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Evaluation of different *Brassica* genotypes under field conditions against white rust disease (*Albugo candida*) of rapeseed-mustard for resistant sources

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Abstract

White rust or white blister disease caused by oomycete fungi, *Albugo candia* is one of the major devastating disease of rapeseed mustard. Continuous emergence of new races of the pathogen is responsible for breaking down of the resistance of already existing resistant cultivars. So there is need for the evaluation of existing resistant cultivars as well as new Brassica cultivars to find out stable resistance sources against the disease. In this context, 82 different Brassica genotypes, including 10 different Brassica species were evaluated in field, under natural conditions for the confirmation of resistance sources against *Albugo candida* in two successive years 2017-18 and 2018-19. Observations of percent disease severity and phenotypic disease reaction were taken at different time intervals of 70, 80 and 90 DAS. Infection rate and area under disease progress curve (AUDPC) were calculated for each genotype. Out of 82 Brassica genotypes evaluated, 26 were found free from the disease and 28 genotypes showed moderately resistant reaction while rest of the genotypes showed susceptible reaction at 90DAS. Minimum infection rate (0.0949) and AUDPC (69.44) was observed in DRMRJ 127 and SIVT-17-19 while maximum infection rate (0.1008) and AUDPC (588.0) was observed in 71 J0002 and RH 30, respectively at 90 DAS.

Keywords: Albugo candida, resistant, AUDPC, white rust, Brassica genotypes

1. Introduction

Oilseed Brassicas are important oilseed crops, grown as fodder, source of oil, condiments and vegetables around the world with global production of 584.3 million tonnes (mt) in 2019-20 (FAO, 2020). In India, oilseed crops comprise 26.20 mha, area with production of 35.35 mt and yield of 1328 kg/ha. Oilseed Brassica includes eight different species namely toria, yellow Sarson, Indian mustard, gobhi Sarson, Taramira, Brown Sarson and Karan Rai. Among them rapeseed-mustard attain prime position with total area of 6.64 mha, total production 8.1 mt and productivity 1980 kg/ha (Anonymous, 2020)^[1]. Rapeseed-mustard is susceptible to a number of diseases eg. Alternaria blight, White rust, Sclerotinia stem rot and Downey mildew which limit its production. Among them, white rust disease caused by Albugo candida (Pers. ex Lev.) Kuntze, is wide spread and highly destructive disease in many agronomically important Brassica species as pathogen can spread systemically and cause severe malformation of the inflorescence through hypertrophy and hyperplasia resulting in staghead formation (Punjabi et al., 2010)^[16]. The disease causes annual yield loss of 20-60 percent in rapeseed mustard crop (Saharan et al., 1984, Saharan and Verma, 1992, Bisht et al. 1994 and Kolte, 1996, Kalpana et al, 2017)^[20, 17, 3, 8]. Protectant fungicides have been recommended for controlling white rust disease in rapeseed-mustard (Kolte and Tewari., 1980)^[9] and Kolte and Awasthi, 1981, Kalpana et al, 2019)^[10,7]. But due to concern of environmental hazards, high cost of chemicals and problem of non-uniform spraying due to plant height, farmers are usually reluctant to use these fungicides for the management of the disease. At present best alternative method for management of this disease is identification of resistant cultivars which is also most ecofriendly and cost effective disease management strategy for this disease. Availability of resistant source has been reported by several workers and different criteria have been used by them to determine the relative resistance of various genotypes in oilseed Brassica

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(Ashrufuzzaman, *et al.*, 1996, Kumar and Kolte., 2001) ^[2, 11]. However, less work has been done to understand the various aspect of disease component in resistant and susceptible genotypes. In this view, it is very important to identify and confirm the resistant sources. So that some promising and potential genotypes could be identified and used as donor sources in resistant breeding programme. Due to variability and wide distribution of white rust pathogen, new races of *Albugo candida* pathogen emerge which challenge the resistance of existing cultivars. Hence, along with screening of new Brassica genotypes, continuous evaluation of already reported resistant cultivars is also needed for finding stable

resistant sources against the pathogen. Considering the problems, the present investigation was undertaken for the confirmation of resistant sources in *Brassica* genotypes against *A. candida*.

2. Material and Method

Brassica genotypes (82 no.) including 10 different Brassica species were evaluated against *A. candida* pathogen in field under natural condition during the crop season 2017-18 and 2018-19 in Crop research centre, GBPUA&T, Pantnagar. Following Brassica genotypes (Table 1) were used for evaluation against white rust disease.

