RESEARCH ARTICLE



Identification and quantification of slow blasting resistance in basmati/aromatic rice germplasm against neck blast (*Pyricularia oryzae* Cavara)

Jyoti Jain*, Manarshroop Kaur Sohal¹, Jagjeet Singh Lore, Sandeep Jain¹, Navjot Sidhu and Sachin Upmanyu²

Abstract

A total of 44 basmati/aromatic germplasm lines were evaluated and quantified for slow blasting type of resistance to neck blast disease (*Pyricularia oryzae*) under both artificial and natural epiphytotic conditions. Among the test genotypes evaluated, significant differences were obtained with respect to Area Under Disease Progress Curve (AUDPC), lesion length (mm), susceptibility index (Sx) value and apparent rate of infection (r). Sx values differed significantly among test genotypes ranging from 2.83 to 12.83. Four genotypes i.e. Tetep, INGR 15001, INGR 15002 and Pusa Basmati 1637 were found to be moderately resistant to neck blast with Sx value < 3, AUDPC value between 70-140, lesion length between 2-5mm and apparent infection rate (r) ranging between 0.31 to 0.34 indicating slow blasting tendencies as compared to Susceptible check (Pusa Basmati 1401) exhibiting AUDPC value of 349.8, lesion length (16.22mm) and apparent infection rate (r) of 0.44. Improved Pusa Basmati also showed slow blasting with r value of 0.41 but exhibited susceptible reaction to the disease with AUDPC value of 249.6 and LL (11.52 mm) respectively. However, three genotypes were found to be moderately susceptible, 18 were susceptible and 19 as highly susceptible to the disease with susceptibility index lying in the range of 3.1-6, 6.1-8 and >8 respectively. Only one entry RYT 3672 showed moderately susceptible reaction to the disease having Sx value of 5.98, AUDPC value of 169.8 and lesion length (mm) and disease incidence (%) while it was negatively correlated with incubation period (IP 50). None of the test entry showed complete resistance to the disease. The newly identified sources exhibiting slow blasting resistance despite moderate disease level with lowest apparent rate of infection can be used as donors for strengthening neck blast breeding programme in basmati rice.

Keywords: Apparent rate of infection (r), AUDPC, Neck blast, Resistance, Susceptibility index (Sx).

Introduction

Rice (Oryza sativa L.) is the most important cereal crop of Graminae family and is cultivated in 113 countries of the world. India is chief exporter of basmati rice in international market but still its yield per unit area is very low due toyield losses caused by various biotic and abiotic stresses. Among the biotic stresses, neck blast disease caused by Pyricularia oryzae Cavara is highly destructive and is estimated to reduce the world's rice production by 8 per cent every year (Wilson and Talbot 2009) which is enough to feed 60 million people (Barnwal et al 1994). Over the past few decade huge yield losses of 20-100 per cent have been reported from India (Vasudevan et al. 2014) and with each unit increase in neck blast disease incidence, there is loss of yield around 0.23 g per plant (Koutroubas et al. 2009). As 50-80 per cent of basmati is exported to European and Arabian countries, increased incidence of neck blast disease can largely impact Indian economy (Salim et al. 2003).

Neck blast disease is prevalent throughout the Punjab state particularly in south-western districts (<u>Singh</u> et al. 2018) and has become a serious bottleneck in successful cultivation of basmati rice in Punjab state due to increased

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Jyoti Jain et al.

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Table 1. Reaction of basmati/aromatic rice germplasm lines against r

