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of the first avirulence gene in the poplar rust fungus
*Melampsora larici-populina***

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POPLAR RUST NEVER SLEEPS: EVOLUTIONARY CHARACTERIZATION OF THE FIRST AVIRULENCE GENE IN THE POPLAR RUST FUNGUS MELAMPSORA LARICI-POPULINA

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Text

Poplar rust, caused by the pathogenic fungus *Melampsora larici-populina* (Basidiomycota, Pucciniales), is the main phytosanitary constraint for commercial poplar cultivation in Europe and other parts of the world. In the last 50 years, many rust-resistant cultivars were bred and released, but all the qualitative resistance genes released were overcome by pathogen evolution within a short period. In 1994, breakdown of the *RMIp7* resistance gene was detected in Belgium and Northern France. New virulent *M. larici-populina* individuals spread all over Western Europe in less than five years, causing very destructive epidemics, and lead to a complete replacement of the pathogen's populations. Through a genome-wide association study (GWAS), we identified a locus in the genome of *M. larici-populina*, that corresponds to the candidate avirulence gene *AvrMlp7*, whose mutation is responsible for *RMIp7* resistance breakdown. To further characterize this effector, we used a population genetics approach on a set of almost 300 individuals collected throughout a 28-year period encompassing the resistance breakdown event. Genotyping at the avirulence locus highlighted two different mutations: a non-synonymous mutation and a complete deletion of this locus. The temporal survey at the candidate locus revealed that both mutations pre-existed long before the breakdown, but at a heterozygous state. Using a reverse ecology approach, we identified the first candidate avirulence gene in this rust fungus.