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Genetic Diversity Analysis for Bacterial Leaf Blight Disease Resistance in Rice (*Oryza sativa* L.)

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ABSTRACT

Background: Rice (*Oryza sativa* L.) gets affected by more than seventy diseases by the infection of bacteria, fungi and viruses. Among, bacterial leaf blight (BLB) caused by *Xanthomonas oryzae* pv *oryzae* (*Xoo*) is the important disease around the rice cultivated areas and causing drastic yield losses ranging between 20 and 30 per cent. Among very few options for increasing yield potential in rice, genetic diversity among the genotypes plays an important role in selection of parents having wider variability for disease resistance.

Methods: The rice genotypes were screened using PDI for bacterial leaf blight (BLB) and subjected to D^2 analysis for nine quantitative traits *viz.,* plant height, number of productive tillers per plant, panicle length, days to fifty per cent flowering, number of grains per panicle, thousand grain weight, grain length, grain breadth and single plant yield.

Result: On the basis of Mahalanobis D^2 statistics, the thirty five genotypes are grouped into VIII clusters. The highest intra cluster distance was recorded for cluster II (41.16) followed by cluster VI (37.73). Out of thirty five genotypes screened under field condition using percentage disease index (PDI), CR 1009 found to be resistant with the lowest PDI value of 9.67 per cent. The genotypes Karsamba, TPS 4 and Kaivara samba registered highest PDI value of 70.67, 67.22 and 66.67 respectively. The BLB resistance in genotype dependent and not cluster based. The resistant genotype CR 1009 under field screening was positioned in VI cluster. The cluster II had susceptible genotypes karsamba and kaivarasamba. Thus, the identified genotypes can be utilized in recombination breeding to provide BLB resistance segregants.

Key words: BLB, Disease resistance, Mahalanobis D^2, PDI, Rice (*Oryza sativa* L.).

INTRODUCTION

Rice (*Oryza sativa* L.) is an important staple food for more than half of the world's population and hence, is referred to as "Global Grain" (Prasad *et al.,* 2018). Globally it is cultivated over 167 million hectares with the production of 780 million tonnes (FAOSTAT, 2017). It gets affected by more than seventy diseases by the infection of bacteria, fungi and viruses. Among, them bacterial leaf blight (BLB) caused by *Xanthomonas oryzae* pv *oryzae* (*Xoo*) is the important disease around the rice cultivated areas (Khan, 1996; Gautam *et al.,* 2015). Disease incidence occurs in all growth stages of rice crop, causing drastic yield losses ranging between 20 and 30 per cent (Noh *et al.,* 2007). The disease severity can cause a yield loss up to 80 per cent and is influenced by various crop stages, environment (28 to 34°C) and degree of susceptibility of the genotypes (Shin *et al.,* 1992; Laha, 2017). Since yield of rice is highly affected by BLB current growth status of rice production can't meet the demand projections in near future, which in coming years is going to be a challenge due to decreasing sources of water, arable land and fertilizer input (Marcaida *et al.,* 2014). Among very few options for increasing yield potential in rice, improvement of genetic potential of the crop cultivars is one of the best. Rice is endowed with rich natural genetic diversity and there is tremendous scope to exploit diversity for improvement of desired traits through goal directed breeding. Genetic divergence among the genotypes plays an important role in selection of parents having wider variability for different characters (Nayak *et al.,* 2002). Genetic diversity is a prerequisite for any crop improvement program and it helps in the development of superior segregants. The importance of genetic diversity in selecting parents to recover transgressive segregants has been repeatedly emphasized by many workers (Devi *et al.*, 2017). Thus, present investigation was carried out to study genetic divergence for BLB disease resistance in rice.

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MATERIALS AND METHODS

A field experiment was conducted during Navarai season of 2020 on D Block at Plant Breeding Experimental Farm of Annamalai University, Faculty of Agriculture, Department of Genetics and Plant Breeding, Chidambaram. The screening was conducted in the paddy field at maximum tillering stage under natural environment condition to check the host pathogen interaction without using any BLB inoculums and there was no artificial favourable condition given to promote the pathogen growth.