S. No.	Designation	AUDPC	RAUDPC	RaR AUDPC	Disease incidenc
1	Super Basmati	329.7 ^(b-g)	0.27	0.95	88 ^(a-b)
2	Punjab Mehak 1	317.4 ^(c-g)	0.26	0.91	88 ^(a-b)
3	NDR 8022	316.2 ^(c-g)	0.26	0.91	90 ^(a-b)
4	R 1432-261-105-2-1-2	242 ^(k-m)	0.20	0.70	90 ^(a-b)
5	Basmati Nepal	359.4 ^(a-e)	0.30	1.03	88 ^(a-b)
6	Basmati 93	305.1 ^(d-j)	0.25	0.88	90 ^(a-b)
7	Basmati Lamo	256.8 ^(h-m)	0.21	0.74	88 ^(a-b)
8	Chanan	299.7 ^(e-k)	0.25	0.86	86 ^(a-b)
9	HKR 240 IET 12021	286.3 ^(g-k)	0.24	0.82	90 ^(a-b)
10	IET 12601	305.1 ^(d-j)	0.25	0.87	88 ^(a-b)
11	Malagkit Sung Song	241.8 ^(k-m)	0.20	0.69	84 ^(a-b)
12	IR 60164-122-3-2-1	298.2 ^(f-k)	0.25	0.86	90 ^(a-b)
13	IR 62871-549-3-1	245.4 ^(k-m)	0.20	0.70	88 ^(a-b)
14	IR 62871-549-3-6	225 ^(m)	0.19	0.64	84 ^(a-b)
15	IR 62873-244-2-2	354.9 ^(a-f)	0.30	1.01	88 ^(a-b)
16	IR 62873-244-2-5	336.3 ^(b-g)	0.28	0.97	86 ^(a-b)
17	Barah	362.7 ^(a-d)	0.30	1.03	90 ^(a-b)
18	Khao Dawk Mali 105	352.8 ^(a-f)	0.29	1.04	92 ^(a-b)
19	Dangar Chudi	299.4 ^(e-k)	0.25	0.87	86 ^(a-b)
20	Ramachandra Boita	257.1 ^(h-m)	0.21	0.74	88 ^(a-b)
21	Bahurupi	307.8 ^(c-i)	0.26	0.89	86 ^(a-b)
22	Nagra	171.6 ⁽ⁿ⁾	0.14	0.50	96 ^(a)
23	Bastul	310.2 ^(c-i)	0.26	0.89	88 ^(a-b)
24	Kerala Sundari	357.6 ^(a-f)	0.30	1.03	92 ^(a-b)
25	Acharamati	347.1 ^(a-f)	0.29	0.99	92 ^(a-b)
26	Gangabali	304.4 ^(d-j)	0.25	0.88	92 ^(a-b)
27	IR 74719-23-3-2-2	358.8 ^(a-f)	0.30	1.03	86 ^(a-b)
28	Seond Basmati	169.5 ⁽ⁿ⁾	0.14	0.49	92 ^(a-b)
29	Improved Pusa Basmati	(im)	0.21	0.72	94 ^(a)
30	Pusa 677	306.4 ^(d-j)	0.26	0.88	92 ^(a-b)
31	Pusa Basmati 6	314.4 ^(c-h)	0.26	0.89	92 ^(a-b)
32	IET 21953	238.2 ^(I-m)	0.20	0.69	88 ^(a-b)
33	Sugandha Mati	299.4 ^(e-k)	0.25	0.86	88 ^(a-b)
34	Basmati 443	368.1 ^(a-c)	0.31	1.06	90 ^(a-b)
35	Acharamati-2	404.7 ^(a)	0.34	1.18	92 ^(a-b)
36	Basmati 349	244.0 ^(k-m)	0.20	0.70	88 ^(a-b)
37	Basmati 370 B	252.6 ^(i-m)	0.21	0.73	88 ^(a-b)
38	Basmati 376	380.7 ^(a-b)	0.32	1.11	84 ^(a-b)
39	Basmati 388	336.9 ^(b-g)	0.28	0.95	88 ^(a-b)
40	Pusa 1401	349.8 ^(a-f)	0.29	1.00	90 ^(a-b)
41	Tetep	104.1 ⁽⁰⁾	0.09	0.30	78 ^(b)
42	Pusa Basmati 1637	91.5 ⁽ⁿ⁾	0.07	0.26	86 ^(a-b)
43	INGR 15001	112.2 ⁽ⁿ⁾	0.09	0.30	86 ^(a-b)
44	INGR 15002	115.5 ⁽ⁿ⁾	0.09	0.32	82 ^(a-b)
	PC = Relative area under d				

- Relative area under disease curve; RaRAUDPC = RAUPDC with respect to susceptible check; Superscripts depict that data followed by same letter(s) are not significantly different (p = 0.05) according to Duncan's multiple range test

7.5^(d-h) 12.96^(d-h)

7.8^(a-f) 16.64^(a-c)

8.2^(a-d)

6.7^(i-k)

7.4^(e-i)

8.2^(a-d)

6.7^(i-k)

7.4^(e-i)

7.4^(e-i)

7.4^(e-i)

9.1^(a)

17.82^(a-b)

19.02^(a)

13.08^(d-g)

12.98^(d-h)

17.36^(a-b)

16.44^(a-c)

16.22^(a-c)

2.92⁽ⁱ⁾

6.11⁽ⁱ⁾

7.6^(d-g) 5.32^(i-j)

8.6^(b-c) 6.70⁽ⁱ⁾

acreage under susceptible genotypes. The disease can be managed effectively through the use of chemical fungicides but may lead to high production cost, pesticide residue in grains as well as environmental pollution. Therefore, breeding for host plant resistance is most economical, ecofriendly and sustainable method to manage neck blast. The complete resistance or vertical resistance to blast disease is of qualitative nature, controlled by one or few major genes and is highly race specific. Since the rice blast pathogen is highly variable therefore, due to frequent development of races, resistant varieties remain effective only for a few years (Ou and Nuque 1985). Therefore, partial resistance, also called horizontal resistance, is more durable as it is race non-specific, quantitative and is mostly controlled by many minor genes (Ezuka 1979; Yeh and Bonman 1986). Therefore, the present study was conducted to identify slow blasting donors for neck blast disease among basmati and aromatic rice germplasm.

