Original Research Article

Genetic diversity analysis of rice (*Oryza sativa* L.) genotypes for yield and sheath blight resistancescreening

ABSTRACT

Sheath blight disease, caused by *Rhizoctoniasolani*Kühn, is considered the second most important disease affecting rice, causing yield reduction globally. In the present study thirty diverse rice genotypes wereinoculated with fungal mycelia during the maximum tillering stage to assess the genetic diversity of rice genotypes for sheath blight reactions. Mahalanobis D^2 statistics was performedfor grain yield and yield contributing features under sheath blight stress to calculate the genetic divergence between the genotypes. Four clusters were formed from the genotypes. Cluster III has the highest number of genotypes (nine). The highest inter-cluster distance was noticed between cluster I and cluster IV (11.41) and minimumbetween cluster III and cluster IV (6.50). The intra-cluster distances were lower, indicating the homogeneity of the genotypes within the clusters. Maximum intra-cluster D^2 value was recorded in cluster IV (6.32) and minimum in cluster II (5.36). Cluster I showed high genetic divergence from all other clusters. Hence, the genotypes from cluster I could be used for hybridization with the genotypes of other clusters to develop high yielding sheath blight resistant rice varieties.

Keywords*: Rice sheath blight resistance, cluster analysis, D^2 statistics, genetic divergence, rice germplasm, rhizoctonoasolani, relative lesion height.*

INTRODUCTION

Rice (*Oryza sativa* L.)isan important cereal crop in the world, playing a vital role in nutrition and food security [1].However, due to climatic changes, rice production is challenged by several emerging diseases, one of the most significant being sheath blight, caused by the soil-borne necrotrophic fungus *Rhizoctoniasolani*Kühn. Sheath blight causes infection from seedling to the heading stage, causing damage to leaves, sheaths, and even panicles affecting plant health and yield[2]. Sheath blight thrives in warm, humid conditions, making it particularly problematic in regions with high rainfall and intensive cultivationreducing both grain yield and quality [3].The yield loss due to sheath blight was estimated to range from 10-40% annually, causing a growing threat to rice cultivation [4]. Effective management strategies, including developing resistant rice varieties, cultural practicesand judicious use of fungicides are essential to mitigate the effects of this disease [5]. However, highly resistant varieties, have not yet been identified which significantly limits the progress of sheath blight resistance

breeding[6]. Only moderate resistance to rice sheath blight has been reported by different researchers [7,8,9].

Genetic diversity is essential for any crop improvement program, as progenies from divergent parents exhibit greater heterosis and broader variability in segregating generations [9]. Diversity analysis is used to assess the genetic divergence existing in the germplasm collections and to identify parental genotypes with greater divergence for hybridization to develop high yielding varieties [10]. Mahalanobis D^2 statistics has been widely recognized as a powerful tool for plant breeders to select suitable parental genotypes with a broader range of variability for various traits [11].The clustering can reveal the pattern of divergenceamong the genotypes and help in selecting diverse parental lines for breeding[12]. Hence, the present investigation was undertaken to estimate the magnitude of genetic divergence among 30 rice genotypes under sheath blight disease incidence.

MATERIALS AND METHODS

Thirty rice genotypes (Table 1) were screened for sheath blight resistance in completely randomized design with two replications at the Department of Genetics and Plant Breeding, College of Agriculture, Vellayani.Atthe maximum tillering stage (approximately 40 days after planting), rice plants were inoculated with *Rhizoctoniasolani*mycelia bits between tillers, 5-10 cm above the waterline and then tied with cotton to maintain highhumidity. Observations were recorded from five randomly selected plants from each replication for different characters *via* days to heading (DH), days to 50 per cent flowering (DF), number of tillers per plant (NT), number of productive tillers per plant (NPT), stem thickness (ST), plant height (PH, cm), lesion height (LH, cm), panicle length (PL, cm), number of grains per panicle (GP), thousand grain weight (TGW, g), grain yield per plant (GY,g), relative lesion height (RLH, %), number of lesions per plant (NLS) and percentage disease index (PDI, %). The lesion height was recorded on the 28^{th}day after inoculation. The relative lesion height (RLH) was calculated using the following formula and expressed in terms of percentage [9].