Each germplasm is evaluated for the BLB resistance by calculating per cent disease index (PDI) and by giving scales to the respective PDI reading. For one genotype, five plants are taken for evaluating the BLB resistance. The PDI and scales for evaluating the BLB resistance was analysed based on the method suggested by Nagendran *et al.,* 2013.

Percentage disease index (PDI) =

$$\frac{\text{Sum of all numerical ratings}}{\text{Total no. of leaves graded}} \times \frac{100}{\text{Maximum Grade obtained}}$$

Scoring system used to evaluate breeding lines for BLB resistance in the field (IRRI, 2006 and Rafi *et al.,* 2013).

Scale	Disease leaf area	Description
0	0	Immune
1	1-10	Resistant
3	11-25	Moderate resistant
5	26-50	Moderate susceptible
7	51-75	susceptible
9	76-100	Highly susceptible

The genetic divergence among thirty five genotypes were estimated by Mahalanobis (1949) D^2 statistics for nine quantitative characters. The D^2 values were calculated using GENRES software. The computed values are tested for significance. The average inter and intra cluster distance tables were obtained from table output. The grouping of the genotypes into cluster was done using Toucher's method (Rao *et al.,* 2002).

RESULTS AND DISCUSSION

Screening for BLB

The morphological screening of thirty five rice genotypes against the bacterial leaf blight (BLB) pathogen under field condition was carried out using PDI (Percentage Disease Index). Among the genotypes CR 1009 found to be resistant with the lowest PDI value of 9.67 per cent. The genotypes Karsamba, TPS 4 and Kaivara samba registered highest PDI value of 70.67, 67.22 and 66.67 respectively. The result of this screening of rice genotypes based on field screening was presented in the Table 1. Of the genotypes three per cent were resistant, forty-six per cent were found to be moderately resistant, thirty seven percent were moderately susceptible and fourteen per cent were susceptible to rice bacterial leaf blight (BLB) which was presented in the Fig 1.

Tamilarasan *et al.,* 2018 morphologically screened one hundred and fourteen rice varieties against bacterial leaf blight (BLB) using PDI and concluded that genotypes CR 1009, PY 5, Kadaikannam, ADT 41, ACK 13005, ACK 12001, Mulampunchan and Veethiruppu were resistant against rice bacterial leaf blight (BLB). Further grouped the genotypes using D^2 statistics and mentioned the position of the resistant genotypes in the respective clusters also pointed out that the BLB resistance is genotype dependent and not cluster based.

D^2 analysis

An effort was made by using D^2 statistic proposed by Mahalanobis (1949), to assess the nature and magnitude of thirty five rice genotypes and to select the suitable genotypes for further utilization in breeding programme. In the cluster diagram formed by the Tocher's method, eight major clusters were formed. The maximum number of genotypes was depicted in cluster I which comprised of ten genotypes followed by cluster VI and II with nine and six genotypes respectively, whereas cluster III, IV, V, VII and VIII comprised two genotypes each. It is presented in the Table 2. The pattern of group constellation proved the existence of significant amount of variability. Similar findings were also reported by Dey *et al.,* 2020.

Table 1: Score for BLB resistance under field screening.

Genotypes	Percentage disease index (PDI)	Scale	Description
IR 20	47.00	5	MS
IR 64	14.00	3	MR
IR 50	32.11	5	MS
CO 39	13.44	3	MR
CO 43	14.67	3	MR
CO 45	61.00	7	S
CO 49	18.11	3	MR
CO 50	25.42	5	MS
CO 51	25.00	3	MR
MDU 5	12.23	3	MR
ADT 37	40.33	5	MS
ADT 39	27.10	5	MS
ADT 43	23.67	5	MS
ADT 46	19.67	3	MR
ADT 48	13.11	3	MR
TPS 4	67.22	7	S
ASD 16	26.00	3	MR
ASD 18	36.14	3	MR
ASD 19	25.33	3	MR
CR 1009	9.67	1	R
BPT 5204	25.57	3	MR
JGL 348	37.00	5	MS
Anjali	14.67	3	MR
Poonkar	63.95	7	S
White Ponni	31.00	5	MS
Thooyamalli	28.44	5	MS
Kullakar	31.00	5	MS
Kitchadi Samba	22.67	3	MR
Kuliyadichan	17.33	3	MR
Mapillai Samba	34.00	5	MS
Seeraga Samba	25.33	3	MR
Kaivara Samba	66.67	7	S
Jaya	35.00	5	MS
Kuruvai Kalanjium	45.57	5	MS
Karsamba	70.67	7	S

R- Resistant; MR- Moderate resistant; MS- Moderate susceptible; S- Susceptible.