Si. No.	Genotypes	Species	Si no.	Genotype	Species	Si no.	Genotype	Species
1	Varuna	B. juncea	29	NBPGR 407	-	57	DRMRIJ-12-06	B. juncea
2	Pusa Bold	B. juncea	30	NBPGR 410	-	58	NPJ 217	B. juncea
3	TL 15	B. rapa var.toria	31	NBPGR 426	-	59	EC 399301	B. juncea
4	Candle	B. rapa var. Brown sarson	32	NBPGR 427	-	60	RMM-09-05-01	B. juncea
5	BSH 1	B. rapa var. Brown sarson	33	NBPGR 428	-	61	DRMRJ 127	B. juncea
6	Kranti	B. juncea	34	NBPGR 429	-	62	RMWR-09-05-01	B. juncea
7	Ragini	B. rapa	35	NBPGR 433	-	63	RH.14.001	B. juncea
8	RL 1359	B. juncea	36	NBPGR 434	-	64	DRMR 2035	B. juncea
9	Pusa Kalyani	B. rapa var. Brown sarson	37	NBPGR 437	-	65	DRMR 2019	B. juncea
10	Torch	B. rapa var. Brown sarson	38	NBPGR 439	-	66	RLC-5	B. juncea
11	Tobin	B. rapa var. Brown sarson	39	PRD.14.16	-	67	DRMR 12.39	B. juncea
12	Bhawani	B. rapa var.toria	40	PRD.14.25	-	68	DRMRIJ 12.40	B. juncea
13	Sinapis alba	S. alba	41	PRD.34.20	-	69	RL-JEB-52	B. juncea
14	DLSC-1	B. carinata	42	PAB.14.57	-	70	NPJ 217	B. juncea
15	YSPB 24	B. rapa var. yellow sarson	43	IC 413293	-	71	DRMR-12-48	B. juncea
16	Wester	B. napus	44	IC 426528	-	72	RMM-09-6-1	B. juncea
17	Heera	B. juncea	45	IC 597932	-	73	PDZ 5	B. juncea
18	Cutlass	B. juncea	46	IC 3175280	-	74	ABS(3)-15	B. juncea
19	Sangam	B. nigra	47	IC 313378	-	75	RTM-10-9-1	B. juncea
20	RH 30	B. juncea	48	IC 313379	-	76	PDZ 3	B. juncea
21	NRCDR 515	B. juncea	49	IC 265495	-	77	DRMR 5206	B. juncea
22	Eureca sativa	E. sativa	50	IC 298024	-	78	71 J0002	B. juncea
23	Donskaja	B. juncea	51	IC 597932	-	79	RTM 16.24	B. carinata
24	EC 41329	B. juncea	52	RMWR-09-05	B. juncea	80	SIVT 17.108	B. carinata
25	NBPGR 1	-	53	DRMRIJ-12-65	B. juncea	81	SIVT 17.19	B. juncea
26	NBPGR 8	-	54	DRMRIJ-12-43	B. juncea	82	SBZ 13 30	B. juncea
27	NBPGR 15	-	55	DRMRIJ-12-02	B. juncea			
28	NBPGR 352	-	56	RH 1231	B. juncea			

Table 1: Brassica genotypes for evaluation against A. candida under field condition

2.1 Evaluation under natural field conditions

The *Brassica* genotypes were sown on Oct.15, 2017 in a Randomized Block Design. Two rows of each with 3 m length were sown with plant to plant distance of 5-10 cm with a susceptible check (Varuna) sown after each two rows. Thinning of plants was done after 15 days of germination and two irrigations were applied during entire crop growth. Recommended doses of $N_{80}P_{40}K_{40}$ sulphur₄₀ Kg/ha was applied in the field. Half dose of nitrozen in the form of Urea was applied as broadcast 5 days after first irrigation. Ten plants were randomly selected in each row of each genotype and tagged to record observations. The observation on disease severity of white rust disease was recorded at 70, 80 and 90 days after sowing (DAS) using 0-9 rating scale (Conn *et al*, 1990)^[4].