Materials and methods

Raising of crop

A set of 42 germplasm lines (Table 1) along with susceptible check (Pusa Basmati 1401) and resistant check (Tetep) were grown under field conditions for two consecutive years in *kharif* 2018 and 2019 at rice experimental fields, Department of Plant Breeding and Genetics, PAU, Ludhiana and at Wheat and Rice Research Centre, Malan, Palampur, Himachal Pradesh (hotspot location). Seeds of each test entry were sown during the second fortnight of June and nursery was raised as per Package of Practices for Kharif crops of Punjab (Anonymous 2017). One month old seedlings of each entry were transplanted in paired rows having 20×20 cm spacing at both the locations.

Disease assessment under artificial epiphytotic conditions

Rice plants of 44 entries raised at Rice Experimental Fields, Department of Plant Breeding and Genetics, PAU, Ludhiana were artificially inoculated with highly virulent isolate of the fungus (NB-7) at 50% per cent flowering stage using bit wrap technique (Jain et al. 2017) during late evening hours. Five plants per entry and five necks per plant were inoculated. Disease assessment was done in terms of disease incidence (%), disease severity (0-9 scale), incubation period (IP 50), lesion length (mm), apparent rate of infection (r), panicle blast severity (PBS) and Area Under Disease Progress Curve (AUDPC) as follows:

Disease incidence (%) was calculated by dividing the number of diseased necks by total number of necks inoculated and then multiplying with 100 for each test entry. Disease score and panicle blast severity was recorded at 4, 7, 10, 13 and 16 days after inoculation (DAI) as per 0-9 scale based on lesion length (Jain et al. 2017) as follows:

Disease Score	Lesion Length (mm)
0	No lesion
1	< 2
3	2.1-5
5	5.1-10
7	10.1-20
9	>20

Panicle blast severity for each test genotype was calculated using formula as per SES scale, IRRI (Anonymous 2002) given below:

Paniele Blast Severity =	$\frac{10 \times \text{NI} + 20 \times \text{N3} + 40 \times \text{N5}}{470 \times \text{N7} + 100 \times \text{N9}}$
Panicle Blast Severity =	Total number of panicles observed

where N1-N9 are the number of panicles with score 0-9 based on lesion length as given above.

Incubation period (IP50) was calculated as the time period between the inoculation and appearance of the disease symptoms (lesions) on 50% of the inoculated necks. Each entry was observed daily for appearance of symptoms upto 15DAI, while lesion length (mm) on necks were measured with a measuring scale at 16 DAI. The values of AUDPC were calculated for each genotype using midpoint method (Campbell and Madden 1990). Disease progression with time was calculated by using the formula given by Shaner and Finney (1977) as follows:

AUDPC =
$$\sum_{i=1}^{n} [(Y_{i+n1} + Y_i)/2] [X_{i+1} + X_i]$$

where,

Yi = Panicle blast severity at the *i*th observation, $X_i = time$ (days) at the *i*th observation and

n = total number of observations.

Based on the AUDPC values the reaction of the test entries was designated as given below (Jain et al. 2017):

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AUDPC Value	Reaction
0-70	Resistant
70.1-140	Moderately Resistant
140.1-210	Moderately Susceptible
210.1-280	Susceptible
>280	Highly Susceptible

To guantify the relative level of resistance among the test genotypes, Susceptibility index (Sx) values were calculated using the following equation given by Yuen and Forbes, 2009:

$$Sx = Sy \frac{Dx}{Dy}$$

where Sy and Dy represent, respectively, the assigned susceptibility scale value and observed disease progress

