adipala, 1999). The direct effect of days to 50% flowering, panicle length and biological yield was observed negligible but correlation coefficient was positive in ENV 1 (Table 3). Interestingly, correlation coefficient between the traits and yield of spikelet

**Table 2. Path coefficient analysis for grain yields under three environments**

| | | DTF | FLA(cm) | PE(cm) | PL(cm) | PH(cm) | PN | SF% | TW(g) | SPP | BY(g) | GY(g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DTF | ENV 1 | 1 | 0.371** | -0.237* | 0.366** | 0.301** | 0.409** | -0.019 | -0.158 | 0.423** | 0.605** | 0.368** |
| | ENV 2 | 1 | 0.397** | -0.231* | 0.056 | 0.285* | 0.316** | -0.228* | -0.227* | 0.291* | 0.599** | 0.146 |
| | ENV 3 | 1 | 0.269* | -0.290* | 0.139 | -0.032 | 0.051 | -0.486** | -0.191 | -0.119 | 0.171 | -0.118 |
| FLA | ENV 1 | 0.371** | 1 | -0.096 | 0.522** | 0.390** | 0.066 | -0.02 | -0.153 | 0.495** | 0.593** | 0.421** |
| | ENV 2 | 0.397** | 1 | -0.029 | 0.315** | 0.377** | 0.024 | -0.148 | 0.149 | 0.384** | 0.423** | 0.148 |
| | ENV 3 | 0.269* | 1 | -0.309** | 0.539** | 0.351** | 0.029 | -0.344** | -0.089 | 0.459** | 0.318** | 0.049 |
| PE | ENV 1 | -0.237* | -0.096 | 1 | 0.16 | -0.174 | -0.436** | 0.136 | 0.199 | -0.1 | -0.236* | -0.026 |
| | ENV 2 | -0.231* | -0.029 | 1 | 0.374** | 0.023 | -0.104 | -0.112 | 0.202* | -0.074 | -0.024 | 0.005 |
| | ENV 3 | -0.290* | -0.309** | 1 | 0.019 | 0.134 | 0.214* | 0.187 | 0.225* | -0.043 | 0.083 | 0.253* |
| PL | ENV 1 | 0.366** | 0.522** | 0.16 | 1 | 0.270* | -0.127 | 0.268* | -0.102 | 0.549** | 0.345** | 0.436** |
| | ENV 2 | 0.056 | 0.315** | 0.374** | 1 | 0.278* | -0.022 | -0.017 | 0.059 | 0.316* | 0.257* | 0.228* |
| | ENV 3 | 0.139 | 0.539** | 0.019 | 1 | 0.629** | -0.029 | -0.092 | -0.011 | 0.422** | 0.300** | 0.029 |
| PH | ENV 1 | 0.301** | 0.390** | -0.174 | 0.270* | 1 | 0.217* | -0.105 | -0.149 | 0.391** | 0.650** | 0.277* |
| | ENV 2 | 0.285* | 0.377** | 0.023 | 0.278* | 1 | 0.08 | -0.121 | -0.009 | 0.228* | 0.441** | 0.033 |
| | ENV 3 | -0.032 | 0.351** | 0.134 | 0.629** | 1 | -0.024 | 0.054 | 0.108 | 0.375** | 0.351** | 0.147 |
| PN | ENV 1 | 0.409** | 0.066 | -0.436** | -0.127 | 0.217* | 1 | -0.251* | -0.236* | -0.01 | 0.521** | 0.208* |
| | ENV 2 | 0.316* | 0.024 | -0.104 | -0.022 | 0.08 | 1 | -0.1 | -0.142 | -0.210* | 0.593** | 0.141 |
| | ENV 3 | 0.051 | 0.029 | 0.214* | -0.029 | -0.024 | 1 | -0.063 | -0.128 | -0.364** | 0.698** | 0.490** |
| SF | ENV 1 | -0.019 | -0.02 | 0.136 | 0.268* | -0.105 | -0.251* | 1 | 0.279* | 0.161 | -0.049 | 0.588** |
| | ENV 2 | -0.228* | -0.148 | -0.112 | -0.017 | -0.121 | -0.1 | 1 | 0.192 | 0.204 | -0.123 | 0.491** |
| | ENV 3 | -0.486** | -0.344** | 0.187 | -0.092 | 0.054 | -0.063 | 1 | 0.339** | -0.166 | 0.077 | 0.389** |
| TW | ENV 1 | -0.158 | -0.153 | 0.199 | -0.102 | -0.149 | -0.236* | 0.279* | 1 | -0.244* | -0.096 | 0.069 |
| | ENV 2 | -0.227* | 0.149 | 0.202* | 0.059 | -0.009 | -0.142 | 0.192 | 1 | -0.084 | -0.006 | 0.267* |
| | ENV 3 | -0.191 | -0.089 | 0.225* | -0.011 | 0.108 | -0.128 | 0.339** | 1 | 0.048 | -0.105 | 0.187 |
| SPP | ENV 1 | 0.423** | 0.495** | -0.1 | 0.549** | 0.391** | -0.01 | 0.161 | -0.244* | 1 | 0.459** | 0.643** |
| | ENV 2 | 0.291* | 0.384** | -0.074 | 0.316* | 0.228* | -0.210* | 0.204* | -0.084 | 1 | 0.369** | 0.520** |
| | ENV 3 | -0.119 | 0.459** | -0.043 | 0.422** | 0.375** | -0.364** | -0.166 | 0.048 | 1 | 0.017 | -0.07 |
| BY | ENV 1 | 0.605** | 0.593** | -0.236* | 0.345** | 0.650** | 0.521** | -0.049 | -0.096 | 0.459** | 1 | 0.493** |
| | ENV 2 | 0.599** | 0.423** | -0.024 | 0.257* | 0.441** | 0.593** | -0.123 | -0.006 | 0.369** | 1 | 0.448** |
| | ENV 3 | 0.171 | 0.318** | 0.083 | 0.300** | 0.351** | 0.698** | 0.077 | -0.105 | 0.017 | 1 | 0.651** |
| GY | ENV 1 | 0.368** | 0.421** | -0.026 | 0.436** | 0.277* | 0.208* | 0.588** | 0.069 | 0.643** | 0.493** | 1 |
| | ENV 2 | 0.146 | 0.148 | 0.005 | 0.228* | 0.033 | 0.141 | 0.491** | 0.267* | 0.520** | 0.448** | 1 |
| | ENV 3 | -0.118 | 0.049 | 0.253* | 0.029 | 0.147 | 0.490** | 0.389** | 0.187 | -0.07 | 0.651** | 1 |