Rating score	Leaf area covered ((%)	Disease reaction
0	No symptoms	Immune (I)
1	<5	Highly resistant (HR)
3	5 - 10	Resistant (R)
5	11 - 25	Moderately resistant (MR)
7	26 - 50	Susceptible (S)
9	>50	Highly susceptible (HS)

With disease observations at different time intervals, Area under disease progress curve (AUDPC) was calculated for each genotypes using formula given by (Wilcox son *et al.*, 1975)^[22].

$$AUDPC = \sum_{i=1}^{k-1} \frac{1}{2} [(x_i) + (x_i + 1) \dots (x_i + n)]$$

Where

 x_i = initial disease index $x_i + 1$ = second disease index

The Apparent infection rate was calculated by using formula given by (Vander plank, 1963)^[21]

$$r = \frac{2.3}{t_2 - t_1} \log_{10} \frac{x_2(1 - x_1)}{x_1(1 - x_2)}$$

Where

However, disease response (resistant/susceptible) in all the genotypes was determined at maximum disease pressure at 90 DAS.

2.2 Statistical Analysis: Data obtained from the experiment was analyzed by using OPSTAT software in RBD at 0.05% probability level.

3. Result and Discussion

3.1 Disease reaction on the basis of percent disease severity at 90 DAS

Among different Brassica genotypes evaluated at different time intervals, out of 82 genotypes, 26 genotypes viz. Donskaja, NRCRD 515, Wester, DLSC 1, NBPGR 8, NBPGR 352, NBPGR 407, NBPGR 410, NBPGR 426, NBPGR 427, NBPGR 428, NBPGR 429, NBPGR 433, NBPGR 434, NBPGR 437, NBPGR 439, IC 298024, IC 313379, IC 317528, IC 313378, IC 313379, IC 265495, IC 298024, IC 597942, SIVT 17.108, RTM 16.24, were found immune or free from disease with 0.0 percent disease severity index, while 28 genotypes viz. Candle (18.33), Cutlasss (20.00), Sinapis alba (16.67), Eureca sativa (11.33), NBPGR 1 (25.0), NBPGR 15 (25.0), IC 597932 (20.0), RMWR-09-05 (15.0), DRMRIJ-12-65 (23.3), DRMRIJ-12-06 (25.0), NPJ 217 (15.0), RMM-09-10 (11.67), DRMRIJ-127(21.4), RMWR-09-5-1(11.67), RH-14-001(15.0), DRMR 2035 (11.67), DRMR 2019 (15.0), RLC 5 15.0), DRMR 12.39 (25.0), RL-JEB-52 (15.0), RH 305 (15.0), DRMR-12-48 (11.67), PDZ-5 (11.67), ABS(3)-15 (15.0), RTM-10-9-1 (15.0), 71J0002 (15.0), SIVT 17.19 (11.67), SBZ 13-30 (15.0) were found moderately resistant at 90 DAS. Rest of the genotypes were found susceptible to highly susceptible (28.0-75.0 percent disease severity) against white rust disease at 90DAS (Table 2). Many earlier workers also evaluated different Brassica genotypes under field conditions and found some genotypes free from disease. Kalpana et al. (2017)^[6] reported different Brassica species viz. turnip red (Brassica napus), Sinapis alba, PBC 9221 (Brassica carinata), PBN 9501 (Brassica napus) free from disease while Katili local, Ornamental Rai, Eureca sativa were found resistant against the disease. Based on field studies Saharan and Kaushik, 1988; Gupta *et al.*, (1994) ^[18, 5] reported *Brasssica* genotypes *viz*. HC-1, PCC-1 (*B. carinata*), GSL-1501 (*B. napus*), EC-129126-1 and Shiva free from white rust disease.

Similarly, different B. napus genotypes viz. EC-338997, PBN-2001, EC-339000, PBN 2002 and DGS-1 and B. carinata cv. PBC 9221 were free from disease and *B. juncea* genotypes viz. CBJ 001, CBJ 003 and CBJ 004 (China), JM06011 (Australia) were found resistant to white rust disease (Kumar and Kalha, 2005; Li et al., 2008.; Meena et al., 2011) [13, 14, 15]. In accordance to the present finding this study reveals that Brassica species viz. Sinapis alba and Eureca sativa which were found free from disease and resistant, respectively by Kalpana et al. (2017)^[6] reduced their resistance level and found to be moderately resistant against A. candida pathogen. Similarly, NBPGR series and IC series which were reported to be immune (0% disease severity) under field conditions were again found free from disease except NBPGR 1, NBPGR 15, IC 597932 which were found moderately resistant with 25.0, 25.0 and 20.0 percent disease severity respectively. Hence continuous screening of resistant genotypes is required to obtain a stable resistant source against the pathogen for effective management (Table 2, figure 1.A & 1.B).

