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RESEARCH ARTICLE

Postulation of resistant genes for powdery mildew (*Blumeria graminis tritici*) in Indian wheats

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ABSTRACT

Two hundred and sixty three genotypes of advanced Indian wheat breeding material comprising *Triticum* spp. and tritcale were screened against seven genetically characterized virulences of *Blumeria graminis* f. sp. t*ritici* and powdery mildew resistant genes were postulated in fifty one genotypes showing differential reaction to the cultures. Gene *Pm5* and some other unidentified gene(s) were postulated in genotype PBW 368. Resistance in genotypes PBW 363 was attributed to gene (s) *Pm3c+Pm8* and some other unidentified gene (s). Resistance in these genotypes, HS 352, HS 365, HPW 93, HUW 435, UP 2359, HP 1740, UP 2358, HW 1089, K 9210, K 9211, K 9116, K 9235, K 9228, HUW 443, WH 615, HUW 446, HD 2644, MP 941, HUW 435, HUW 454, HW 1087, PBW 369 and HP 1729 was found to be controlled by gene *Pm8* individually or in combination with unknown gene(s). Resistance in 24 genotypes, behaving differentially to the cultures, could not be attributed to any of the known gene(s). Eight genotypes UP 2374, PBW 361, HW 1093, UP 2375, TL 2853, TL 2780, HPT 6 and DT 46 were resistant to all the test cultures, hence, the resistance in these genotypes could not be attributed to any of the genotypes. Rest of the genotypes were susceptible to all the isolates.

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INTRODUCTION

Wheat powdery mildew, *Blumeria graminis* f.sp. *tritici* (Bgt), was confined mainly to northern and southern hills in India. However, with the introduction and spread of high yielding, semi-dwarf varieties under high fertility conditions , the disease has posed a potential threat in North Western Plain Zone (NWPZ) and North Hill Zone (NHZ) (Bahadur and Aggarwal, 1997, DWR, 2009). Cultivation of resistant varieties is a practically feasible, economically viable and environmentally safe method to manage this disease (Svec *et al*., 2002). More than 45 gene loci (*Pm1 to Pm45*) with more than 60 genes/alleles for resistance to powdery mildew have been identified and catalogued in bread wheat and its relatives (Alam *et al*., 2011), some of which have been utilized in various breeding programmes throughout the world to evolve resistant varieties. However, resistance of genes in the varieties are frequently overcome by new *Bgt* virulences, as the presence and frequency of virulence genes in the pathogen population changes continuously (Alam *et al*., 2011, Rax Paul *et al*., 2000, Identification and genetic characterization of resistant donors is a pre- requisite to evolve powdery mildew resistant varieties and their proper exploitation in the deployment, constitution of multilines and varietal mixtures. Preliminary assumptions on resistance genes in donors can be drawn from pedigree relationships (Heun and Fischbeck, 1987). Infection – type matching technique (Browder, 1973) based on gene- for –gene concept (Flor, 1955) using genetically characterized *E. graminis tritici* cultures confirms the presence of genes responsible for resistance. Powdery mildew resistance genes using this technique have been identified in wheat genotypes of Europe (Heun and Fischbeck, 1987, Lutz *et al*., 1995a, Hovmoller, 1989, Lutz *et al*., 1995b, Zeller *et al*., 1998, Svec