$$\text{Relative lesion height (RLH)} = \frac{\text{Lesion height (cm)}}{\text{plant height(cm)}} \times 100$$

Percentage disease index(PDI) was calculated using the following equationand expressed in terms of percentage[13].

$$\text{PDI} = \frac{\text{Sum of individual ratings}}{\text{No.of plants examined} * \text{Maximum disease scale}} \times 100$$

The data was analyzed following Mahalanobis's (1936) generalized distance (D^2) extended by Rao [14]. The grouping of the genotypes into clusters was carried out using Ward's methods. Statistical analysis was carried out usingRStudio 3.6.1.

Table 1: List of rice genotypes used in the study

Treatments	Name of Genotypes	Treatments	Name of Genotypes
T1	Remanika	T16	Prathyasa
T2	Gouri	T17	Karthika
T3	Chenthadi	T18	Chenkayama
T4	Krishnanjana	T19	Vyttila-9
T5	Panchami	T20	Pournami
T6	Karishma	T21	Chettivirippu
T7	Revathy	T22	Vyttila-6
T8	Bhagya	T23	Onam
T9	Vyttila-7	T24	Makom
T10	Karuna	T25	Uma
T11	White Ponni	T26	Bhadra
T12	Sreyas	T27	Vyttila-8
T13	Vyttila-1	T28	Vyttila-4
T14	Vyttila-10	T29	Pokkali
T15	Vyttila-3	T30	Kuthiru

RESULTS AND DISCUSSIONS

Distribution and grouping of genotypes

The cluster analysis was conducted for 30 genotypes (Table 2) for fourteen charactersnamely days to heading (DH), days to 50 per cent flowering (DF), number of tillers per plant (NT), number of productive tillers per plant (NPT), stem thickness (ST), plant height (PH, cm), lesion height (LH, cm), panicle length (PL, cm), number of grains per panicle (GP), thousand grain weight (TGW, g), grain yield per plant (GY,g), relative lesion height (RLH, %), number of lesions per plant (NLS) and percentage disease index (PDI, %).Based on the distribution pattern,the 30 genotypes were grouped into four clusters. The clustering pattern of the genotypes is depicted through the dendrogram (Fig 1). Cluster III with nine genotypes was the largest followed by cluster I (eight genotypes) and cluster IV (seven genotypes). The clusters IIhadthe least number of genotypes (six). Based on the inter-cluster distances, clusters III and IV had the lowest divergence (6.50) while clusters I and IV recorded the highest divergence (11.41). The highest intra cluster distance was noticed among genotypes of cluster IV (6.32) and lowest was noticed among genotypes of cluster II (5.36).Similar results were obtained by Dey et al., 2020[9], where the 29 accessions are divided into six clusters and highest intra cluster distance was observed in cluster IV.

Table 2: Clustering pattern of 30 rice genotypes based on 14traits

Cluster	No.of genotypes	Genotypes
I	8	Remanika, Chenthadi,Krishnanjana,Panchami, Karishma, Revathy, White Ponni, Bhadra
II	6	Gouri, Karuna, Sreyas, Karthika, Chenkayama, Onam
III	9	Bhagya, Vyttila-7, Vyttila-10, Prathyasa, Vyttila-9, Pournami, Vyttila-6, Makom, Uma
IV	7	Vyttila-1, Vyttila-3, Chettivirippu ,Vyttila-8, Vyttila-4, Pokkali , Kuthiru

Intra and inter cluster D^2 values

Based on D^2 values, the average inter-cluster and intra-cluster distances were computed and are presented in the Table 3. The intra-cluster distance varied from 5.36 (cluster II) to 6.32 (cluster IV). The lower intracluster values indicated lowervariation among the genotypes within the cluster. The inter-cluster distances extended from 6.50 to 11.41. The minimum divergence was noted between cluster III and cluster IV (6.50), while the highest inter-cluster distance was noticed between cluster I and cluster IV (11.41). The inter cluster distances were depicted in the cluster diagram (Fig.2).