3.2 Infection rate and area under disease progress curve (AUDPC) in different Brassica genotypes

Disease severity in different Brassica genotypes at different time intervals (70, 80 & 90 DAS) clearly revealed gradual progression of disease over time up to 90 DAS. Minimum (0.0949) and maximum (0.1008) infection rate were observed in DRMRJ 127 and 71 J0002 respectively. However, AUDPC for different genotypes was clearly in synchronization with percent disease severity at maximum disease pressure (90 DAS) with minimum AUDPC in SIVT-17-19 (69.44) and maximum in RH 30 (588.0). (Table 2, fig. 1 A& 1 B)). Present finding are in accordance with Kalpana *et al* (2017)^[6] who reported low infection rate and AUDPC in EC 399299 and *Raphanus sativus*. Kumar *et al* (2004) ^[12] also reported resistant genotypes *viz*. RC 781, RH 819, RC 1425, RH 781 and RH 8119 containing low infection rate and AUDPC in comparison to susceptible genotypes.

 Table 2: Disease severity, disease reaction and AUDPC of A. candida on different Brassica species/genotypes under field conditions (Pooled data of 2017-18 and 2018-19)

C No	Decenter Constant	% Disease severity									Lefe d'an Dete	
5. INO.	Brassica Genotype	70DAS	Ang*	DR	80DAS	Ang*	DR	90DAS	Ang*	DR	infection kate	AUDPC
1	Varuna	40.33	39.41	S	53.33	46.89	HS	73.33	58.91	HS	0.0299	575.56
2	Pusa Bold	39.33	38.82	S	48.33	44.03	S	65.00	53.74	HS	0.0251	498.89
3	TL 15	15.33	23.00	MR	21.67	27.70	MR	33.00	35.05	S	0.0383	235.56
4	Candle	8.33	16.59	R	15.00	22.59	MR	18.33	25.18	MR	0.0394	138.89
5	BSH 1	16.00	23.56	MR	16.67	24.04	MR	31.67	34.22	S	0.0341	207.22
6	Kranti	42.33	40.57	S	51.67	45.94	HS	65.00	53.74	HS	0.0214	515.00
7	Ragini	20.00	26.55	MR	25.00	29.98	MR	32.00	34.43	S	0.0235	245.56
8	RL 1359	30.00	33.20	S	33.33	35.24	S	53.33	46.89	HS	0.0288	369.44
9	Pusa Kalyani	22.67	28.40	MR	21.67	27.70	MR	36.67	37.24	S	0.0241	254.44
10	Torch	16.33	23.81	MR	15.00	22.78	MR	30.00	33.15	S	0.0304	193.89
11	Tobin	14.00	21.96	MR	17.33	24.56	MR	28.00	29.91	MR	0.0290	187.22
12	Bhawani	22.00	27.93	MR	32.67	34.83	S	41.67	40.18	S	0.0319	315.00
13	Sinapis alba	3.33	8.61	HR	10.00	18.04	R	16.67	24.04	MR	0.0805	113.89
14	DLSC 1	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00
15	YSPB 24	32.33	34.63	S	28.33	32.13	S	43.33	41.15	S	0.0146	315.00
16	Wester	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00
17	Heera	33.33	35.24	S	30.00	33.20	S	43.33	41.15	S	0.0131	325.00
18	Cutlass	8.33	16.59	MR	16.67	23.73	MR	20.00	26.44	MR	0.0438	155.56
19	Sangam	14.33	22.23	MR	18.33	25.30	MR	28.00	29.91	S	0.0278	185.56

