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## Research Article

# Diversity analysis for yield traits and sheath blight resistance in rice genotypes

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**Abstract**
Genetic diversity play a crucial role in crop improvement as progeny from divergent parents show greater heterosis and provide a wide range of variability in segregating generation. It also provides a chance to obtain new recombination of genes in the gene pool. The present study was conducted with 29 genotypes and observations were recorded for plant height, the number of tillers/plant, the number of productive tillers/ plant, panicle length, grain number/panicle, test weight and grain yield/ plant. Genetic divergence among the genotypes was estimated by Mahalanobis $D^2$ analysis. The genotypes were grouped into six clusters. The maximum number of genotypes (eight) was found in cluster 4, followed by seven in cluster 2, six in cluster 3, four in cluster 1, three in cluster 5 and one in cluster 6. Maximum intra-cluster $D^2$ value was recorded in cluster 4 (166.93) and minimum in cluster 6 (0.00). The $D^2$ value of inter-cluster ranged from 204.20 to 1861.92. Maximum inter-cluster $D^2$ value was found between cluster 4 and 5 (1861.92), followed by cluster 5 and 6 (1548.42). It indicated a very wide range of genetic diversity among genotypes. These genotypes may be utilized for the hybridization programme for sustaining rice production. Moreover, from this study, we also recommend crossing of genotypes belong to cluster 5 and two genotypes of cluster 4 (Ngonolasha and Phougak) for developing high yielding genotype with sheath blight resistance.

**Keywords**
Rice, Genetic diversity, Sheath blight, $D^2$ statistics

## INTRODUCTION

Rice is the staple food crop for more than half of the global population. India is one of the world's largest rice producers. In India, it is grown in an area of about 42.95 million hectares with a production of 112.905 million tonnes and productivity of 2585 kg ha⁻¹ (Anonymous, 2017-18). Sheath blight is one of the major diseases occurring in most rice-producing areas and is second in importance, next to rice blast in reducing both grain yield and quality. This disease is caused by *Rhizoctonia solani* AG1-1A Kühn. The yield penalty for this disease can be up to 50% under favourable environmental conditions (Richa *et al.*, 2016). Till now no absolute resistance to sheath blight disease was reported. Only moderate resistance to rice sheath blight has been reported by different researchers (Sha and Zhu, 1990; Zou *et al.,* 2000; Sharma *et al.*, 2009; Liu *et al.*, 2009; Channamallikarjuna *et al.,* 2010, Dey *et al.*, 2016). In our previous study, we reported some moderate resistance genotypes for sheath blight *viz.*, SM 801 (N 22 mutant), Ngnololasha, Wazuhophek, Gumdhan and Phougak (landraces from the northeast), RP 2068-18-3-5 (gall midge biotype differential) and Tetep (cultivar).

Genetic diversity is a prerequisite of any crop improvement programme. Progeny obtained from divergent parents shows greater heterosis and provide a wide range of variability in segregating generation. Plant Breeders utilize the knowledge of genetic diversity for choosing parents for hybridization programme. Knowledge obtained from genetic diversity analysis will also be helpful for developing high yielding genotypes with sheath blight resistance. Genetic divergence can be studied by $D^2$ statistics developed by Mahalanobis (1936). The present investigation was carried out to estimate the magnitude of genetic divergence present in 29 rice genotypes.

## MATERIALS AND METHODS

Twenty-nine (29) rice genotypes (**Table 1**) comprising landraces from the northeast, introgression lines (ILs) from wild species and improved cultivars were transplanted in Randomized Block Design (RBD) with 3 replications at Indian Institute of Rice Research (IIRR) farm, ICRISAT campus during *Kharif* 2014. In each replication, the single seedling was transplanted with the spacing of 20 X 15 cm

at 30 days after sowing. The recommended agronomic practices and plant protection measures were followed to maintain normal crop growth. Observations were recorded on five randomly selected plants in each replication for plant height (cm), number of tillers/ plant, number of productive tillers/ plant, panicle length (cm), grain number/ panicle, test weight (g) and grain yield/ plant (g). Genetic divergence among the 29 genotypes was estimated by Mahalanobis D² analysis (Mahalanobis, 1936). The grouping of these genotypes into clusters was carried out by Tocher's methods (Rao, 1952). Intra and inter-cluster distances mean performances and contribution % of individual traits to the divergence of clusters of different characters were also calculated.

