Indian J. Genet., 76(2): 205-208 (2016)
DOI: 10.5958/0975-6906.2016.00024.9

Short Communication

Resistance to powdery mildew (*Blumeria graminis* f. sp. *tritici* E. Marchal.) in bread wheat, durum, dicoccum and triticale genotypes

Daisy Basandrai*, Ashwani K. Basandrai, S. K. Rana[1], B. K. Sharma[2], Amar Singh[1], Dhirender Singh[3] and P. D. Tyagi[1]

Rice and Wheat Research Centre, Malan 176 047, [1]Department of Plant Pathology, CSKHPAU, Palampur 176 062, [2]Research Sub Station, Akrot, Una 177 211, [3]HAREC, Dhaulakuan, Sirmour 173 031

(Received: November 2015; Revised: February 2016; Accepted: March 2016)

Abstract

Powdery mildew resistance genes were postulated in 63 Indian genotypes belonging to *Triticum aestivum* L., *T. durum*, *T. dicoccum* and triticale. Gene *Pm3c* in combination with some unidentified gene(s) was postulated in genotype, K 9441. Some unknown gene(s) alongwith *Pm5* were identified in eight genotypes, while *Pm 5+Pm 8* were detected in genotype WH 681. Resistance in 22 genotypes was attributed to gene *Pm8* while, 12 genotypes showed additional resistance ascribed to the unknown gene(s). Seven genotypes *viz*., K 9453, HD 2689, HW 3003, HD 2680, MACS 3011, MACS 3018 and HD 2700 showing differential behavior to the test cultures. However, infection type matching technique, could not attribute resistance in these gnotypes. Triticale genotypes *viz*., DT 95, DT 46 and DT 91, *Triticum dicoccum* genotypes namely, DDK 1013, DDK 1014, MACS 2574, MACS 2912, MACS 2919, DDK 1009 and DDK 1015 and *T. aestivum* genotype UP 2450 were resistant to all the cultures and hence, no resistance gene in these genotypes could be postulated.

Key words : *Blumeria graminis tritici*, race specific resistance, *Triticum aestivum*, *T. durum*, triticale, *T. dicoccum*, wheat

Powdery mildew (PM), caused by the *Blumeria graminis* (DC.) E.O. Speer f.sp. *tritici* (Bgt) em. Marchal (syn. *Erysiphe graminis* DC. ex Merat f.sp. *tritici* Marchal), results in 13-100% yield losses affecting stable wheat production in areas with cool and maritime climates (Mwale et al. 2014). Cultivation of resistant varieties is economical, practically feasible and environmentally safe method to reduce crop losses. More than 60 PM resistance genes/alleles have been reported and few have been utilized in the development of commercial varieties (Mwale et al. 2014). However, such varieties loose their resistance shortly due to emergence of new virulent pathogen strains. Therefore, new and genetically diverse sources of resistance needs to be characterized. Keeping this in view, resistance genes were identified in advanced breeding lines of wheat (*Triticum aestivum*, *T. durum*, *T. dicoccum*) and triticale using infection type matching technique (ITMT) (Nayar et al. 2001) and the results are reported herein.

The host comprised advanced Indian breeding genotypes of wheat (*Triticum* spp.) and triticale. The pathogen comprised 10 genetically characterized single colony cultures of Bgt identified among the PM populations from north western Himalayas. The avirulence/virulence formulae of the cultures is given in Table 1. The experiment was conducted in the glass house of the Department of Crop Improvement, CSKHPKV, Palampur and HAREC Dhaulakuan. The seedlings of test genotypes, susceptible cv. Agra Local along with international powdery mildew differential lines (*Pm* lines) *viz*., Axminister xCc^8 and CI 13836 x Cc^8 (*Pm1*), Ulka x Cc^8 (*Pm2*), Asosan x Cc^8 (*Pm3a*), Chul x Cc^8 (*Pm3b*), Sonora x Cc^8 (*Pm3c*), Khapli x Cc^8 (*Pm 4*), Yuma x Cc^8(*Pm4*), Hope/CS (*Pm5*), Timgalin (*Pm6*), TP 114 (*Pm2+6*), Transec (*Pm7*), Kavkaz, Veery and Kavkaz/4Fd (*Pm 8*) were