Table 2: Composition of D^2 cluster for rice genotypes.

Cluster	Number of genotypes	Name of the genotypes
I	10	IR 20 , IR 64, IR 50, CO 39, CO 43, CO 45, CO 49, C0 50, ADT 39,ADT 43
II	6	CO 51, MDU 5, ADT 37, ADT 46, Kaivara Samba, Karsamba
III	2	Anjali, Whiita Ponni
IV	2	Kitchadi Samba, Jaya
V	2	TPS 4, Kulliyadichan
VI	9	ADT 48, ASD 16, ASD 18, ASD 19, CR 1009, BPT 5204, JGL 348, Poonkar, Kuruvai Kalanjium
VII	2	Kullakar, Seeraga Samba
VIII	2	Thooyamalli, Mapillai Samba

Table 3: Inter and intra cluster distances for rice genotypes.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	31.62	43.13	45.08	38.92	40.92	34.72	33.94	55.54
II		41.16	35.70	35.10	32.96	47.78	50.52	44.31
III			16.76	22.03	27.14	49.69	48.32	37.45
IV				18.65	32.14	42.19	39.10	40.59
V					19.16	42.28	49.96	30.84
VI						37.73	38.37	57.06
VII							32.09	60.80
VIII								36.76

Table 4: Cluster means among rice genotypes for various biometric traits.

Cluster	PH	NPT	PL	DFF	NGP	TGW	GL	GB	SPY
I	105.96	16.07	22.00	76.77	147.90	14.08	8.21	2.87	33.96
II	139.05	13.06	22.22	80.78	153.56	16.00	8.08	3.14	41.00
III	135.88	13.17	25.95	95.67	137.50	14.71	7.92	2.62	44.39
IV	158.51	17.33	25.23	93.00	157.33	15.68	7.75	2.53	43.25
V	138.57	15.17	21.18	85.83	121.67	16.91	8.62	3.42	44.50
VI	123.17	16.07	22.28	76.70	142.37	15.07	8.72	2.68	32.16
VII	106.43	21.17	23.09	88.00	146.00	14.77	7.15	2.45	34.59
VIII	169.90	13.67	21.85	93.83	111.00	23.10	8.25	3.28	43.58
Grand Mean	134.68	15.71	22.97	86.32	139.67	16.29	8.09	2.87	39.68

PH- Plant height; TGW- Thousand grain weight; NPT- No. of productive Tillers; GL-Grain length; PL- Panicle length; GB-Grain breadth; DFF- Days to 50% flowering; SPY- Single plant yield; NGP-No of grains per panicle.

The highest intra cluster distance was recorded for cluster II (41.16) followed by cluster VI (37.73) and lowest intra cluster average distance was recorded by cluster III (16.76) and IV (18.65) which is furnished in Table 3 and Fig 2. The genotypes belonging to the clusters separated by high genetic distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants (Solanki *et al.,* 2019). Maximum inter cluster distance was observed between VII and VIII (60.80), followed by cluster VI and VII (57.06). The minimum inter cluster distance was observed between clusters III and IV (22.03) and this was followed by the clusters V and III (27.14). Among the nine traits studied, maximum contribution was made by single plant yield (66.72%) which is in agreement with Banumathy *et al.,* 2010. The cluster mean for all the nine biometric traits were studied character wise and furnished below in Table 4. Hybridization among the genotypes which had the maximum inter-cluster distances could produce