Additionally, at maximum tillering stage (approximately 40 days after planting), rice plants were inoculated with *R. solani* by placing five typha pieces between tillers in the central region of rice hills 5-10 cm above the waterline and then tied with a rubber band to maintain high humidity in the microclimate. For scoring the sheath blight disease reaction, data on plant height and lesion height were recorded at 20 days after inoculation (DAI) to calculate relative lesion height. The relative lesion height (RLH) was calculated by the following formula for scoring disease reaction and graded as per the 0-9 Standard Evaluation System (SES) (Table 6).

$$RLH \% = \frac{\text{Lesion height (cm)}}{\text{Plant height (cm)}} \times 100$$

**Table 1. List of rice genotypes along with disease scoring**

| SN | Genotype | Type | Scoring | Disease Reaction | SN | Genotype | Type | Scoring | Disease Reaction |
|---|---|---|---|---|---|---|---|---|---|
| 1 | SM-801 | N-22 mutant | 3 | Moderately Resistant | 16 | BG-380-2 | Cultivar | 5 | Moderately susceptible |
| 2 | 9(B) | Wild introgression line | 7 | Susceptible | 17 | MR 1523 | Cultivar | 9 | Highly Susceptible |
| 3 | 16(B) | Wild introgression line | 7 | Susceptible | 18 | RP-2068-18-3-5 | Elite breeding line | 3 | Moderately Resistant |
| 4 | 61(B) | Wild introgression line | 5 | Moderately susceptible | 19 | GSR-137 | Elite breeding line | 7 | Susceptible |
| 5 | Tetep | Cultivar | 3 | Moderately Resistant | 20 | RPBIO226 | Cultivar | 9 | Highly Susceptible |
| 6 | BPT 5204 | Cultivar | 9 | Highly Susceptible | 21 | MTU 1010 | Cultivar | 9 | Highly Susceptible |
| 7 | Swarna | Cultivar | 9 | Highly Susceptible | 22 | Swarnadhan | Cultivar | 5 | Moderately susceptible |
| 8 | IR 50 | Cultivar | 9 | Highly Susceptible | 23 | Kavya | Cultivar | 7 | Susceptible |
| 9 | Ching Chakhao | Landrace | 5 | Moderately susceptible | 24 | Sumi special | Landrace | 5 | Moderately susceptible |
| 10 | Ngonolasha | Landrace | 3 | Moderately Resistant | 25 | Haorei Machang | Landrace | 5 | Moderately susceptible |
| 11 | Jasmine 85 | Cultivar | 7 | Susceptible | 26 | Talong | Landrace | 5 | Moderately susceptible |
| 12 | Wazuho Phek | Landrace | 3 | Moderately Resistant | 27 | Phougak | Landrace | 3 | Moderately Resistant |
| 13 | Meghalaya Lefara | Landrace | 7 | Susceptible | 28 | Machang Kaoyeng | Landrace | 5 | Moderately susceptible |
| 14 | Gumdhan | Landrace | 3 | Moderately Resistant | 29 | Zunhiboto | Landrace | 5 | Moderately susceptible |
| 15 | ARC 6605 | Landrace | 5 | Moderately susceptible | | | | | |

## RESULTS AND DISCUSSION

The genotypes were grouped into six clusters (**Table 2**). The genotypes within the same cluster are closely related to each other. The maximum number of genotypes (eight) was included in cluster 4 followed by seven in cluster 2, six in cluster 3, four in cluster 1, three in cluster 5 and one cluster 6. Grouping of genotypes in different clusters is shown in **Fig 1.** Genotypes originated from the same geographic region fell into different clusters, indicating that clustering of populations does not follow their geographic distribution. Average intra and inter-cluster values have been shown in **Table 3.** The maximum intra-cluster distance was recorded in cluster 4 (166.93). The inter-cluster distance ranged from 204.20 to 1861.92 indicating that genetic materials are quite diverse. Crosses between parents belonging to the most diverse clusters would be expected to show maximum heterosis (Souroush *et al.*, 2004).

**Table 2. Cluster composition of 29 genotypes (Tocher's method)**

| Cluster | Number of Genotypes | Name of Genotypes |
|---|---|---|
| 1 | 4 | 16(B), 61(B), 9(B), Swarna |
| 2 | 7 | MR 1523, GSR-137, SM-801, Tetep, RP-2068-18-3-5; Swarnadhan, BG-380-2 |
| 3 | 6 | Gumdhan, MTU 1010, Machang Kaoyeng, Wazuho Phek, Haorei Machang, Meghalaya Lefara |
| 4 | 8 | Sumi special, Zunhiboto, Ngonolasha, Phougak, Ching Chakhao, Talong, ARC 6605, Jasmine 85 |
| 5 | 3 | BPT 5204, RPBIO226, Kavya |
| 6 | 1 | IR 50 |