Table A: Information on pedigree of wheat genotypes used

Sr. No.	Varieties/ genotypes	Parentage
1.	VL 733	ALD"S"/OW "S"
2.	Hs 365	HS 207/Sonalika
3.	HPW 93	PJ/HN4//GLL/3/YACO"S"/4/VEE
4.	HD 2610	VEE'S'/HD 2402
5.	HI 977	Gu/Aust#261-15??Cno/No.66/3/Kal/Bb
6.	HD 2639	CN 079/PRL'S'//GAA
7.	HD 2641	CN 079/PRL'S'//CHILL'S'
8.	HD 2644	YL54/NIOB//NAR'S13/ND/C13438/4/HD 2329/5/Hb 2160
9.	HP 1633	RL 6010/6*Ska
10.	RW 674	HP 1633/CC 492
11.	RW 575	WH 377/Janak/WG 377/HI 385
12.	K 9116	DW 5046/Celaya/Celava/K 8434
13.	K 9006	CPAN 168 /HD 2204
14.	K 9210	VEE'S'/WL 711
15.	K 9211	K 7917/UP 2003/HUW 206
16.	K 9253	JUP/EMU//GLO/TRM 73
17.	K 9262	WH 147/HD 2204
18.	K 9264	HP 1633/Kalyan sona//UP 262
19.	PBW 361	PBW 129/WL 1763/CCBS 57
20.	PBW 363	SERI 3/BUC/BJY 'S'
21.	PBW 368	WG 2702/CROW'S'
22.	PBW 369	WL 711/HD 2285//CCBS 122
23.	PBW 372	HP 1209/CB 96
24.	K 9228	K 8202/K 8181//K 816
25.	K 9107	K 8101/K 68
26.	UP 2358	CNO. 67/MPO//MON'S'/3/SERI
27.	K 9235	HUW 319/CPAN 1556//CPAN 1556
28.	MP 941	SERI/4TA'S'-DUR69/3/SERI
29.	HP 1729	MRL "S"/BUC "S" //VEE 7.
30.	HP 1740	BAU "S"/LIRA "S"//KAUZ
31.	HUW454	HUW 300/HUW 355//VEE 'S'
32.	HUW 446	HUW 37/HD 2204//HUW 284
33.	HUW 435	K 7903/HUW 37//K 7903
34.	HUW 443	HUW 207/HUW 202
35.	HUW 446	HUW 37//HUW 206//C 306
36.	GW 1104	AA'S'/CR'S'//CIT'S'/3/SEBON
37.	GW 1106	HI 6490/JWJ80//HI 8112
38.	DT 46	JNIT 140/DTS 1209
39.	HPT 6	JNIT 79/ CPAN 1922
40.	TL 2780	Cinnamon/WL-394/TL 174/TCL MAYA II
41.	TL 2853	TL 1969/WHITE RYE//TL 707
42.	UP 2374	CPAN 1987/WL 1829
43.	WH 615	Kauz Selection
44.	UP 2375	MgA 513-2B/PBW 174
45.	HD 2610	VEE 'S'/HD2402
46.	HW 1093	-
47.	DL 803-3	HUW 202/K 7537/HD 2160
48.	HW 1087	HW 680XVSM 346
49.	UP 2359	CPAN 1985/HD2375
50.	HW 1089	HW 680X VSM 346
51.	HP 1209	E 4871/Pj 62
52.	UP 2363	Kauz 'S'
53.	HW 1093	-
54.	BW 1087	-
	HS 352	Bow "S"/Buc "S"

Table B : List of the near-isogenic lines/cultivars having known genes for resistance to *Blumeria graminis* f. sp. *tritic*.

Line	CI/PI number	Designated gene
Axminister xCc[8],	CI 14114	*Pm 1*
CI 13836 x Cc[8]	CI 14115	*Pm 1*
Ulka x Cc[8]	CI 14118	*Pm 2*
Asosan x Cc[8]	CI 14120	*Pm 3a*
Chul x Cc[8]	CI 14121	*Pm 3b*
Sonora x Cc[8]	CI 14122	*Pm 3c*
Khapli x Cc[8]	CI 14123	*Pm 4*
Yuma x Cc[8]	CI 14124	*Pm 4*
Hope/CS	-	*Pm 5*
Timgalin	-	*Pm 6*
TP 114	PI 405718	*Pm 2+6*
Transec	CI 14189	*Pm 7*
Kavkaz, Veery	PI 361879	*Pm 8*
Kavkaz/4Fd	-	*Pm 8*
Agra Local	A collection from Uttar Pradesh	Universal susceptible

et al., 2002, Gordei *et al*., 1998) and America (Leath and Heun, 1990) and China (Zhou-Yi Lin *et al*., 2002). In India, resistance genes have been identified in some exotic and Indian wheat stocks (Basandrai *et al.*, 1996, Pathania *et al.*, 1998, Rax Paul *et al.*, 1999). This paper embodies information on powdery mildew resistance in some advanced Indian breeding material.