0		Ų			
nst neck blast	disease ui	nder artificial ir	noculation condit	ions	
Disease	IP50	Lesion	Apparent rate	Sx	Host response
incidence (%)	(days)	length (mm)	of infection		based on Sx)
₈₈ (a-b)	7.6 ^(c-g)	15.98 ^(a-d)	0.47 ^(a,b,c,d,e,f)	8.55	HS
₈₈ (a-b)	6.9 ^(g-k)	16.18 ^(a-c)	0.44 ^(c,d,e,f)	8.20	HS
90 ^(a-b)	6.5 ^(k-l)	16.60 ^(a-c)	0.47 ^(a,b,c,d,e,f)	8.22	HS
90 ^(a-b)	6.5 ^(k-l)	12.56 ^(e-h)	0.43 ^(d,e,f)	6.28	S
₈₈ (a-b)	6.6 ^(j-l)	17.14 ^(a-c)	0.47 ^(a,b,c,d,e,f)	9.31	HS
90 ^(a-b)	7.3 ^(f-j)	16.34 ^(a-c)	0.45 ^(b,c,d,e,f)	8.04	HS
88 ^(a-b)	6.6 ^(j-l)	12.76 ^(e-h)	0.42 ^(e,f)	6.66	S
86 ^(a-b)	7.5 ^(d-h)	15.86 ^(a-d)	0.47 ^(a,b,c,d,e,f)	7.76	S
90 ^(a-b)	5.9 ^(I)	17.76 ^(a-b)	0.48 ^(a,b,c,d,e,f)	7.41	S
₈₈ (a-b)	7.7 ^(b-f)	15.98 ^(a-d)	0.45 ^(c,d,e,f)	8.02	HS
₈₄ (a-b)	8.4 ^(a-b)	13.92 ^(c-f)	0.44 ^(c,d,e,f)	6.21	S
90 ^(a-b)	8.0 ^(a-f)	16.82 ^(a-c)	0.50 ^(a,b,c,d)	7.73	S
₈₈ (a-b)	8.2 ^(a-d)	11.90 ^(f-h)	0.43 ^(d,e,f)	6.34	S
₈₄ (a-b)	7.5 ^(d-h)	12.22 ^(f-h)	0.46 ^(a,b,c,d,e,f)	5.76	MS
₈₈ (a-b)	8.4 ^(a-b)	17.62 ^(a-b)	0.53 ^(a,b)	9.05	HS
86 ^(a-b)	7.9 ^(a-f)	16.30 ^(a-c)	0.50 ^(a,b,c,d)	8.73	HS
90 ^(a-b)	7.6 ^(c-g)	17.62 ^(a-b)	0.48 ^(a,b,c,d,e,f)	9.28	HS
92 ^(a-b)	6.6 ^(j-l)	18.62 ^(a-b)	0.48 ^(a,b,c,d,e)	9.33	HS
86 ^(a-b)	6.5 ^(k-l)	17.58 ^(a-b)	0.45 ^(c,d,e,f)	7.80	S
₈₈ (a-b)	8.1 ^(a-e)	15.32 ^(b-e)	0.48 ^(a,b,c,d,e)	6.66	S
86 ^(a-b)	8.2 ^(a-d)	16.96 ^(a-c)	0.53 ^(a)	7.92	S
96 ^(a)	8.5 ^(a)	10.32 ^(g-h)	0.45 ^(c,d,e,f)	4.46	MS
88 ^(a-b)	8.0 ^(a-f)	17.34 ^(a-b)	0.50 ^(a,b,c,d)	7.99	S
92 ^(a-b)	6.8 ^(h-k)	17.50 ^(a-b)	0.50 ^(a,b,c,d)	9.28	HS
92 ^(a-b)	8.4 ^(a-b)	18.34 ^(a-b)	0.51 ^(a,b,c)	8.90	HS
92 ^(a-b)	6.4 ^(k-l)	17.66 ^(a-b)	0.48 ^(a,b,c,d,e)	7.92	S
86 ^(a-b)	6.6 ^(j-l)	16.72 ^(a-c)	0.47 ^(a,b,c,d,e,f)	9.26	HS
92 ^(a-b)	8.5 ^(a)	9.92 ^(h)	0.45 ^(c,d,e,f)	4.40	MS
94 ^(a)	7.4 ^(e-i)	11.52 ^(f-h)	0.41 ^(g)	6.50	S
92 ^(a-b)	7.4 ^(e-i)	17.10 ^(a-c)	0.47 ^(a,b,c,d,e,f)	7.88	S
92 ^(a-b)	8.3 ^(a-c)	16.78 ^(a-c)	0.48 ^(a,b,c,d,e,f)	8.01	HS
	5.5		0.10	0.01	

 $0.46^{(b,c,d,e,f)}$

0.50^(a,b,c,d)

0.51^(a,b,c)

0.44^(c,d,e,f)

0.50^(a,b,c,d)

0.45^(c,d,e,f)

0.44^(c,d,e,f)

0.31^(h)

0.30 ^(h)

0.32 ^(h)

0 34 ^(h)

0.48^(a,b,c,d,e,f)

0.47^(a,b,c,d,e,f) 7.72 S

6.21 S

9.57 HS

10.61 HS

6.30 S

6.56 S

10.01 HS

8.59 HS

9.00 HS

2.72 MR

2.36 MR

2.78 MR

2.97 MR

November, 2021]

value (AUDPC or RaRUDPC) for the standard genotype (Pusa Basmati 1401, susceptible check). Whereas, Sx and Dx represent, respectively, the calculated susceptibility scale value and observed disease progress value for the genotype in question (individual test entry). The susceptible check Pusa Basmati1401 was used as a reference entry and susceptibility scale value was formulated to test the susceptibility level among basmati rice genotypes against neck blast.