**Table 3. Intra (bold) and inter-cluster (diagonal) average of D² and D values (parenthesis) of 29 genotypes**

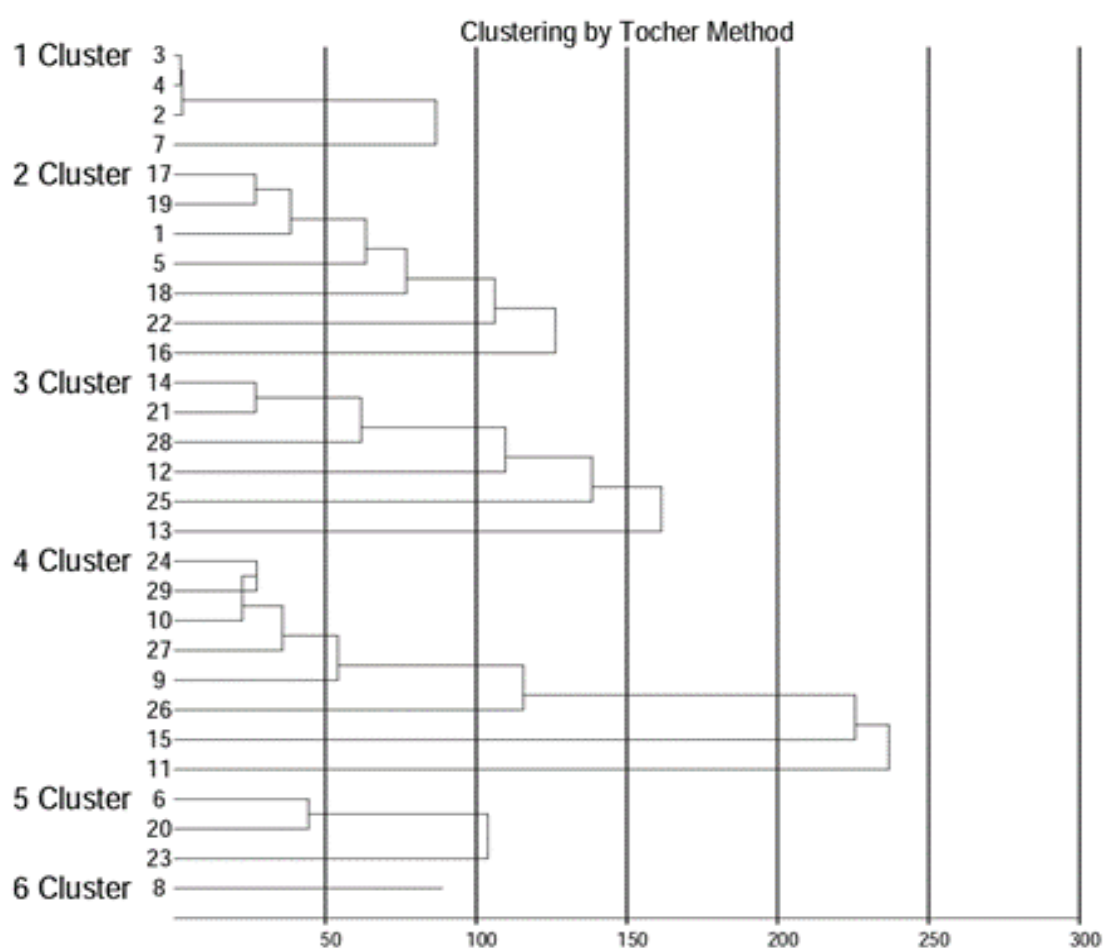| | Cluster. 1 | Cluster. 2 | Cluster. 3 | Cluster. 4 | Cluster. 5 | Cluster. 6 |
|---|---|---|---|---|---|---|
| Cluster.1 | **59.44** **(7.71)** | 592.92 (24.35) | 279.22 (16.71) | 1080.44 (32.87) | 256.64 (16.02) | 841.58 (29.01) |
| Cluster.2 | | **109.62** **(10.47)** | 472.19 (21.73) | 349.69 (18.70) | 1207.56 (34.75) | 204.20 (14.29) |
| Cluster.3 | | | **154.01** **(12.41)** | 594.38 (24.38) | 581.29 (24.11) | 916.88 (30.28) |
| Cluster.4 | | | | **166.93** **(12.92)** | 1861.92 (43.15) | 737.67 (27.16) |
| Cluster.5 | | | | | **118.59** **(10.89)** | 1548.42 (39.35) |
| Cluster.6 | | | | | | **0.00** **(0.00)** |



**Fig1. Clustering of Genotypes** (1-SM-801; 2- 9(B); 3-16(B); 4- 61(B); 5- Tetep; 6-BPT 5204; 7-Swarna; 8-IR 50; 9-Ching Chakhao; 10-Ngonolasha; 11-Jasmine 85; 12-Wazuho Phek; 13-Meghalaya Lefara; 14-Gumdhan; 15-ARC 6605; 16-BG-380-2; 17-MR 1523; 18- RP-2068-18-3-5; 19- GSR-137; 20-RPBIO226; 21-MTU 1010; 22- Swarnadhan; 23-Kavya; 24-Sumi special; 25-Haorei Machang; 26-Talong; 27-Phougak; 28-Machang Kaoyeng; 29-Zunhiboto)

Maximum inter-cluster distance observed between cluster 4 and cluster 5 (1861.92), followed by cluster 5 and cluster 6 (1548.42) suggesting wide genetic diversity between these clusters. In this study, the inter-cluster distances were higher than the intra-cluster distances which indicate the presence of considerable diversity among the genotypes. Similar kinds of results for inter and intra-cluster distances in rice were reported by different researchers like Kuchanur *et al.* (2009); Shahidullah *et al.* (2009); Vennela *et al.* (2017) and Behera *et al.* (2018).