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20	РН 3 0	40.00	30.22	S	58 33	40.78	ЦС	75.00	60.05	Цζ	0.0314	588 80
20	KII 30	40.00	39.22	5 T	38.33	49.70	115	73.00	00.05	115	0.0314	388.89
21	NRCDR 515	0.00	0.00	1	0.00	0.00	I	0.00	0.00	1	0.00	0.00
22	Eureca sativa	3.33	8.61	HR	6.67	14.75	R	11.33	16.59	MR	0.0803	91.41
23	Donskaja	0.00	0.00		0.00	0.00	T	0.00	0.00	I	0.00	0.00
24	EC 41220	26.67	27.24	ЦС	41.67	40.19	c	45.00	42.10	c	0.0102	201.67
24	NDDCD 1	30.07	11.02	IID	41.07	40.10	5	45.00	42.10	5	0.0102	391.07
- 25	NBPGR I	4.33	11.93	HK	11.6/	19.88	MR	25.00	29.91	MK	0.0876	140.56
26	NBPGR 8	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00
27	NBPGR 15	12.33	20.49	MR	12.33	20.49	MR	25.00	29.91	MR	0.0353	157.22
28	NBPGR 352	0.00	0.00	T	0.00	0.00	T	0.00	0.00	I	0.00	0.00
20	NIDDCD 407	0.00	0.00	T	0.00	0.00	T	0.00	0.00	T	0.00	0.00
29	NBPGR 407	0.00	0.00	1	0.00	0.00	1	0.00	0.00	1	0.00	0.00
30	NBPGR 410	0.00	0.00	Ι	0.00	0.00	I	0.00	0.00	I	0.00	0.00
31	NBPGR 426	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00
32	NBPGR 427	0.00	0.00	T	0.00	0.00	I	0.00	0.00	I	0.00	0.00
33	NBPGP 428	0.00	0.00	T	0.00	0.00	T	0.00	0.00	T	0.00	0.00
24	NDPCD 420	0.00	0.00	T	0.00	0.00	T	0.00	0.00	T	0.00	0.00
34	NBPGR 429	0.00	0.00	1	0.00	0.00	1	0.00	0.00	1	0.00	0.00
35	NBPGR 433	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00	I	0.00	0.00
36	NBPGR 434	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00
37	NBPGR 437	0.00	0.00	T	0.00	0.00	T	0.00	0.00	I	0.00	0.00
38	NBPGR 439	0.00	0.00	T	0.00	0.00	T	0.00	0.00	I	0.00	0.00
20	DPD 14 16	42.00	40.29	c c	52.22	46.80	ЦС	66.67	54.76	ЦС	0.0221	407.78
39	I KD.14.10	42.00	40.30	0	33.33	40.09	115	45.00	12.10	115	0.0231	497.78
40	PRD.14.25	38.33	38.23	2	38.33	38.23	2	45.00	42.10	3	0.0080	312.22
41	PRD.34.20	51.67	45.94	HS	53.33	46.89	HS	66.67	54.76	HS	0.0127	530.56
42	PAB.14.57	40.00	39.20	S	41.67	40.18	S	45.00	42.10	S	0.0059	391.67
43	IC 313379	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00
44	IC 298024	0.00	0.00	T	0.00	0.00	T	0.00	0.00	I	0.00	0.00
45	IC 507032	6.67	13 70	P	12.67	20.81	MR	20.00	27.22	MR	0.0240	126.06
40	IC 317529	0.07	0.00	T	0.00	20.01	I	20.00	0.00	T	0.0240	0.00
40	IC 31/528	0.00	0.00	I	0.00	0.00	I	0.00	0.00	1	0.00	0.00
47	IC 313378	0.00	0.00	1	0.00	0.00	I	0.00	0.00	I	0.00	0.00
48	IC 313379	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00
49	IC 265495	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00
50	IC 298024	0.00	0.00	I	0.00	0.00	I	0.00	0.00	I	0.00	0.00
51	IC 597942	0.00	0.00	T	0.00	0.00	T	0.00	0.00	T	0.00	0.00
52	DMWD 00 05	2.00	0.00	IID	5.00	12.02	IID	15.00	22.50	MD	0.00	76.67
52	RMWR-09-03	5.00	9.72	пк	5.00	12.92	ПK	13.00	22.39	MK	0.0803	/0.0/
53	DRMRIJ-12-65	10.00	18.43	R	11.67	19.88	MR	23.33	28.65	MR	0.0424	144.44
54	DRMRIJ-12-43	20.00	26.55	MR	30.00	33.15	S	41.67	40.18	S	0.0367	300.00
55	DRMRIJ-12-02	18.33	25.30	MR	21.67	27.70	MR	36.67	37.19	S	0.0347	252.78
56	RH 1231	26.67	31.06	S	31.67	34.22	S	38.33	38.23	S	0.0181	313.89
57	DRMRII 12-06	12.33	20.49	MR	15.67	23.20	MR	25.00	29.91	MR	0.0353	170.56
50	NDL 217	4.22	11.02	IID	6.67	14.75	D	15.00	22.50	MD	0.0533	92.79
50	NFJ 217	4.55	11.95	пк	0.07	14.75	N G	13.00	22.39	MIK	0.0021	02.70
59	EC 399301	26.67	31.06	S	35.00	36.22	S	50.00	44.98	S	0.0178	335.56
60	RMM-09-10	3.00	9.72	HR	6.67	14.75	R	11.67	19.88	MR	0.0679	72.22