The apparent rate of infection (r/unit/day) was computed at 7 days interval after the appearance of the disease during both the years as follows:

 $r = (log x_1 - x_0)/(t_1 - t_2) \times 2.303$

where, x_0 and x_1 were the disease index at time t, and t, respectively (Vanderplank 1963).

Disease assessment under natural epiphytotic conditions at hotspot location

The disease severity of all the test entries grown at Wheat and Rice Research Centre, Malan, Himachal Pradesh (hotspot location) for neck blast was recorded under natural epiphytotic conditions. Ten plants per replication were randomly selected for disease scoring based on disease severity and 0-9 rating scale was followed for disease rating as per SES scale IRRI (Anonymous 2002) as follows:

Score	Disease symptoms	Reaction
0	No visible lesion or observed lesions on only a few pedicels	Immune
1	Lesions on several pedicels or secondary branches	Highly Resistant
3	Lesions on a few primary branches or the middle part of panicle axis	Resistant
5	Lesion partially around the base (node) or the uppermost internode or the lower part of panicle axis near the base	•
7	Lesion completely around panicle base or uppermost internodeor panicle axis near base with more than 30% of filled grains	Susceptible
9	Lesion completely around panicle base or uppermost internode or the panicle axis near the base with less than 30% of filled grains	
	0 1 3 5 7	 No visible lesion or observed lesions on only a few pedicels Lesions on several pedicels or secondary branches Lesions on a few primary branches or the middle part of panicle axis Lesion partially around the base (node) or the uppermost internode or the lower part of panicle axis near the base Lesion completely around panicle base or uppermost internodeor panicle axis near base with more than 30% of filled grains Lesion completely around panicle base or uppermost internode or the panicle axis near the base with less

Statistical analysis of the data was done with SPSS version 20 (Statistical Package for the Social Sciences) and analysis of variance was calculated at 95% confidence interval for each parameter. Hierarchical cluster analysis was performed on the data using between group linkage method with SPSS 20 software.

Results

Screening under artificial inoculation conditions

A total of 44 genotypes were quantified for slow blasting type of resistance under artificial epiphytotic conditions based on disease severity recorded at 4, 7, 10, 13 and 16 DAI. Susceptibility index (Sx) was calculated to measure relative level of resistance among all the test entries. The disease incidence (%) and IP 50 (days) among all the genotypes showed variation from 78-96 per cent and 5.9-9.1 days, respectively. Four MR genotypes, namely, Tetep, INGR 15001, INGR 15002 and Pusa Basmati 1637 scored susceptibility index (Sx) value of < 3. Three entries viz., IR 62871-549-3-6, NAGRA and Seond Basmati exhibited moderately susceptible reaction with susceptibility index value ranging between 3 and 6 (Table 1). Eighteen genotypes were found to show susceptible reaction andninteen genotypes were found to exhibit highly susceptible reaction against the disease with susceptibility index values in the range of 6.1-8 and more than 8 respectively. Four test genotypes viz., Tetep, INGR 15001, INGR 15002 and Pusa Basmati 1637 showed moderately resistant reaction exhibiting lowest apparent rate of infection (r) varying from 0.31 to 0.34 and slow lesion development indicating slow blasting tendencies compared to susceptible check (Pusa Basmati 1401) exhibiting r value=0.44 with Sx value of 9.00. Similarly, Improved Pusa Basmati showed slow blasting tendency with low r value (0.41) but showed S reaction to the disease with Sx value of 6.50.

The symptoms of the disease started appearing first on susceptible genotypes namely Dangar Chudi and Acharmati with minimum IP 50 of 6.5 days. It was followed by 6.6 days on highly susceptible genotypes viz., Khao Dawk Mali and IR 74719-23-3-2-2. Incubation period of 6.7 days was recorded on 2 highly susceptible genotypes Acharmati-2 and Basmati 376. Symptoms were observed on 6 genotypes, namely, Improved Pusa Basmati, Pusa 677, Basmati 349, Pusa 388, Pusa Basmati 1401 and Tetep with IP of 7.4 days and were statistically at par with each other. Whereas maximum IP of 9.1 days was observed on genotype, INGR 15002.

