IDENTIFICATION OF A NEW RESISTANCE GENE TO SEPTORIA TRITICI BLOTCH IN WHEAT

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Septoria tritici blotch (STB) caused by the ascomycete *Mycosphaerella graminicola* is one of the most devastating foliar diseases of bread wheat in North-Western Europe, Central- and West Asia and also of durum wheat in North Africa. STB can cause 10-15% yield losses, but under conducive weather conditions it can easily exceed 50%. Disease control is mainly achieved with fungicides that cost hundreds of millions of dollars globally each year, only 600 M€ in Western Europe and 35.5 M£ in England, but resistance development in the fungal populations is a continuous concern. Disease management can be strongly supported by growing resistant cultivars and hence, breeding for resistance to STB is important, particularly for areas where access to fungicide control is limited. In recent years, 15 major resistance genes and QTLs, *Stb1-Stb15*, were identified and are currently being used by breeders in breeding programs. However, this is still a very limited number compared to other cereal diseases. Hence, the identification of new genes is crucial to enable breeders to diversify STB resistance in new wheat cultivars. This can be achieved by rigid screening on available adapted germplasm but also by screening wild relatives or derived synthetic hexaploids. We screened a wide range of germplasm including 54 hexaploid wheat lines as well as several synthetic hexaploids (SH) with a global set of 18 *M. graminicola* isolates. Some of these SHs showed an extraordinary high and broad level of resistance. We subsequently screened a population of recombinant inbred lines (RILs) derived from the SH M3 and the highly susceptible cv. Kulm with isolates of *M. graminicola* and identified a novel QTL with major effects on chromosome 3D. This chromosome has not previously been reported to carry *Stb* genes and hence, we consider the 3D QTL to be a novel *Stb* gene that can be easily deployed once closely linked markers have been developed. Ongoing progress on the analysis of this RIL population will be presented.