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Adaptive dynamics of populations of Leptosphaeria maculans under resistance selection pressure: insights from two decades of surveys in France

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Leptosphaeria maculans is responsible for stem canker, a major disease of oilseed rape (canola, Brassica napus). Major genes for resistance (Rlm) are used in commercial varieties to control the disease. The effectiveness of a given resistance gene is a function of the frequency of the corresponding avirulent allele in field populations of the pathogen. After the release of Rlm1 in the 1990's in France, a very rapid increase in the frequency of isolates virulent towards this gene was observed. More recently, a new resistance gene, Rlm7, was introduced into commercial hybrid varieties, at a time when most (>99.5%) of the L. maculans isolates possessed the corresponding avirulent allele AvrLm7. Since 2000, the frequency of isolates virulent against Rlm7 has been monitored in populations of L. maculans in either experimental fields with increased selection pressure, or at a national scale in standard agronomic situations. While a rapid increase in frequency of virulent isolates was observed in an experimental field with minimum tillage and continuous oilseed rape cropping (36% of isolates virulent after 3 years), the breakdown of Rlm7 resistance appeared much slower than that observed previously for Rlm1 (less than 20% of isolates were virulent on Rlm7 after 10 years of widespread use of Rlm7). Among the possible reasons for the longer durability of Rlm7, the role of the negative interaction between AvrLm7 and AvrLm3 was explored. A detailed knowledge of molecular mechanisms responsible for virulence against Rlm3 and Rlm7 was obtained and suggested that stacking the two resistance genes in the same variety could have a negative impact on Rlm7 durability while the use of both resistance genes in different varieties could have slowed down the breakdown. These population and molecular information are currently used in an epidemiological model to test and confirm our hypotheses.