Longest lesion length was also recorded on genotype Acharamati-2 (19.02 mm) followed by Khao Dawk Mali 105 (18.62 mm) which was significantly higher than all other genotypes except HKR 240 IET 12021, IR 62873-244-2-2, Barah, Dangar Chudi, Bastul, Kerala Sundari, Acharamati and Gangabali and hence were found to be highly susceptible to neck blast disease. Whereas minimum lesion length was measured on Tetep (2.92 mm) followed by Pusa Basmati 1637 (5.32 mm), INGR 15001 (6.70 mm), INGR 15002 (6.11 mm) respectively and were designated as moderately resistant. The average lesion length produced on all the genotypes ranged from 2.92-18.62 mm and the disease incidence was

calculated ranging between 82-96 per cent respective (Table 1). On artificial inoculation with Pyricularia oryza only 4 genotypes viz., Tetep, INGR 15001, INGR 15002 ar Pusa Basmati 1637 showed moderately resistant reaction Similarly, 3 genotypes namely IR 62271-549-3-6, NAGRA an Seond Basmati were found moderately susceptible to nee blast disease. However, 18 genotypes were susceptible ar 19 were highly susceptible to the disease (Table 2).

Correlation studies

Т

Correlation analysis between all the parameters viz., are under disease progress curve (AUDPC), Incubation period (50), lesion length (LL) and per cent disease incidence (DI) wa done and significant differences were obtained among th 43 genotypes with respect to AUDPC value and lesion lengt (mm). But results were insignificant in terms of IP 50 (day and per cent disease incidence (Table 3). However, AUDPO lesion length and disease incidence were found positive correlated with each other but negatively correlated wi IP 50 as shown in Table 4 AUDPC was significantly positive

Table 2. Resistance level of basmati/aromatic rice germplasm lines against neck blast disease under artificial epiphytotic conditions

Reaction	Number of genotypes	Genotypes
Resistant	None	-
Moderately resistant	4	Tetep, INGR 15001, INGR
Moderately susceptible	3	IR 62871-549-3-6, NAGR
Susceptible	18	R 1432-261-105-2-1-2, Ba 3-2-1, IR 62871-549-3-1, Pusa Basmati,Pusa 677, I
Highly susceptible	19	Super Basmati, Punjab N IR 62873-244-2-5, Barah Basmati 6, Basmati 443, J
Table 3. Analysis of varianc	e of different p	parameters

Source		Type III Sum of Squares	df	Mean Square	F value	P value		
Varieties	AUDPC	1293184.42	44	29390.55	20.46*	.000		
	Lesion length (mm)	3188.427	44	72.464	16.34*	.000		
	I.P. 50 (days)	124.260	44	2.82	10.72 ns	.000		
	Disease Incidence (%)	2326.22	44	52.86	0.561 ns	.987		

Alpha= 0.05; * = P < 0.05 (significant) ns = not significant

Table 4. Correlation Coefficient between AUDPC, Disease Incidence

		AUDPC	Disease Incidence	IP50	Lesion Length
AUDPC	Pearson correlation	1	.320*	386**	.947**
	Sig (2-tailed)		.032	.009	.000
Disease incidence	Pearson correlation		1	089	.404**
	Sig (2-tailed)			.559	.006
IP50	Pearson correlation			1	361*
	Sig (2-tailed)				.015
Lesion length	Pearson correlation				1
	Sig (2-tailed)				

* Correlation is significant at the 0.05 level (2-tailed).** Correlation is significant at the 0.01 level (2-tailed).

 IP50. Hierarchical cluster analysis based on AUDPC values using between group linkage method grouped genotypes into 2 distinct clusters viz., Cluster I and Cluster II. Cluster I consisted of 28 genotypes and was categoria 	esion antly JDPC with
5 71	d 44 uster rized
 as highly susceptible to neck blast. Cluster II was furt classified into three sub clusters i.e. Cluster IIa contain ten genotypes such as Basmati Lamo, Ramachandra Bo Improved Pusa Basmati, Basmati 370 B, IR 62871-549-3-6, 21953, R 1432-261-105-2-1-2, Malagkit Sung Song, IR 628 549-3-1 and Basmati 349 showed susceptible reaction, w Cluster IIb contained Nagra and Seond Basmati genoty showed moderately susceptible reaction and Cluster chaving four genotypes (Pusa Basmati 1637, Tetep, IN 15001 and INGR 15002 with moderately resistant react to the disease. 	ining Boita, 6, IET 2871- while otype ter II INGR

R 15002 and Pusa Basmati1637

RA and Seond Basmati

Basmati Lamo, Chanan, HKR 240 IET 12021, Malagkit Sung Song, IR 60164-122-, Dangar Chudi, Ramachandra Boita, Bahurupi, Bastul, Gangabali, Improved , IET 21953, Sugandha Mati, Basmati 349 and Basmati 370 B

