

Genotypic Diversity of European *Phytophthora ramorum* Isolates Based on SSR Analysis¹

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Abstract

Genotyping of NA1 isolates of *Phytophthora ramorum* has provided valuable information regarding the introduction, evolution, and the pathways of spread of this pathogen in North America. So far, genotyping of European isolates of *P. ramorum* has only been reported for the Belgian and Spanish populations. Until the epidemic of *P. ramorum* in Japanese larch (*Larix kaempferi* (Lam.) Carrière), the European *P. ramorum* population was mostly confined to nurseries. This population may have different rates of evolution and selection and different pathways of spread than the NA1 population, which is mostly derived from the natural environment. The objective of this study was to genotype and analyze a wider European collection of *P. ramorum*, which was in part made possible via the collection of DNA samples as part of the EU COST Action FP0801 (Established and emerging *Phytophthora*: increasing threats to woodland and forest ecosystems in Europe.).

In total, over 1,300 samples from 17 European countries were analyzed using seven EU1 polymorphic microsatellite loci. The majority of the samples were collected after 2001 from *Rhododendron* in nurseries. At least 66 EU1 genotypes were identified. Approximately 64 percent of the isolates belonged to multilocus genotype EU1MG1, which was present in all countries. Isolates with single repeat shifts in the most variable markers were the second most abundant and widespread, but at frequencies of less than 6 percent and in a maximum of 11 countries. As in the NA1 population, the structure of the genotype network is indicative of a clonal, expanding population that accumulated microsatellite mutations after a single introduction of the EU1MG1 genotype. The population structure and genetic diversity was similar in most of the countries represented by a sizeable number of samples. The population structure of the United Kingdom isolates is unique in that it is characterized by a large subpopulation with a unique mutation in one of the markers, a mutation that presumably arose relatively soon after the introduction of the pathogen in the United Kingdom. Based on the finding of unique genotypes in time and space, local evolution followed by national or international spread, was also observed for other countries. In general, however, the level of diversity was too small and the amount of international exchange was too extensive to draw detailed conclusions on the primary origin of specific isolates. There were no clear indications of sexual recombination within the EU1 lineage. Three isolates with highly deviating marker profiles were identified. Further analysis of these isolates revealed that they belong to a new (EU2) lineage, as detailed in a separate report (Van Poucke et al., EU2, a fourth evolutionary lineage of *Phytophthora ramorum*, this proceedings).

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