*Corresponding author's e-mail: bunchy@rediffmail.com
Published by the Indian Society of Genetics & Plant Breeding, F2, First Floor, NASC Complex, PB#11312, IARI, New Delhi 110 012
Online management by indianjournals.com

Table 1. Avirulence/virulence formulae of the *Blumeria graminis tritici* cultures used

Culture	Avirulence/virulence formulae
1	*Pm 1, 2, 3b, 4a, 4b, 5/Pm 3a, 3c, 6, 7, 8*
2	*Pm 1, 2, 4a, 4b/Pm 3a, 3b, 3c, 5, 6, 7, 8*
3	*Pm 1, 2, 3b, 4a, 4b/Pm 3a, 3c, 5, 6, 7, 8*
4	*Pm 1, 2, 4a, 4b, 8/Pm 3a, 3b, 3c, 5, 6, 7*
5	*Pm 1, 2, 3b, 3c*, 4a, 4b/Pm 3a, 5, 6, 7, 8*
6	*Pm 1, 2, 3a, 3c, 4a, 4b, 7, 8/Pm 3b, 5, 6*
7	*Pm 1, 2, 3a, 4a, 4b/Pm 3b, 3c, 5, 6, 7, 8*
8	*Pm 1, 2, 3a, 3b, 4a, 4b, 6, 7/Pm 3c, 5, 8*
9	*Pm 1, 3b, 4a, 4b/Pm 2, 3a, 3c, 5, 6, 7, 8*
10	*Pm 1, 2, 3b, 4a, 4b, 6, 7/Pm 3a, 3c, 5, 8*

raised in galvanized iron trays filled with mixture of field soil and FYM (10:1). The raising of seedlings of test genotypes and differential lines, their inoculation separately with each culture, incubation for disease development in glasshouse and data recording on infection type (IT) was undertaken following Paul et al. (1999). The data on IT of the test genotypes and the gene(s) speculated are given in Table 2 and the results are described here under.

Genotype K 9441 developed IT'2' to cultures 2, 5 and 6 and IT= ';' to cultures 8 and 9. These IT suggested that the gene *Pm3c* individually or in combination with some unidentified gene(s) was responsible for its resistance. K 9441 involved leaf rust resistance gene *Lr23* (Nayar et al. 2001). Gabo, the differential line for gene *Lr23,* involved Sonora in its pedigree (Zeven and Zeven, 1979), having gene *Pm3c* (McIntosh et al. 2008), thereby, confirming its presence. Genotypes *viz*., GW 173, GW 273, and GW 291 developed IT= ';' to culture 1, whereas HS 369, GW 279, GW 1128, HD 2688, UP 2464 and DWR 225 produced IT '2' to it. Additionally, the genotypes, UP 2464, GW 273, GW 279, GW 1128, HD 2688, GW 173 showed resistant reaction to various cultures (Table 2). Infection type matching technique (ITMT) indicated the involvement of gene *Pm5* and some other unknown gene (s) in these genotypes. GW 291 and GW 279 involved cvs. HD 2402 and WL 2265, respectively in their pedigree having Kalyanasona possessing gene *Pm5* (McIntosh et al. 2008). Resistance to yellow rust in GW 173 and HD 2688 was attributed to gene *Yr2KS+*. Kalyansona, the carrier of gene *Yr2KS*, involved Hope (Nayar et al. 2001), in its pedigree carrying gene *Pm5* (McIntosh et al. 2008) confirming its presence.

WH 681 showed IT ';' to culture 4 and 6 and IT '2' to culture 1, 2 and 7 suggesting the presence of genes *Pm5, Pm8* and some other unidentified gene(s). This genotype involved Phoebee and WL 410 in its pedigree which carried Kalyansona and Kavkaz having genes *Pm 5* and *Pm 8*, respectively (McIntosh et al. 2008). *Pm8* was further confirmed by the postulation of closely linked gene *Lr26* (Nayar et al. 2001) in it.