MATERIALS AND METHODS

Material :

Host :

The host material comprised 263 genetic stocks of wheat (*Triticum* spp.) and triticale comprising advanced Indian wheat breeding material. The information on pedigree details of the selected genotypes used in the present studies is given in Table A.

Pathogen :

Seven genetically characterized single colony cultures of *Blumeria graminis tritici* (Bgt) cultures from the powdery mildew populations were collected from north western Himalayas. The avirulence/virulence formulae of the cultures is given in Table B.

– *Pm1, 2, 3b, 3c, 4, 2+6/ 3a, 5, 6, 7, 8*
– *Pm1, 2, 3b, 4, 5, 2+6, / 3a, 3c, 6, 7, 8*
– *Pm1, 2, 3b, 4, 2+6, / 3a, 3c, 5, 6,7, 8*
– *Pm1, 2, 3b, 4, 5, 7, 8/ 3a, 3c, 6, 2+6*
– *Pm1, 2, 3b, 4, 2+6, 8*/ 3a, 3c,5, 6, 7*
– *Pm1, 2, 3a, 3c, 4, 5, 2+6/ 3b, 6, 7, 8*
– *Pm1, 2, 3b, 4, 2+6, 7/3a, 3c,5, 6, 8*

Methods :

The experiment was conducted in the glass house of the Department of Plant Breeding and Genetics, C.S.K. Himachal Pradesh Krishi Vishvavidyalaya, Palampur. The seedlings of test genotypes were raised in galvanized iron trays (18 x 9 x 4²) having a mixture of field soil and FYM (10:1). Each tray accommodated 13 rows of test genotypes and a row of susceptible cv Agra Local. Seedlings of international powdery mildew differential lines (*Pm* lines) having genes *Pm1* to *Pm8* (Table B) were also grown separately to confirm the virulence spectrum of the cultures. Ten days old seedlings, at one leaf stage, of the test genotypes and the differential lines were dust inoculated with mass inoculum of each single colony culture separately. The inoculated trays were incubated in spore proof muslin cloth chambers under natural light conditions in the glass house. The maximum and minimum temperature during the experimentation varied from 25±4°C and 5± 3°C, respectively.

The data were recorded on infection – type, 10 days after the inoculations following a modified '0-4' scale (Smith and Blair, 1950). The genotypes showing disease reaction 0-2 were categorized as resistant whereas, those with '3-4' as susceptible. The observations were recorded when the susceptible check developed infection type '4'. The resistance genes were identified based on the differential reaction, following Browder (1973).

RESULTS AND DISCUSSION

Two hundred sixty three genotypes of *T. aetivum*, *T durum* and triticale were subjected to seven genetically

characterized single colony cultures of *Blumeria graminis* f. sp.*tritici*. Forty three genotypes behaved differentially to the cultures and eight genotypes were resistant to all the cultures. Rest of the genotypes were susceptible to the test cultures. Based on the infection- type, matching technique powdery mildew resistant gene(s) were postulated in these genotypes and are given in Table 1. Based on the differential interaction these genotypes were categorized into six resistance spectrums (Spectrum I-VI).

Spectrum I :

Only one genotype PBW 368 comprised this spectrum. It developed infection-type ';-1' to cultures 1, 2, 3 and 6 and was susceptible to rest of the cultures indicating the presence of gene *pm5* in combination with some unidentified gene(s). The pedigree analysis of the genotype showed the involvement of Lerma Rojo 64 as one the parents which in turn has Newthach having cultivar Hope as one of the parents (Zeven and Zeven, 1976). Genotype Hope possessed gene *pm 5* (McIntosh *et al*., 2008).

