

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 triticale were screened against seven genetically characterized virulences of *Blumeria graminis* f. sp. *tritici* 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