Twenty two genotypes *viz*., HS 345, VL 772, HS 375, VL 780, PBW 438, PBW 440, WH 671, WH 672, HD 2687, K 9548, HP 1805, HP 1815, HD 2690, HUW 488, NW 1033, NW 1043, RW 3445, K 9555, GW 285, PBW 429, HP 1807 and HD 2667 showed IT ';' to cultures 4 and 6. The differential reaction of the cultures revealed the presence of gene *Pm8* in these genotypes. The genotypes, HS 385, K 9465 and DWR 229 produced IT ';' to cultures 4, 5, 6 and 7. UP 2435, K 9508 and K 9550 developed IT ';' and '2', UP 2440; and UP 2425, K 9564 and VL 768 produceed IT ';' '2' and '2' or either cultures 4 or 6, respectively. UP 2398 developed IT '2', ';' and '1' against the cultures 4, 6 and 8, respectively, whereas HD 2501 produced IT '1' to culture 4 and 8 and ';' against 5 and 6. ITMT suggested the presence of gene *Pm8* and some other unknown gene(s) for resistance in these genotypes. Pedigree analysis revealed the involvement of Veery (HP 1815, VL 768 and UP 2435), Alondra (RW 3445), Genaro (VL 780 and WH 672), Seri (WH 671 and DWR 229), Kauz (HP 1805, K 9508), Lira (NW 1043), Raj 1972 (HUW 488), CPAN 1961 (UP 2398), Bob White (K 9548) and CPAN 3004 (UP 2450) in their parentage. Genotype VL 772 involved var. Thornbird, having Kavkaz in its pedigree. Genotypes Veery, Kavkaz, Bobwhite, Alondra, Seri, Lira, Kauz, Genaro, Chil 'S' carry powdery mildew resistance gene *Pm8* (McIntosh et al. 2008). Moreover, leaf rust and yellow rust resistance genes, *Lr26* and *Yr9* were postulated in genotypes VL 780, UP 2435, PBW 438, PBW 440, WH 672, WH 671, K 9548, HP 1815, HD 2690, HUW 488, NW 1043, GW 285, WH 681, HS 375, NW 1033, DWR 229, K 9508, K 9548, K 9550, VL 768, HD 2667, PBW 429, HS 345 and VL 772 (Nayar et al. 2001) thereby, authenticating the postulation of closely linked gene *Pm8* in these genotypes.

Genotypes, K 9453, HW 3003, HD 2689, HD 2680, MACS 3011, MACS 3018 and HD 2700 developed varied ITs to the test cultures, however,

Table 2. Reaction of advanced breeding material to 10 cultures of *Blumeria graminis tritici* and genes postulated

