Identification and genetic characterisation of a powdery mildew resistance gene in wheat

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Studies were conducted to determine the inheritance of resistance to powdery mildew (PM) by Blumeria graminis f.sp. tritici in a resistant (R) CIMMYT line 6HRWSN125 and in the resistant cultivar Meri. Resistance was assessed at the seedling stage in a doubled haploid (DH) population (6HRWSN125/WAWHT2074) and in three Meri-based crosses including Meri/Ajana, Meri/Wyalkatchem and Meri/6HRWSN125. Line WAWHT2074 and cultivars Ajana and Wyalkatchem are susceptible (S) to powdery mildew strains in Western Australia. The DH population showed a segregation ratio not significantly different from 1R:3S ($\chi^2 = 1.5$, P = 0.22) indicating complementary gene interaction of two genes for PM resistance. Crosses Meri/Ajana and Meri/Wyalkatchem produced S F₁ progeny and an F₂ segregation ratio of 1R:3S $(\chi^2 = 0.5 \text{ and } 3.6, P = 0.48 \text{ and } 0.06)$, suggesting the presence of a single recessive gene in Meri. The hypothesis was confirmed in the F₃ where a non-random selection of F₃ families was examined for segregation of resistance. F₃ families arising from R F₂ plants were all true breeding R while F₃ families from S F₂ plants either segregated or were true breeding S. The Pm locus was mapped in Meri/Ajana and Meri/Wyalkatchem to the proximal region on chromosome 3BS, a region not previously identified to contain Pm resistant genes. The cross between the resistant cultivar Meri and the resistant line 6HRWSN125 produced R F₁ progeny. The F₂ progeny segregated in a ratio of 43R:21S ($\chi^2 = 0.8$, P = 0.36) which supports the hypotheses of two dominant complementary genes in 6HRWSN125 and one recessive gene in Meri. Presence of different resistant genes in parents 6HRWSN125 and Meri was confirmed in F₃ where F₃ families from R F₂ plants either segregated or were true breeding R while F₃ families from $S F_2$ plants were all true breeding S.