(*) = significant at 5% level of significant; (**) = significant at 1% level of significant

fertility was almost equal to its direct effect. So, direct selection through this trait will be effective. Among the component traits, spikelet fertility had highest direct effect (0.579) to grain yield along with positive indirect effects through days to 50% flowering, panicle exsertion, test weight, spikelet per panicle, biological yield and negative indirect effect through flag leaf area, panicle length, plant height, panicle number. Biological yield, indirect effect of panicle number (0.233) and spikelet per panicle (0.251) had more correlation towards grain yield. It was observed that plant height (0.031) had no direct effect to grain yield but it was supported by positive indirect effect of high magnitude via spikelet per panicle (0.213) which is highly correlated to grain yield. In ENV 2, following partitioning of individual correlation values of the traits into direct and indirect effects, spikelet fertility (0.394), spikelet per panicle (0.374), biological yield (0.436) and test weight exhibit direct effect of correlation to grain yield. Among these, biological yield (0.436) had high magnitude of direct effect. Days to flowering had recorded a negligible contribution via direct effect to grain yield but high correlation via indirect effect on biological yield (0.261). Panicle number (0.055) was not directly correlated to grain yield but indirectly correlated via biological yield (0.259). Among the component traits, spikelet fertility (0.279) and biological yield (0.649) contributed direct effects on yield but biological yield had more directly correlated on yield with high magnitude in ENV 3. Flag leaf area (0.100) and panicle number (0.044) had negligible correlation via direct effect to grain yield but it was indirectly correlated with biological yield. Similarly,

direct effect of plant height (-0.080) was not correlated to grain yield but indirectly correlated through biological yield (0.227). The direct effect of spikelet fertility was highest and also highly correlated to grain yield in the three environments. These results are similar to the finding of (Pallavi *et al*., 2017; Shoumik *et al*., 2017).