Genotypes	Reaction to cultures										Gene postulated
	1	2	3	4	5	6	7	8	9	10	
K 9441	3	2	3	3	2	2	3	;	;	4	*Pm 3c+*
HS 369	2	2	3	4	4	4	2	4	3	3	*Pm 5+*
GW 273	;	-	4	4	4	3	3	;	;	;	*Pm 5+*
UP 2464	2	4	4	2	;	4	4	4	4	4	*Pm 5+*
GW 279, GW 1128	2	4	4	4	4	;	3	4	;	4	*Pm 5+*
GW 173	;	2	2	4	4	4	4	;	;	4	*Pm 5+*
HD 2688	2	4	2	4	4	;	4	4	4	4	*Pm 5+*
DWR 225	2	;	4	4	3	4	4	4	4	4	*Pm 5+*
GW 291	;	3	4	3	;	3	4	4	3	3	*Pm 5+*
WH 681	2	2	4	;	4	;	2	4	4	4	*Pm 5+8*
HS 345, VL 772, HS 375, VL 780, PBW 438, PBW 440, WH 671, WH 672, HD 2687, K 9548, HP 1805, HP 1815, HD 2690, HUW 488, NW 1033, NW 1043, RW 3445, GW 285, K 9555, PBW 429, HP 1807 and HD 2667	3	3	3	;	4	;	3	4	4	4	*Pm 8*
HS 385, K 9465, DWR 229	3	3	3	;	;	;	;	4	3	3	*Pm 8+*
UP 2435, K 9508, K 9550	4	4	4	;	4	2	3	4	3	3	*Pm 8+*
UP 2440	4	4	4	2	4	;	3	4	4	4	*Pm 8+*
UP 2425, VL 768, K 9564	3	3	3	2	3	2	4	4	3	3	*Pm 8+*
UP 2398	3	4	4	2	4	;	3	1	4	4	*Pm 8+*
HD 2501	3	4	4	1	;	;	3	1	4	4	*Pm 8+*
K 9453	4	;	4	3	3	2	4	4	4	4	?
HD 2689	4	4	4	4	4	4	;	4	3	4	?
HW 3003	3	4	3	3	4	;	4	;	1	4	?
HD 2680	4	4	4	4	3	;	3	4	4	4	?
MACS 3011, MACS 3018	4	;	4	3	3	4	4	4	4	4	?
HD 2700	4	;	4	4	4	;	;	4	4	4	?
DT 46, DT 91, DT 95, UP 2450, DDK 1009, DDK 1013, DDK 1014, DDK 1015, MACS 2574, MACS 2912, MACS 2919	;	;	2	;	;	;	;2	;	;	;	?
Sonora x Cc[8]	3	4	4	4	2	;	4	4	4	4	*Pm 3c*
CS/Hope	;	4	4	4	4	4	4	4	4	4	*Pm 5*
Veery, Aurora	4	4	4	;	4	;	4	4	4	4	*Pm 8*

present set of cultures could not identify any of the known genes in these genotypes. Genes, *Lr26*, *Yr9* and *Sr31* were reported in K 9453, HD 2689 and HW 3003 (Nayar et al. 2001), however, in the present studies linked gene *Pm8* could not be postulated in these lines. The higher reaction of these genotypes to PM cultures avirulent on *Pm8* may be due to presence of suppressor gene in wheat genome, identified as a major QTL (QSuPm.uga-1AS) as *Pm3a.* The inhibiting effect of this gene has also been reported in some Mexican and Chinese wheats carrying *Pm8* (Hao et al. 2013).

Three triticales genotypes, *viz*., DT 46, DT 91 and DT 95 and seven dicoccum wheats, DDK 1009, DDK 1013, DDK 1014, DDK 1015, MACS 2574, MACS 2912, and MACS 2919 and bread wheat UP 2450 showed resistant reaction (IT = ;-2) to all the cultures.

Absence of differential interaction in these genotypes implied that resistance in the above mentioned genotypes could not be attributed to any of the known genes. As has been observed in the present study high level of resistance has been reported in Triticale and *T. dicoccum* (Bahadur, and Aggarwal 1997; Tomar et al. 2004; Mwale et al. 2014; Anonymous 2014).

Ten cultures of *Bgt* could speculate only three PM resistance genes namely, *Pm3c, Pm5* and *Pm8,* individually or in combination with unknown genes in 63 advanced wheats and frequency of *Pm8* gene was the highest, indicating narrow genetic base of PM resistance in Indian wheats. During the last three decades varieties having leaf rust and yellow rust resistance genes, *Lr26* and *Yr9 viz*., PBW 343, HPW 42, HS 240, HS 277, HUW 206, K 8804, HW 318, MACS 2496, VL 738, UP 2338, WH 542, VL 829, VL 907 etc. and gene *Lr23 viz*., HPW 251, HD 2967, WH 1021, K 8027, GW 322, HD 2285, HS 295, PBW 154, RAJ 3777 etc., having Kalyansona and Sonora as one of the parents, were widely cultivated throughout the country (Bhardwaj 2011; Anon. 2014). Hence, genes *Pm3c, Pm5* and *Pm8* must have got inadvertently introgressed in wheat varieties alongwith closely linked *Lr* and *Yr* resistance genes. Virulences against genes, *Pm3c, pm5* and *Pm8* are quite prevalent in India (Bahadur and Aggarwal 1997; Paul et al. 2000; Basandrai et al. 2003), due to selection pressure exerted by wide cultivation of such varieties. Powdery mildew has emerged as a major threat in the northern hills and north-western plains of India and majority of the varieties under cultivation are susceptible (Anonymous 2014). However, gene and gene combinations *Pm1*, *Pm1 + Pm9, Pm2 + Pm6, Pm4a, Pm4b + Pm8* etc. remained effective (Paul et al. 2000; Basandrai et al. 2003). Durability of resistance may be enhanced and prolonged by time and space deployment of diverse resistant sources, breeding cultivars with adult plant resistance and by using molecular markers to pyramid effective major genes in suitable agronomic backgrounds.

