

The European population of *Phytophthora infestans* in a global context

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SUMMARY

Late blight, caused by *Phytophthora infestans*, causes significant losses to potato and tomato crops on a global scale. The timing and effectiveness of blight management depends on the pathogen's response to the environment, primary inoculum type, virulence to host resistance and sensitivity to fungicide active ingredients. However, the pathogen population is continually evolving and emerging clonal lineages with new traits highlights the need to tailor management to the local pathogen population. This is the rationale behind the EuroBlight consortium's collection of data on the genetic diversity of *P. infestans*, analysed with simple sequence repeat (SSR) genetic markers. Our surveys of late blight infected crops alongside those of partner research institutes and agrochemical companies from 2013–2018 has generated a database of over 8400 geo-tagged European samples. Standardised protocols, SSR allele scoring and a single data format remain critical to the utility of the database and its associated analysis tools and the mapping interface used to view the data.

Currently, much of the pathogen genotyping has been conducted at the James Hutton Institute in Dundee but the effective expansion of this database to other regions depends on sharing the experiences of this lab to ensure the standardised naming of the alleles at each of the 12 SSR loci. We have been working closely with partners in other laboratories within all five networks (EuroBlight, AsiaBlight, Tizon Latino, USABlight and AfricaBlight) to harmonise the methods. Recent updates to the EuroBlight web page include a detailed step-by-step guide to scoring the SSR alleles (fluorescently labelled peaks) with sample images and explanations of the common scoring challenges. A list of the names and expected peak sizes of every allele reported to date is also provided. In addition, a list and the allele combinations of the commonly occurring clonal lineages, examples of minor variants and other known names from the literature are provided. This central data resource should prove a valuable asset for the community of late blight researchers and enable the effective sharing of data across and within networks.

A complex population structure is observed in Europe with around 70% of the sampled population dominated by a few widely disseminated clonal lineages; see maps at www.euroblight.net. The most obvious change in the years 2016-2018 was the overall decline in

the combined frequency of the clones EU_13_A2, EU_6_A1 and EU_1_A1 from 60 to 40% of the population. Over the same time period, the clones EU_36_A2, EU_37_A2 and EU_41_A2 have increased from 10 to 36% of the sampled population and research is underway on the drivers and management implications of this change. The SSR diversity within lineages has also been tracked over time and demonstrates the local spread of some sub-clonal variants. In contrast to the clones, 20–30% of the sampled European population comprises genetically diverse pathogen populations consistent with local, ephemeral oospore-derived sexual populations. These 'Other' diverse populations are more prevalent in some parts of Europe than others. Deeper insights into pathogen diversity at a range of scales in Europe is being investigated via the integration of the R-based population genetics application *poppr* into the Potato Tool Box in the pathogen database.

The flexible structures, systems and tools developed by EuroBlight partners for tracking populations of *P. infestans* in potato and tomato cropping systems across the globe are proving valuable tools. When combined with phenotypic data on the traits, the EuroBlight population tracking approach provides a crucial early warning system that helps mitigate against management failures due to the emergence and spread of new clones. Two recent cases were presented; the dominance of the EU_33_A2 lineage in Plateau State in Nigeria and the appearance of the EU_13_A2 clone in potato crops in Senegal. These are the first reports of these recently emerged European lineages in sub-Saharan Africa and are a cause for concern for crop production in these regions.