With an intra-cluster distance of 5.83 Cluster I recorded the greatest inter-cluster value with cluster IV (11.41) and minimum with cluster II (8.36). Cluster II had an intra- cluster distance of 5.36. This cluster recorded the greatest divergence with cluster IV (8.31) and lowest with cluster III (6.68). With an intra-cluster distance of 5.87, cluster III had the highest inter-cluster distance of 6.50 with cluster IV. Cluster IV recorded the greatest intra cluster value. In this study, the inter-cluster distances were higher than the intra-cluster distances which indicated the presence of considerable genetic diversity among the genotypes of different clusters.Maximum heterosis and segregants could be developed by crossing genotypes from clusters I and IV that exhibited the greatest genetic distance. The least genetic distancewas observed between clusters III and IV, indicating that the genotypes within these clusters are closely related.Similar reports were made byVennela*et al*. (2017)[15], Dey *et al*., (2020)[9]and Chaudhary *et al*., (2023)(16) in rice.

Table 3:Intra and inter-cluster (D^2)distances of 30 rice genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	**5.83**			
Cluster II	8.36	**5.36**		
Cluster III	9.23	6.68	**5.87**	
Cluster IV	11.41	8.31	6.50	**6.32**

Table 4 :Cluster means for fourteen characters in rice genotypes

Cluster	DH	DF	NT	NPT	ST	PH	LH	PL	GP	TGW	GY	RLH	PDI	NLS
I	78.00	90.68	3.87	3.62	6.08	84.25	7.96	21.77	144.46	23.20	7.10	20.50	12.22	3.06
II	66.75	79.83	2.75	2.41	5.40	89.03	12.69	21.38	126.00	22.42	6.11	21.95	11.85	3.70
III	63.05	76.72	3.33	3.11	5.19	79.88	17.85	20.41	87.36	19.53	4.32	34.54	21.23	5.75
IV	56.50	67.14	3.00	2.35	4.95	97.44	20.39	17.00	42.02	14.54	2.47	36.57	24.12	6.53

DH-Days to heading, DF- Days to 50 per cent flowering, NT- Number of tillers per plant, NPT- Number of productive tillers per plant, ST- Stem thickness, PH- Plant height, LH- Lesion height, PL- Panicle length, GP- Number of grains per panicle, TGW-Thousand grain weight, GY-Grain yield, RLH-Relative lesion height,PDI-Percentage disease index, NLS-Number of lesions per plant

The cluster means were calculated for fourteen characters and presented in Table 4.The maximum and minimum cluster mean values were distributed in different clusters.Cluster I was observed to have the highest cluster average for days to heading (78.00), days to 50 per cent flowering (90.68), number of tillers per plant (3.87), number of productive tillers per plant (3.62),stem thickness(6.08cm), panicle length (21.77cm), number of grains per panicle (144.46), thousand grain yield (23.20g) and grain yield per plant (7.10g). Cluster IV had the highest cluster average for plant height(97.44cm), lesion height(20.39cm),relative lesion height(36.57%), percentage disease index(24.12) and number of lesions per plant(6.53). Similar results for maximum clustermeans for plant height (140.08) was recorded in cluster 4 by Dey et al., 2020 [9], Rathan et al., (2020) [17].

The lowest cluster mean for days to heading (56.50),days to 50 percent flowering (67.14), number of productive tillers per plant(2.43), stem thickness (4.95cm), panicle length (17.00cm), number of grains per panicle (42.02), thousand grain weight (14.54g) and grain yield per plant (2.47 g) was recorded in cluster IV. The lowest cluster mean for lesion height (7.96 cm), relative lesion height (20.50 cm), number of lesions per plant (3.06) was observed in cluster I. Lowest cluster mean for number of tillers per plant (2.75) and percentage disease index was seen in cluster II. The cluster mean for plant height (79.88 cm) was minimum in cluster III[18].

Cluster I exhibited desirable mean values for yield contributing traits including grain yield per plant, number of grains per panicle, thousand grain weight, panicle length and

number of productive tillers. The mean values for sheath blight disease resistance reactions such as lesion height, relative lesion height and percentage disease index were low in cluster I. Cluster I consist of sheath blight tolerant genotypes Chenthadi, Krishnanjana, Panchami and White Ponni, moderately resistant genotypes Karishma, Revathy, Bhadra and moderately susceptible genotype Remanika. Hence, the sheath blight tolerant genotypes in cluster 1 can be utilized in hybridization for developing high yielding sheath blight resistant rice varieties.