Mehak 1, NDR 8022, Basmati Nepal, Basmati 93, IET 12601, IR 62873-244-2-2, , Khao Dawk Mali 105, Kerala Sundari, Acharamati, IR 74719-23-3-2-2, Pusa Acharamati-2, Basmati 376, Basmati 388 and Pusa Basmati 1401

e (%), IP	50 (days)	and Lesion	Length (mn	(ו
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Screening under natural epiphytotic conditions at hotspot location

Field screening under the natural epiphytotic conditions at hotspot location as presented in Table 4 revealed that 5 genotypes viz., INGR 15001, INGR 15002, IR 62871-549-31, Dangar Chudi and IR 74719-23-3-2-2 showed resistant reaction with disease score of 3 and twelve genotypes namely Basmati 93, Chanan, HKR 240 IET 12021, IR 62871-

549-3-6, Bastul, Ganga Bali, Pusa 677, Sugandha Mati, Tetep, Super Basmati, Basmati 443, Basmati 349 and Pusa Basmati 1637 showed moderately resistant reaction with disease score of 5. However, out of 44 test entries, 25 genotypes showed susceptible reaction and only 2 genotypes viz., Acharmati-2 and Pusa Basmati 1401were observed as highly susceptible with disease score of 9 (Table 5 and Table 6).

S. No.	Designation	Disease incidence	Disease score	Host response*	S. No.	Designation	Disease incidence	Disease score	Host response*
1	Super Basmati	25	5	MR	23	Bastul	15	5	MR
2	Punjab Mehak 1	49	7	S	24	Kerala Sundari	54	7	S
3	NDR 8022	46	7	S	25	Acharamati	48	7	S
4	R1432-261-105-2-1-2	54	7	S	26	Gangabali	12	5	MR
5	Basmati Nepal	36	7	S	27	IR 74719-23-3-2-2	8	3	R
6	Basmati 93	20	5	MR	28	Seond Basmati	42	7	S
7	Basmati lamo	44	7	S	29	Improved Pusa Basmati	42	7	S
8	Chanan	18	5	MR	30	Pusa 677	22	5	MR
9	HKR 240 IET 12021	15	5	MR	31	Pusa Basmati 6	40	7	S
10	IET 12601	48	7	S	32	IET 21953	46	7	S
11	Malagkit Sung Song	28	7	S	33	Sugandha Mati	25	5	MR
12	IR 60164-122-3-2-1	46	7	S	34	Basmati 443	20	5	MR
13	IR 62871-549-31	5	3	R	35	Acharamati-2	68	9	HS
14	IR 62871-549-3-6	18	5	MR	36	Basmati 349	21	5	MR
15	IR 62873-244-2-2	7	3	R	37	Basmati 370 B	34	7	S
16	IR 62873-244-2-5	48	7	S	38	Basmati 376	38	7	S
17	Barah	32	7	S	39	Basmati 388	42	7	S
18	Khao Dauk Mali 105	46	7	S	40	Tetep	18	5	MR
19	Dangar Chudi	5	3	R	41	Pusa Basmati 1637	15	5	MR
20	Ramachandra Boita	38	7	S	42	INGR 15001	8	3	R
21	Bahurupi	32	7	S	43	INGR 15002	7	3	R
22	Nagra	33	7	S	44	Pusa Basmati 1401	65	9	HS

*Based on disease incidence per cent

Disease score	Disease reaction	No of genotypes	Genotypes
0	Immune	Nil	-
1	Highly resistant	Nil	-
3	Resistant	5	IR 62871-549-31, Dangar Chudi, IR 74719-23-3-2-2, INGR 15001 and 15002
5	Moderately resistant	12	Basmati 93, Chanan, HKR 240 IET 12021, IR 62871-549-3-6, Bastul, Gangabali, Pusa 677, Sugandha Mati, Tetep, Super Basmati, Basmati 443, Basmati 349 and Pusa Basmati 1637
7	Susceptible	25	Punjab Mehak 1, NDR 8022, R1432-261-105-2-1-2, Basmati Nepal, Basmati Lamo, IET 12601, Malagkit Sung Song, IR 60164-122-3-2-1, IR 62873-244-2-2, IR 62873-244-2-5, Barah, Khao Dawk Mali 105, Ramachandra Boita, Bahurupi, Nagra, Kerala Sundari, Acharamati, Seond Basmati, Improved Pusa Basmati, Pusa Basmati 6, IET 21953, Basmati 370 B, Basmati 376, Basmati 388 and Pusa Basmati 1401
9	Highly susceptible	2	Acharamati2, Pusa Basmati 1401