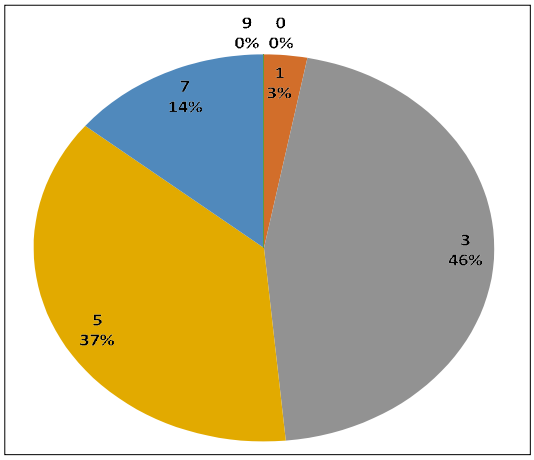

Fig 1: Distribution of the genotypes in different BLB grads. 0: Immune; 1: Resistant; 3: Moderate Resistant; 5: Moderate Susceptible; 7: Susceptible; 9: Highly Susceptible.

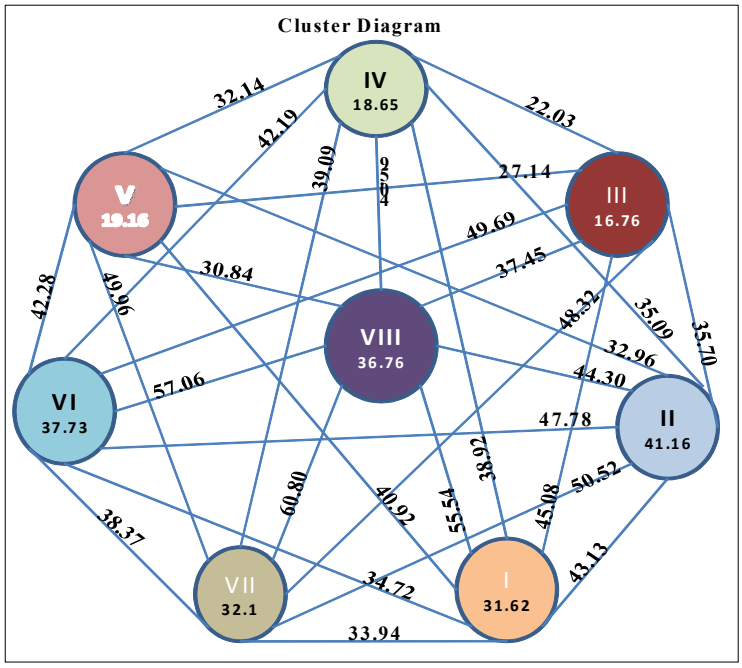

Fig 2: Cluster Diagram by Tocher Method.

heterotic combinations and wide variability in segregating generations for many beneficial traits (Anandan *et al.,* 2011). Thus, the divergence of the thirty five rice genotypes used in the study may be due to involvement of different ancestral pedigree or uncommon parentage.

On the basis of Mahalanobis D^2 statistics, the thirty five genotypes were grouped into eight clusters. The BLB resistance in genotype dependent and not cluster based. The resistant genotype CR 1009 under field screening was positioned in VI cluster. The cluster II had susceptible genotypes karsamba and kaivarasamba.

CONCLUSION

Since Rice is highly affected by Bacterial Leaf Blight (BLB), genetic diversity is tremendous scope to exploit diversity for improvement of disease resistance through goal directed breeding. Thus studies on genetic divergence for BLB disease resistance in rice is one of the important objective in rice breeding. Among thirty five rice genotypes studied for Bacterial Leaf Blight (BLB) disease resistance, CR 1009 found to be resistant under field screening with the lowest PDI value of 9.67 per cent while genotypes Karsamba, TPS 4 and Kaivara samba registered highest PDI value of 70.67, 67.22 and 66.67 respectively. On the basis of Mahalanobis D^2 statistics, the resistant genotype CR 1009 under field screening was positioned in VI cluster, the cluster II had susceptible genotypes karsamba and kaivarasamba. Thus, the identified genotypes with wider variability for disease resistance can be utilized in recombination breeding to provide BLB resistance segregants.

Conflicts of interest: None.

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