61	DRMRJ 127	2.00	8.13	HR	10.00	18.04	R	13.33	21.14	MR	0.0949	87.22
62	RMWR-09-5-1	5.00	12.92	HR	6.67	14.75	R	11.67	19.88	MR	0.0424	74.44
63	RH 14 001	6.67	14 75	R	6.67	14 75	R	15.00	22 59	MR	0.0406	88 33
64	DPMP 2025	6.67	14.75	D	6.67	14.75	D	11.67	10.88	MD	0.0280	77.22
6	DDMD 2010	5.07	12.02	ID	7.02	15.50	D D	15.00	17.00	MD	0.0200	07.79
00	DRMR 2019	5.00	12.92	HK	7.55	15.59	ĸ	15.00	22.59	MR	0.0549	87.78
66	RLC-5	4.00	11.32	HR	6.67	14.75	K	15.00	22.59	MR	0.0661	82.22
67	DRMR 12.39	8.33	16.59	R	13.00	21.10	MR	25.00	29.91	MR	0.0549	151.67
68	DRMRIJ 12.40	18.33	25.30	MR	26.67	31.06	S	45.33	42.30	S	0.0453	292.78
69	RL-JEB-52	5.00	12.92	HR	6.67	14.75	R	15.00	22.59	MR	0.0549	85.56
70	RH 305	4 00	11 32	HR	10.33	18.46	R	15.00	22.59	MR	0.0661	99.44
70	DDMD 12 40	5.00	12.02	ЦП	9 22	16.50	D	11 47	10.99	MD	0.0001	74.44
/1	DRMR-12-46	3.00	12.92	пк	8.33	10.39	ĸ	11.07	19.00	MK	0.0108	/4.44
12	KMM-09-6-1	35.00	36.22	5	50.00	44.98	5	55.00	47.86	HS	0.0226	452.78
73	PDZ 5	6.67	14.75	R	10.00	18.04	R	11.67	19.88	MR	0.0280	85.56
74	ABS(3)-15	6.67	14.75	R	8.33	16.59	R	15.00	22.59	MR	0.0294	92.22
75	RTM-10-9-1	3.00	9.72	HR	8.33	16.59	R	15.00	22.59	MR	0.0805	91.11
76	PDZ 3	15.00	22.59	MR	23.33	28.84	MR	35.00	36.22	S	0.0424	241.11
77	DRMR 5206	16.67	24.04	MP	36.67	37.24	S	35.00	36.22	s S	0.0371	305 56
70	71 10002	2.00	0 1 2		0.07	17.01	о П	15.00	22.50	ND ND	0.0371	01.77
/8	/1 J0002	2.00	0.15	пк	9.0/	1/.91	ĸ	15.00	22.39		0.1008	91.0/
79	KIM 16.24	0.00	0.00	1	0.00	0.00	1	0.00	0.00	1	0.00	0.00
80	SIVT 17.108	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00	Ι	0.00	0.00
81	SIVT 17.19	2.00	8.13	HR	6.67	14.75	R	11.67	19.88	MR	0.0882	69.44
82	SBZ 13 30	6.67	14.75	R	13.33	20.95	MR	15.00	22.59	MR	0.0406	107.78
	CD 5%	3.49			3.68	-		4.37	1		-	
				•		1			1	1	1	

*Angular transformed value I: Immune, HR: Highly resistant, MR: Moderately resistant, R: Resistant, S: Susceptible, HS: Highly susceptible



Fig 1(A): Percent disease severity (90DAS) and AUDPC of A. candida on different Brassica species under field conditions



Fig 1(B): Percent disease severity (90DAS) and AUDPC of A. candida on different Brassica genotypes under field conditions

4. Conclusion

The present investigation on evaluation of different Brassica genotypes under natural field conditions against white rust disease revealed that continuous evaluation of new genotypes as well as existing resistant genotypes is needed as evolution and emergence of new pathogenic races, may cause break down of existing resistant sources. However, for the final confirmation of resistance, the genotypes which have been found free from disease or resistant under field conditions need to be evaluated in glasshouse also under artificial epiphytotic conditions to assure if absence of disease in field condition is due to true resistance in that genotype or an escape from disease due to unfavorable environmental conditions for disease development. The Brassica species which are free from disease or highly resistant against A. candida pathogen can not only be used as resistant sources against the disease but also as potential sources for selection of differential hosts for finding out A. candida pathotypes/races.

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