November, 2021]

slow blasting tendencies with reduced r values (0.02-0.12) Discussion compared to susceptible checks (r=0.20-0.23) and terminal Only few resistant and moderately resistant genotypes of disease severities (1.4-16.1% for slow blasting cultivars vs rice and basmati rice have been reported across the world 88% for susceptible checks). The results also corroborate with varying amount of resistance to neck blast disease. the findings of Sarkhel (2010) who observed 5 test entries Therefore, identification of novel sources of resistance to viz., Punjab Mehak 1, Seond Basmati, Punjab Basmati 2, Pusa rice blast has been a major objective for many researchers Sugandh 5 and Pusa Sugandh 3 as resistant against all the involved in rice breeding programs (Rama Devi et al. 2015; isolates of Pyricularia oryzae. Vasudevan et al. 2014). In the present investigation, a Breeding for disease resistance is most effective method significant variation in degree of disease susceptibilities for blast management. Though many resistant varieties to was observed among 44 basmati/aromatic lines. Of these, P. oryzae have been developed, the resistance is not long only four entries viz., Pusa Basmati 1637, INGR 15001, INGR lasting, because of highly variable nature of the pathogen 15002 and Tetep exhibited moderate level of resistance (Lang et al 2009). Hence, development of broad spectrum based on lesion length (mm), AUDPC, rAUDPC, Susceptibility and durable resistant varieties is essential for containing this index (Sx), per cent disease incidence and apparent rate of disease. Thus, the genotypes exhibiting substantially lower infection. Results presented here revealed that genotypes apparent rate of infection (r) and reduced susceptibility were significantly differed with respect to level of resistance index (Sx) value indicating slow blasting type of resistance under both artificial inoculation conditions as well as natural to neck blast identified in this study can be exploited further epiphytotic conditions. for blast resistance breeding programmes. Various research workers have evaluated rice/basmati

genotypes for blast resistance using different assessment Author's contribution criteria from different parts of the world. Zewadu et al. Conceptualization of research (JJ, SJ, JSL), Designing of (2017) evaluated a set of 46 Korean rice accessions against experiment (JJ, SJ, JSL), Contribution of experimental blast disease and reported that only three genotypes like materials (JJ, JSL, SU, NS), Execution of field/lab experiments SRHB-133, SPHB-93 and SRHB-78 showed resistant reaction and data collection (JJ, MS, JSL, SU), Analysis of data and under both the field and screenhouse conditions. Turaidar interpretation (JJ, SJ, MS), Preparation of Manuscript (JJ, SJ). et al. (2018) reported only two varieties namely Baigan Munji and Adri Batta as moderately resistant and Tetep as resistant Acknowledgements to blast disease among 30 traditional rice varieties.

The authors are thankful to the University Grant Commission Similarly, Barnwal et al. (2012) screened 193 rice (UGC), New Delhi for the financial support and School of genotypes against blast disease under natural epiphytotic Agricultural Biotechnology, PAU, Ludhiana for providing conditions and reported that only five genotypes were aromatic rice germplasm. found to be highly resistant to the disease. Ghimire et al (2014) evaluated 72 genotypes against leaf as well as neck References Anonymous. 2002. Standard evaluation system for rice. blast and reported that only one genotype namely NR 11100-International Rice Research Institute, Los Banos, Manila, B-B-3-3-2 exhibited resistance to both leaf and neck blast. Philippines. Sabin K et al. (2016) screened 50 rice accessions under natural Anonymous. 2017. Package of Practices for kharif crops of Punjab. epiphytotic conditions against the disease and reported only pp 1-20. Punjab Agricultural University, Ludhiana. one cultivar namely Sabitri as resistant and two cultivars viz., Taichung 176 and Sankharika as susceptible to neck blast disease. Pandey (2016) observed highest apparent rate of infection, disease incidence and disease severity of leaf Phytopathol., 65(1): 56-59. Campbell C. L. and Madden L. V. 1990. Introduction to Plant Disease blast on highly susceptible cultivars Gurmatia, Dehula and Epidemiology. John Wiley and Sons, New York. Indrajal as compared to improved cultivars.

The results also corroborate with the findings of Singh et al. (2018) and Devi et al. (2014) who reported INGR 15001 and INGR 15002 as moderately resistant to neck blast disease. Similarly, Kumar et al. (2010) evaluated 22 elite indica rice genotypes against blast disease under artificial inoculation conditions and reported 13 rice genotypes as resistant to neck blast with disease severity less than 46 % and AUDPC value of 1000 respectively. Villareal et al. (1980) evaluated 16 rice genotypes for slow blasting type of resistance and reported that out of 16 genotypes, 9 were possessing

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