### *Principal Component Analysis (PCA)*

Based on the six characters and their relative values (value in ENV 3/ value in ENV 1), principal component analysis for data reduction was performed and the genotypes were plotted across the first two principal components (Fig. 1). The first two components explained 33% of total variability, PC 1 contributing 18.7% and PC 2 contributing 14.93%. Similar findings were obtained by (Gana *et al*., 2013; Sanni *et al*., 2010). The genotypes were distributed with respect to the first two components and genotypes showing high value for first two principal components UR 100, BAM 4115, BAM 759, BAM 4483 and LR 11 were selected as potential reproductive stage cold tolerant genotypes.

### *Pollen Viability Test*

Pollen viability test of different mini core rice genotypes under cold stress condition relative to timely sown condition were studied and tolerant and susceptible genotypes were identified according to their viability of pollen at reproductive stage separately for timely and late sown environment (Fig. 2). The ratio of pollen viability under ENV 3 and pollen viability under ENV 1 led to the identification of superior genotypes with respect to the trait. Genotypes performing well in cold stress were BAM 5889, BAM 5179, and BAM 4408 whereas genotypes with inferior performances were BAM 56, BAM 811 and BAM 4138. Pollen viability under cold stress has been reported to be an important indicator for cold tolerance (Zhou *et al.,* 2010).

