

EU2, a fourth evolutionary lineage of *Phytophthora ramorum*

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Studies in North America and Europe over the past decade have demonstrated the occurrence of three lineages of *Phytophthora ramorum* informally designated the NA1, NA2 and EU1 lineages. Each lineage appears to represent a reproductively isolated population, but whether they have come from different geographic regions is unknown. Only the EU1 lineage had been found in Europe until recently. EU1 is believed to have been introduced into Europe around 1990. Since then it has spread widely and rapidly across the continent, including the UK and Ireland, via the plant trade. In 2011 *P. ramorum* isolates from Northern Ireland and a closely adjacent area of western Scotland, mostly from *Larix* but also from *Quercus*, *Rhododendron* and *Vaccinium*, were found to have molecular profiles not matching those of any known lineage. Following a phylogenetic study based on eleven polymorphic loci and an SSR analysis they were assigned to a new lineage, informally designated EU2. This analysis indicates the EU2 lineage may be ancestral to the other lineages. No SSR-based intra-EU2 lineage genotypic diversity was detected. All EU2 isolates examined to date have all been of A1 mating type. As this is the same mating type as that of EU1 in Europe, sexual recombination with EU1 lineage genotypes already resident in the UK is unlikely. The earliest isolation dates to 2007. Present evidence points to a recent introduction of EU2 in the context of ongoing phytosanitary emergency measures. The arrival of EU2 highlights an urgent need to identify the geographic origins of *P. ramorum* in order to understand the organism's natural ecology, the processes that have produced the lineages, and whether further lineages exist. Presently, studying the organism in the context of introduction and invasion, we may only be looking at half the picture.

Characterization of *Phytophthora* hybrids from ITS clade 6 associated with riparian ecosystems in South Africa and Australia

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Recent surveys of Australian and South African rivers have revealed numerous Clade 6 *Phytophthoras*, which either have ITS gene regions that were highly polymorphic or could not be sequenced. These isolates were suspected to be hybrids. In order to establish the hybrid nature of these isolates, three nuclear loci and one mitochondrial locus were amplified and, in the case of the nuclear gene regions cloned, and sequenced. Abundant recombination within the ITS region was observed and this combined with phylogenetic comparison of other three loci confirmed the presence of four distinct hybrids involving three known parental species: *P. amnicola*, *P. thermophila* and *P. taxon PgChlamydo*. In each case the hybrid is between two parental species. For the single copy nuclear genes (ASF and GPA) examined, two alleles were obtained, one of which corresponded to each of the parental species. In all cases, only a single *cox1* allele was obtained indicating that mitochondria were always uniparentally inherited from one of the nuclear parents. This pattern of nuclear and mitochondrial inheritance suggests that each hybrid is a result of an independent hybridization event involving two parental species. The hybrid species are sterile and have physiological traits similar to those of the maternal parental. The pathogenicity of these hybrids is unknown, but several isolates from Western Australia were obtained from the rhizosphere soil of dying plants. The serendipitous and simultaneous discovery of the same hybrid complex on two continents is intriguing. However, the wide geographic distribution,



The Sixth Meeting of the International Union of Forest Research Organizations

IUFRO Working Party 7-02-09

Phytophthora in Forests and Natural Ecosystems

Córdoba (Spain)
9th - 14th September
2012