Fig 1: Hierarchical Wards method dendrogram showing the cluster pattern of 30 rice genotypes

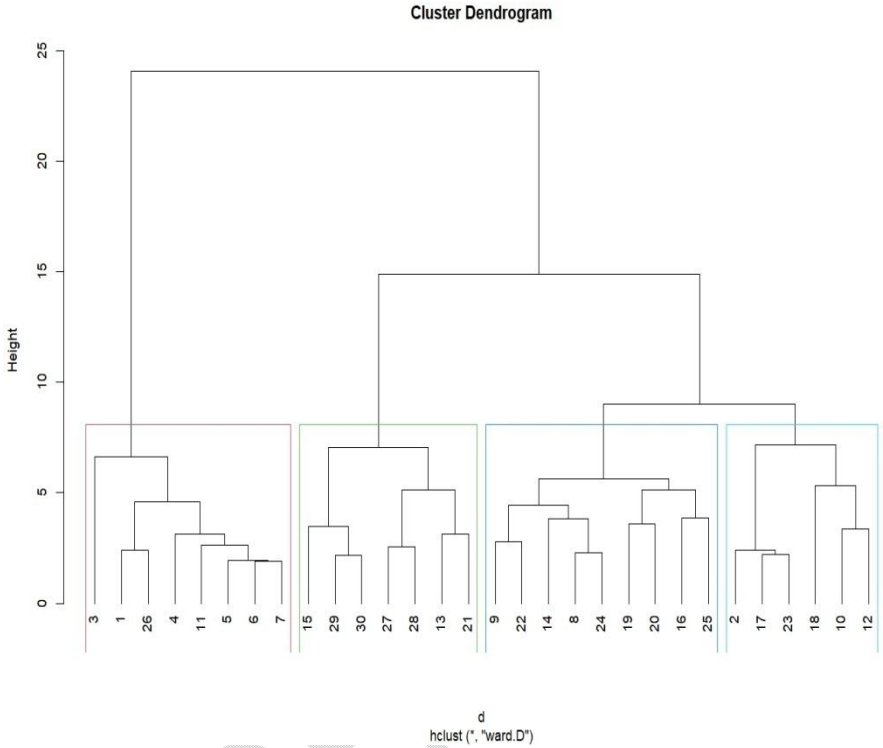
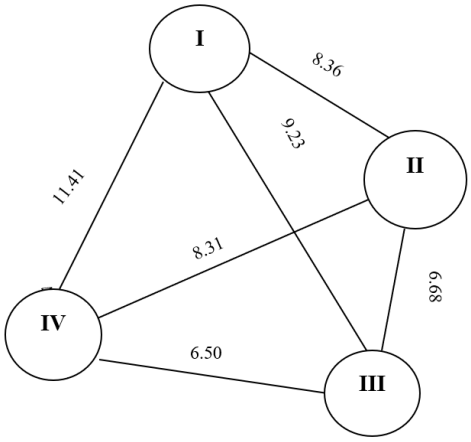


Fig 2: Cluster diagram of rice genotypes



CONCLUSION

The study concluded that broad genetic variability existsamong the genotypesresulting in four clusters with significant genetic distances in the diversity analysis. For future breeding programmes genotypes should be selected from different clusters rather than within the cluster. The results indicated that the genotypes in cluster I and IVweredivergent and therefore future breeding programs can focus on hybridizing the genotypes from diverse clusters as parentsfor developing desirable segregants for grain yield and sheath blight resistance. Intra cluster distance was recorded highest in cluster IV followed by cluster III, indicating that within the cluster the genotypes have low genetic diversity and hybridization among the genotypes may not be useful.Cluster I, comprising Chenthadi, Krishnanjana, Panchami and White Ponniwith significantlyhigher grain yield per plant and tolerance to sheath blight could be used in future hybridization programs to develop high yielding sheath blight resistant rice varieties.

Disclaimer (Artificial intelligence)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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