**Table 3. Path Coefficient studies**

| | | | Indirect Effect Through | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Direct Effect | DTF | FLA | PE | PL | PH | PN | SF | TW | SPP | BY | GY (g) |
| DTF | ENV 1 | -0.028 | | 0.082 | -0.034 | -0.028 | 0.009 | 0.183 | -0.011 | -0.022 | 0.231 | -0.014 | 0.368** |
| | ENV 2 | -0.001 | | -0.045 | -0.005 | 0.004 | -0.05 | 0.017 | -0.09 | -0.054 | 0.109 | 0.261 | 0.146 |
| | ENV 3 | -0.033 | | 0.027 | -0.041 | -0.021 | 0.003 | 0.002 | -0.136 | -0.027 | -0.003 | 0.111 | -0.118 |
| FLA | ENV 1 | 0.221 | -0.011 | | -0.014 | -0.04 | 0.012 | 0.029 | -0.012 | -0.022 | 0.27 | -0.014 | 0.421** |
| | ENV 2 | -0.113 | 0 | | -0.001 | 0.022 | -0.066 | 0.001 | -0.058 | 0.036 | 0.143 | 0.185 | 0.148 |
| | ENV 3 | 0.1 | -0.009 | | -0.044 | -0.08 | -0.028 | 0.001 | -0.096 | -0.013 | 0.011 | 0.206 | 0.049 |
| PE | ENV 1 | 0.144 | 0.007 | -0.021 | | -0.012 | -0.005 | -0.195 | 0.079 | 0.028 | -0.055 | 0.005 | -0.026 |
| | ENV 2 | 0.02 | 0 | 0.003 | | 0.026 | -0.004 | -0.006 | -0.044 | 0.048 | -0.028 | -0.011 | 0.005 |
| | ENV 3 | 0.141 | 0.01 | -0.031 | | -0.003 | -0.011 | 0.009 | 0.052 | 0.032 | -0.001 | 0.054 | 0.253* |
| PL | ENV 1 | -0.077 | -0.01 | 0.115 | 0.023 | | 0.008 | -0.057 | 0.156 | -0.015 | 0.3 | -0.008 | 0.436** |
| | ENV 2 | 0.068 | 0 | -0.036 | 0.008 | | -0.049 | -0.001 | -0.007 | 0.014 | 0.118 | 0.112 | 0.228* |
| | ENV 3 | -0.149 | -0.005 | 0.054 | 0.003 | | -0.05 | -0.001 | -0.026 | -0.002 | 0.01 | 0.195 | 0.029 |
| PH | ENV 1 | 0.031 | -0.009 | 0.086 | -0.025 | -0.021 | | 0.097 | -0.061 | -0.005 | 0.213 | -0.015 | 0.277* |
| | ENV 2 | -0.176 | 0 | -0.043 | 0 | 0.019 | | 0.004 | -0.047 | 0.002 | 0.085 | 0.192 | 0.033 |
| | ENV 3 | -0.08 | 0.001 | 0.035 | 0.019 | -0.093 | | -0.001 | 0.015 | -0.009 | 0.009 | 0.227 | 0.147 |
| PN | ENV 1 | 0.447 | -0.012 | -0.021 | -0.063 | 0.01 | 0.097 | | -0.146 | -0.033 | -0.005 | -0.012 | 0.208* |
| | ENV 2 | 0.055 | 0 | 0.003 | -0.002 | -0.001 | 0.004 | | -0.039 | -0.034 | -0.079 | 0.259 | 0.141 |
| | ENV 3 | 0.044 | -0.002 | -0.031 | 0.03 | 0.004 | -0.001 | | -0.018 | -0.018 | -0.009 | 0.453 | 0.490** |
| SF | ENV 1 | 0.579 | 0.001 | -0.004 | 0.02 | -0.021 | -0.003 | -0.112 | | 0.04 | 0.088 | 0.001 | 0.588** |
| | ENV 2 | 0.394 | 0 | 0.017 | -0.002 | -0.001 | 0.021 | -0.005 | | 0.046 | 0.076 | -0.054 | 0.491** |
| | ENV 3 | 0.279 | 0.016 | -0.034 | 0.026 | 0.014 | -0.004 | -0.003 | | 0.049 | -0.004 | 0.05 | 0.389** |
| TW | ENV 1 | 0.142 | 0.004 | -0.034 | 0.029 | 0.008 | -0.005 | -0.106 | 0.162 | | -0.134 | 0.002 | 0.069 |
| | ENV 2 | 0.24 | 0 | -0.017 | 0.004 | 0.004 | 0.002 | -0.008 | 0.075 | | -0.031 | -0.003 | 0.267* |
| | ENV 3 | 0.143 | 0.006 | -0.009 | 0.032 | 0.002 | -0.009 | -0.006 | 0.095 | | 0.001 | -0.068 | 0.187 |
| SPP | ENV 1 | 0.546 | -0.012 | 0.109 | -0.014 | -0.042 | 0.012 | -0.004 | 0.093 | -0.035 | | -0.01 | 0.643** |
| | ENV 2 | 0.374 | 0 | -0.043 | -0.001 | 0.022 | -0.04 | -0.012 | 0.08 | -0.02 | | 0.161 | 0.520** |
| | ENV 3 | 0.024 | 0.004 | 0.046 | -0.006 | -0.063 | -0.03 | -0.016 | -0.046 | 0.007 | | 0.011 | -0.07 |
| BY | ENV 1 | -0.023 | -0.017 | 0.131 | -0.034 | -0.027 | 0.02 | 0.233 | -0.028 | -0.014 | 0.251 | | 0.493** |
| | ENV 2 | 0.436 | -0.001 | -0.048 | 0 | 0.018 | -0.078 | 0.033 | -0.048 | -0.001 | 0.138 | | 0.448** |
| | ENV 3 | 0.436 | -0.001 | -0.048 | 0 | 0.018 | -0.078 | 0.033 | -0.048 | -0.001 | 0.138 | | 0.651** |

(*) = significant at 5% level of significant; (**) = significant at 1% level of significant

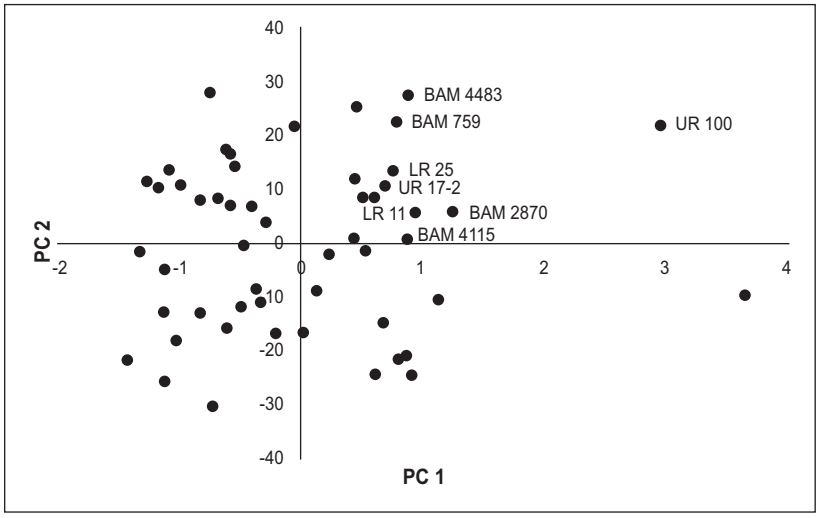


**Fig.1. Principal Component Analysis based on rice characters found to be important under late sown condition and their relative value as compared to timely sown condition**