Spectrum II :

Genotype PBW 363 showed resistant reaction to all the cultures except cultures 3 and 7. Infection-type matching technique suggested the presence of genes *Pm3c* and *Pm8* along with some unidentified gene (s) in this stock . Pedigree analysis indicated the presence of 'Seri' and Sonora 64 in its parentage reported to have genes *Pm3c* and *Pm8*, respectively (McIntosh *et al*., 2008) . The presence of gene *Pm8* in this genotype was further confirmed by the postulation of gene *Lr26+23* and *Yr9+* for leaf rust and yellow rust resistance, respectively (Nayar *et al*., 2001) which are closely linked with gene *Pm8* (McIntosh *et al.*, 2008, Tomar *et al*., 2004).

Spectrum III:

The genotypes, HS 352, HS 365, HPW 93, UP 2359, HP 1740, UP 2359, HW 1089, K 9210, HUW 443, K 9211, WH 615, UP 2358, HUW 446, HD 2644, MP 941, BW 1087 and UP 2363,

Table 1: Reaction of enteries of AVT-I and II year to cultures of *Blumeria graminis* f. sp. *tritici* and probable resistance genes

Group	Enteries	Reaction to cultures							Probable gene(s)
		1	2	3	4	5	6	7	
I	PBW 368	;	1	;	4	4	;	4	*Pm5*
II	PBW 363	;	;	3	;	2	;	4	*Pm3c+8*
III	HS 352, HS 365, HPW 93, UP 2359, HP 1740, UP 2358, HW 1089, K 9210, HUW 443, K 9211, WH 615, HUW 446, HD 2644, MP 941, BW 1087, UP 2363	3	4	3	;	2	4	4	*Pm8*
IV(a)	HUW 435	3	4	;	;	;	2	4	*Pm8+*
(b)	HUW 454	4	4	3	;	;	2	4	*Pm8+*
(c)	K 9235, K 9228	4	4	4	;	2	2	4	*Pm8+*
(d)	PBW 369	;	3	;	;	;	4	4	*Pm8+*
	HP 1729	4	4	4	;	;	4	4	*Pm8+*
(f)	UP 2358, K 9116	4	2	;	;	;	3	4	*Pm8+*
V (a)	HD 2639, HD 2641 HP 1209	;	;	;	4	4	3	3	?
(b)	PBW 372, RW 674	;	;1	3	3	;2	4	3	?
(c)	HP 1633, GW 1104, RW 575, K 9253, Raj 1265,	4	4	;	4	4	4	3	?
(e)	GW 1106, HW 2004, K 9264	;	4	4	4	3	4	3	?
(f)	K 9262, DL 803, K 9107, HI 977, HD 2610	4	4	3	4	3	;1	3	?
VI a	UP 2375, UP 2374, PBW 361, HW 1093	;	;	2	;	2	1	;	?
b	TL 2853, TL 2780, HPT 6, DT 46	;	;	;	;	;	;	;	?
	Sonora/cc[8]	1	4	3	4	3	2	3	*Pm3c*
	CS/Hope	4	;	4	;	4	;	;	*Pm5*
	Fd/Kav	3	3	4	;	2	4	;	*Pm8*
	WL711/Agra Local	4	4	4	4	4	4	4	-

showed infection-type ';' and 2 to cultures '4' and '5' and were susceptible to rest of the cultures. Based on infection-type matching technique gene *Pm8* was postulated in these genotypes. Genotypes HPW 93, UP 2359 and K 9210 involved Veery, genotypes UP 2358 and MP 941 had Seri in their pedigree. Genotypes K 9211, WH 615 and HUW 446 involved Kavkaz in their pedigree through the involvement of var. HUW 206 as one the parents . HP 1740 had Lira's' and 'Kavkaz' as the parents. In genotypes, HS 365, HPW 93, *UP 2359*, HP 1740, UP 2358, K 9210, HUW 443, K 9211, WH 615, HUW 446, HD 2644, MP 941 and UP 2363 leaf rust and yellow rust resistance genes *Lr 26* and *Yr 9* were postulated (Nayyar *et al.*, 2001). Since, genes *Lr 26, Yr 9* and *Pm 8* are closely linked hence, it confirmed the presence of gene *Pm 8* in these genotypes (Tomar *et al*., 2004, McIntosh *et al*., 2008).