The genetic divergence among genotypes was also supported by cluster means for different characters (**Table 4**). Maximum cluster means for plant height (140.08) and test weight (27.08) was recorded in cluster 4. Desirable traits like maximum grain number /panicle (280.33) and grain yield/plant (41.56) were observed in genotypes of cluster 5. Although maximum tillers/plant and productive tillers/plant noted in cluster 1. In the present study genotypes of clusters, 3 showed maximum panicle length with minimum grain yield/plant which is not desirable

**Table 4. Cluster Means**

|  | Plant Height | Tillers/ Plant | Productive Tillers/ Plant | Panicle length | Grain number/ Panicle | Test weight | Grain Yield/ Plant |
|---|---|---|---|---|---|---|---|
| **Cluster 1** | 100.17 | 21.25 | 20.92 | 20.08 | 228.50 | 21.67 | 26.92 |
| **Cluster 2** | 97.57 | 15.62 | 14.90 | 21.10 | 127.71 | 21.86 | 34.48 |
| **Cluster 3** | 125.39 | 8.83 | 8.33 | 23.06 | 198.28 | 24.94 | 22.67 |
| **Cluster 4** | 140.08 | 9.75 | 9.25 | 22.54 | 104.00 | 27.08 | 23.87 |
| **Cluster 5** | 95.56 | 14.11 | 13.33 | 20.00 | 280.33 | 17.56 | 41.56 |
| **Cluster 6** | 58.33 | 20.33 | 19.33 | 22.33 | 109.33 | 20.33 | 33.00 |

**Table 5. Contribution % of the individual trait to the divergence**

| Source | Contribution % | Times Ranked 1st |
|---|---|---|
| Plant Height (cm) | 22.91 % | 93 |
| Tillers/ Plant | 4.43 % | 18 |
| Productive Tillers/ Plant | 0.00 % | 0 |
| Panicle length (cm) | 0.99 % | 4 |
| Grain number/ Panicle | 64.04 % | 260 |
| Test weight (g) | 4.43 % | 18 |
| Grain Yield/ Plant (g) | 3.20 % | 13 |

Character contribution towards the divergence was assessed based on the ranking method. Contribution (%) of individual traits to the divergence is presented in **table 5**. Grain number/ Panicle contributed the maximum towards genetic divergence (64.04%), followed by plant height (22.91%), test weight (4.43%), tillers/ plant (4.43%) grain yield/ plant (3.20%) and panicle length (0.99%).

Productive tillers/ plant showed no contribution (0.00%) toward the divergence. Similar kind of results for plant height was also reported by Kumari *et al* (2018). Hence, the Grain number/Panicle and Plant height were found to be potential contributors to genetic divergence in the genotypes.

**Table 6. Standard Evaluation System (SES) (IRRI 2002) for sheath blight of rice**

| Disease score | Disease Reaction | Description (based on relative lesion height-RLH %) |
|---|---|---|
| 0 | Immune | No infection |
| 1 | Resistant | Vertical spread of lesion up to 20% of plant height |
| 3 | Moderately Resistant | Vertical spread of lesion up to 21-30% of plant height |
| 5 | Moderately Susceptible | Vertical spread of lesion up to 31-45% of plant height |
| 7 | Susceptible | Vertical spread of lesion up to 46-65% of plant height |
| 9 | Highly Susceptible | Vertical spread of lesion up to 66-100% of plant height |

Crosses between divergent parents from the different cluster are likely to produce considerable range variability and transgressive segregations. The present study recommends that the parental lines could be selected from cluster 4 and cluster 5 for hybridization programme. In our previous study, we reported some genotypes as moderate resistance to sheath blight based on three years of testing (Dey *et al.,* 2016). These genotypes are well distributed in cluster 2, cluster 3 and cluster 4. Several researchers reported that the number of grains/panicle showed a positive direct effect on grain yield per plant

(Naseer *et al.,* 2015). As we mentioned above, genotypes of cluster 5 recorded with a maximum grain number/ panicle. Intercluster distance between cluster 4 and cluster 5 was also recorded maximum (1861.92). Therefore, crossing between genotypes of cluster 5 and two genotypes of cluster 4 (Ngonolasha and Phougak) may result high yielding genotype with sheath blight resistance.

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