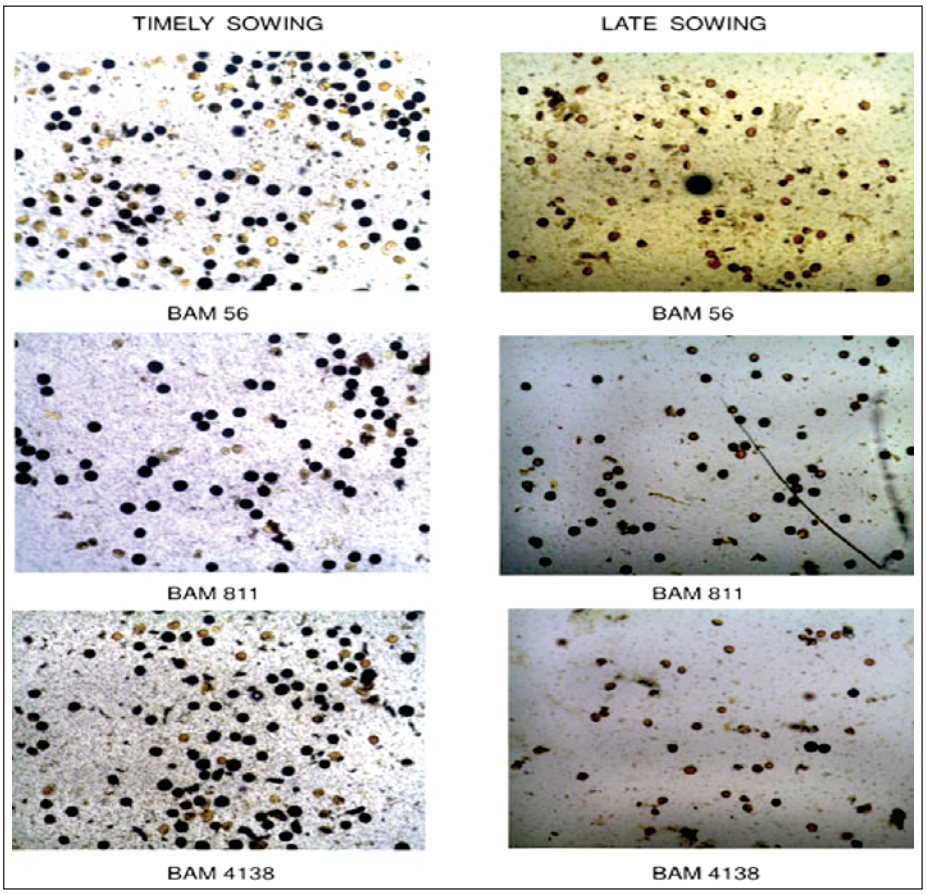


**Fig. 2. Identification of tolerant and susceptible genotypes with respect to pollen viability**

### *Identification of Important Genotypes under Cold Stress at Reproductive Stage*

Important characters having significant correlation and path coefficient values with respect to grain yield under low temperature at flowering stage (late sown condition) were identified. The characters which were identified were biological yield, spikelet fertility, panicle exsertion, test weight, grain yield and spikelet per panicle. Among the

mini core rice accessions studied, genotypes performing well under both timely (ENV 1) and late sown (ENV 2/ ENV 3) environment identified from the selected six traits were BAM 4115, UR 100, BAM 5179, BAM 3808, LR 11, BAM 4483 and UR 3.

## Conclusion

The genotypes identified in the study, especially the local landraces, can be used as potential donors for breeding cold tolerant varieties for mid- and high altitude areas of the North Eastern Hill Region. The important characters identified should help designing effective selection indices in such breeding programmes. Selected tolerant and susceptible genotypes could be further utilized and studied in detail to elucidate the genetic, molecular and physiological basis of cold tolerance at both, seedling and reproductive stage.

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