

Commentary on Powdery Mildew Resistance Genes In Food Crop Plants

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Commentary

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Powdery mildew leads to serious economic loss in wheat production. Exploration of plant resistance to wheat mildew over several decades has led to the invention of a wealth of resistance genes and quantitative trait loci (QTLs). We've provided a comprehensive summary of over 200 mildew genes (permanently and temporarily designated genes) and QTLs reported in common bread wheat. This highlights the various and rich resistance sources that exist across all 21 chromosomes. To manage different data for breeders, here we also present a bridged mapping result from previously reported mildew resistance genes and QTLs with the appliance of a printed integrated wheat map. This can provide important insights to empower further breeding of mildew resistant wheat via marker-assisted selection (MAS).^[1]

Powdery mildew caused by obligate biotrophic fungi of the fungus order may be a widespread disease that infects a good type of angiospermic plant species. In crops, the effect of mildew is commonly devastating, leading to a high percentage of unmarketable products and heavy yield reduction. The employment of crops that are genetically proof against pathogens not only decreases the cultivation costs but also reduces the environmental pollution caused by chemical control of plant diseases. Novel sources of genetic resistance to mildew are continuously being identified. In some species, resistance is conferred by dominantly inherited pre-invasive and post-invasive defense mechanisms that directly target the pathogen. In other cases, mildew resistance was found to be determined by QTLs or by a dominantly inherited single locus.^[2]

The foremost impressive resistance is conferred by the recessive mildew resistance locus present or experimentally induced mutations during this locus can lead to the loss of function of the coded transmembrane protein MLO, leading to strong broad-spectrum immunity to the fungus. Common to monocotyledonous and dicotyledonous plants, the MLO family is encoded by a variable number of loci from which only 1 locus or, in some cases, multiple loci needs to be mutated to attain complete immunity. The simplicity of the Mlo-associated recessive resistance has attracted multiple experimental mutagenic and gene editing projects that are currently being implemented. Common wheat is one among the three major grain crops worldwide, and its high and stable yield plays a vital role in food security. However, various diseases, including mildew, rusts, and fusarium blight, can have devastating impacts on yield. Mildew caused by *Blumeria graminis* f. sp. *tritici* (Bgt) is one in every of the foremost damaging diseases, typically decreasing wheat yield by 10–15% and up to 50% in severe cases.^[3]

The world of winter wheat affected annually by mildew has exceeded 6 m ha in recent decades, causing 300,000 a lot of crop loss every year. Although the pesticides are commonly used for mildew control, resistance to drugs and environmental pollution became increasingly prominent. Improved host resistance provides a beautiful opportunity for the event of a good and environmentally acceptable means to manage this disease. In wheat production, the mildew resistance (Pm) genes exhibit mainly race-specific resistance, which was often short lived, as they were defeated by the fast-evolving virulent pathogen. The ratio of broad-spectrum resistance in wheat cultivars/breeding lines isn't yet satisfactory in wheat production. Therefore, there's an urgent have to mine and utilize simpler resistance sources to extend the genetic diversity of Pm genes.

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