References

Anonymous. 2014. Progress Report of All India Coordinated Wheat and Barley Improvement Project 2013-14, Vol. III, Crop Protection. (Eds. M. S. Saharan, Sudheer Kumar, R. Selvakumar, Subhash Katare and Indu Sharma), Directorate of Wheat Research, Karnal, India. pp 261.

Bahadur P. and Aggarwal R. 1997. Powdery mildew of wheat: A potential disease in north western India. pp. 17-30. *In*: Management of threatening plant diseases of natural importance (Eds. V. P. Agnihotri, A. K. Sarabhoy and D. V. Singh) Malhotra Publishing House, New Delhi.

Basandrai Ashwani K., Tyagi P. D., Singh Amar, Singh B. M. and Sharma B. K. 2003. Pathogenic variation in conidial populations of *Erysiphe graminis* f. sp. *tritici* in Himachal Pradesh. J. Mycol. Pl. Pathol., **33**: 80-83.

Bhardwaj S. C. 2011. Resistance genes and adult plant resistance of released wheat varieties of India. Research Bulletin No. 5: 31 pp. Regional Research Station, Flowerdale, Directorate of Wheat Research, Shimla-171002 (India).

Hao, Yuanfeng, Chen Zhenbang, Wang Yinggying, Bland Dan, Parks Wesley, Cowger Christina and Johnson Jerry 2013. Identification of Pm 8 suppressor at Pm 3 locus in Soft Red winter wheat. Crop Sci., **52**: 2438-2444.

McIntosh R. A., Yamazaki Y. and Dubcovsky J. 2008. Catalogue of gene symbols for wheat. http://wheat.pw.usda.gov/GG2/Triticum/wgc/2008/. Verified 17 March 2010.

Mwale V. M., Chilembwe E. H. C. and Uluko H. C. 2014. Wheat powdery mildew (*Blumeria graminis* f. sp. *tritici*): Damage effects and genetic resistance developed in wheat (*Triticum aestivum*). Int. Res. J. Plant Sci., **5**: 1-16.

Nayar S. K., Nagarajan S., Prashar M., Bhardwaj S. C., Jain S. K. and Datta D. 2001. Revised catalogue of genes that accord resistance to *Puccinia* spp. in wheat. Research Bulletin No. 3: 48 pp. Directorate of Wheat Research, Regional Research Station, Flowerdale, Shimla 171002 (India).

Paul Rax, Basandrai Ashwani K. and Tyagi P. D. 1999. Identification of resistance genes against *Erysiphe graminis tritici* in Indian and exotic wheats. Indian J. Genet., **59**: 125-134.

Paul Rax, Basandrai Ashwani K. and Tyagi P. D. 2000. Virulence spectrum of *Erysiphe graminis* f. sp. *tritici* in Himachal Pradesh. Indian Phytopath., **53**: 126-129.

Tomar S. M. S., Kumar Vinod and Singh B. 2004. Distant hybridization in wheat. pp 160. Indian Agricultural Research Institute, New Delhi.

Zeven A. C. and Zeven Hissink Nineke. 1979. Genealogies of 14000 wheat varieties. pp. 119. The Netherlands Cereal Centre - NGC, Wageningen and CIMMYT.