Spectrum IV:

Seven genotypes comprised this spectrum. Genotypes PBW 369 and HS 352 exhibited infection- type ';' to cultures 1, 3, 4, 5, whereas, genotype HP 1729 developed infection-type ';' to cultures 4, 5. Genotypes UP 2358 and K 9116 developed infection-type '2' against culture 2 and ';' to cultures 3, 4 and 5. Genotypes HUW 435 developed infection-type ';' to cultures 3, 4, 5 and '2' to culture 6 whereas, genotypes HUW 454 showed infection–type ';' to cultures 4, 5 and '2' to culture 6. These genotypes were susceptible to the rest of the cultures. Based on differential reaction following infection-type matching techniques, genes *Pm8* and some unidentified genes were identified in these cultivars. Genotypes HUW 454 and HP 1729 possessed Veery whereas, genotype HS 352 possessed Bob white in their pedigree. Genotypes Veery and Bob white are known to have gene *Pm8* (Mclntosh *et al*., 2008). Presence of gene *Pm8* in cvs HUW 435, K 9235, PBW 369, HP 1729 and K 9116 was confirmed by the identification of genes *Lr 26* and *Yr9* for resistance to leaf rust and yellow rust, respectively (Nayyar *et al*., 2001) as genes *Lr26* and *Yr9* are closely linked (Tomar *et al.,* 2004, Mclntosh *et al.,* 2008).

Spectrum V:

Eighteen genotypes comprised this spectrum. Genotypes HD 2639, HD 2641, HP 1209 showed resistant reaction to cultures 1, 2 and 3 whereas, genotype PBW 372 and RW 674 showed resistant reaction to cultures 1, 2 and 5. Genotypes HP 1633, GW 1104, RW 525, K 9253, Raj 1265 were resistant to culture 3. Genotypes GW 1106, HW 2004 and K 9264 showed resistant reaction to culture 1. Five genotypes, DL 803-3, K 9262, K 9107, HI 977and 2610 showed resistant reaction to culture 6. The test genotypes were susceptible to rest of the cultures. The data revealed that though these genotypes behaved differentially to the cultures, but the present array of cultures could not attribute the resistance in these genotypes any of the known gene (s).

Spectrum VI :

Triticale genotypes TL 2853, TL 2780, HPT 6 and DT 46 and *T. aestivum* genotypes UP 2374, PBW 361, HW 1093 and UP 2374 showed resistant reaction to all the test cultures. The absence of differential interaction, using the present set of cultures, could not postulate the underlying resistance genes in these stocks.

Seven genetically characterized cultures of *Blumeria graminis tritici* used in the present studies could, postulate three known powdery mildew resistance genes *Pm3c, Pm5* and *Pm8,* individually or in combination with unknown genes in 51 advanced wheat material and gene *Pm 8* was the most frequent. Virulence against genes *Pm3c, pm5* and *Pm8* is quite prevalent in *B. graminis tritici* populations in India and abroad (Alam *et al*., 2011, Bahadur and Aggarwal, 1997, Rax Paul *et al.,* 2000 and Svec *et al.,* 2002). During the last two decades powdery mildew has emerged as a major threat in the North hills and north western plains of India. All the commercially grown varieties of bread and durum wheat are susceptible (DWR, 2009). Interestingly, resistance has been reported in same *Triticum* spp. and allied genera (Alam *et al*., 2011, Tomar *et el*., 2004). Therefore, new and diverse sources of resistance against the disease are required to be identified and characterized for their utilization in the breeding programme to evolve resistant varieties.

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