Potato blight tracking in Europe

EuroBlight is continuously investigating the evolution of the European population of the potato late blight pathogen and now reports on the 2019 results. In general, blight pressure was low which reduced sample numbers in many regions. However, episodes of high disease pressure resulted in serious outbreaks in other areas such as northern Britain and Denmark. With contributions from 17 groups, 1816 samples were genotyped from 27 countries. Around 75% of the samples belonged to defined clonal lineages observed in previous seasons. Some clones are widespread and have been present in Europe for more than a decade, but three more recent clones (37_A2, 36_A2 and 41_A2) increased their combined frequency from 10% in 2016 to 40% of the population in 2019. These more recent clones are displacing the established 13_A2, 6_A1 and 1_A1 clones which reduced from 60 to 30% of the samples over the same period. A quarter of the population comprised ephemeral, genetically diverse isolates consistent with oospore-borne inoculum. A regional pattern in the dominance of clones versus sexual recombinants was observed across Europe. Some implications of these displacements and ongoing changes are discussed.

Since its arrival in the nineteenth century, *Phytophthora infestans,* the cause of potato late blight, has remained a serious threat to European potato production. Although we are now better equipped to control the disease than in the past, evolving pathogen populations continue to challenge integrated management practices. The changes in *P. infestans* populations are directly influencing the development and deployment of resistant cultivars, the performance of disease warning systems and the efficacy of plant protection products.

Therefore, coordinated and continuous pathogen monitoring was proposed by the EuroBlight consortium at its meeting in 2013 and is now implemented as an EU-wide monitoring activity, including many stakeholders. We continue to monitor populations and characterise the invasive genotypes to help optimise IPM strategies, as required by EU Directive 2009/128/EC on the sustainable use of plant protection products.

FTA sampling cards with pressed lesions were returned to laboratories at the James Hutton Institute, Dundee and INRAE, Rennes for pathogen DNA fingerprinting using simple sequence repeat markers. Comparisons with prior fingerprint data enabled samples to be assigned to existing clonal lineages or defined as new genotypes. All results were uploaded to the EuroBlight database. Support from international groups is also generating similar data for parts of Asia, South America and Africa, allowing for a more global understanding of pathogen population changes.

Despite the overall low disease pressure in 2019, 17 partner organisations collected over 1900 card samples from 27 European countries, from which 1816 generated genotype data. The genotype data from 2013-2019 now comprises over 10K samples from 35 European countries.

Over the last seven years, 60-79% of the sampled population comprised known clonal lineages that recur over multiple seasons. The remaining samples were novel, genetically diverse genotypes found at a single location in one season and grouped in a category termed 'Other' (Figure 1).

For the first time since 2013, the clonal lineage EU_13_A2 (blue-13) was not the most frequently sampled and dropped to 9.3% of the samples. Although in decline, this widespread, metalaxyl-resistant clone continues to affect management efficacy in Europe, parts of Asia and North Africa, reinforcing the need for pathogen data to support IPM best practices. The frequency of EU_6_A1 rose to 20.4% due to severe outbreaks in parts of Britain where it remains dominant. The frequency of EU_1_A1 further decreased from 1.6 to 0.4% of the population. A progressive displacement of these three lineages is occurring.

Figure 1. Genotype map - 2019. Go to live map.
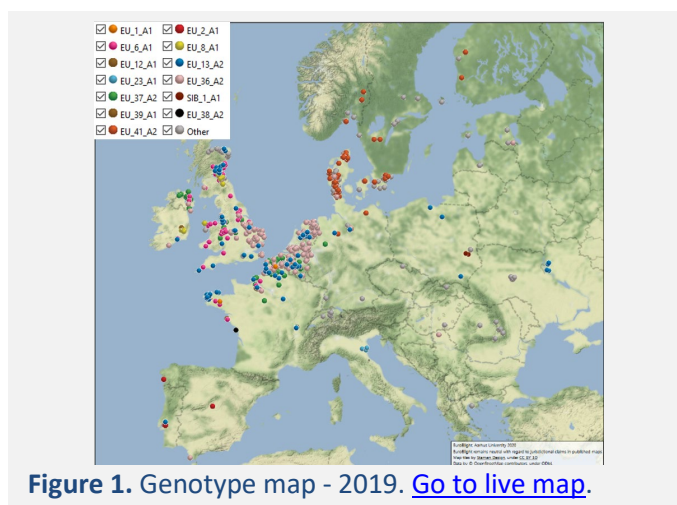
Despite the low blight pressure across many areas, two of the newer clones (EU_36_A2 and EU_41_A2) again increased in frequency in 2019. Clone EU_36_A2, which was first sampled at a low frequency in the starch potato areas in Germany and the Netherlands in 2014, has spread rapidly over the last five seasons. In 2019, it comprised 26% of the European pathogen population, and it was distributed across 15 countries but with a very low incidence in Northeast Europe. Clone EU_41_A2, first recorded in Denmark in 2013, has now spread to six neighbouring states but has not yet spread west to the low countries. In 2019, its frequency rose from 4.6 to 5.7% of the European population. The survival and spread of these clones, when others are decreasing or have failed to establish, suggests they are evolutionarily fit and supports anecdotal evidence that they are more challenging to manage in the field. Conversely, the overall frequency of clone EU_37_A2 declined for the first time since its detection in 2013. It peaked at 14.4% of the sampled population in 2018 but dropped to 8.4% in 2019. The reduced sensitivity of isolates of EU_37_A2 to fluazinam reported by Wageningen University in 2017 confers a selective advantage to this clone when this product is applied, and probably explained its increasing prevalence in Europe over the 2016 to 2018 seasons. However, widespread reporting of the reduced sensitivity has led to a marked decline in fluazinam use across many countries and the removal of this positive selection pressure possibly explains the overall drop in EU_37_A2 frequency in 2019. This change in product use and the population response suggests management failures have been avoided by using more effective chemistry and indicates a strong positive benefit of the EuroBlight monitoring approach. Regional differences, which may relate to current patterns of fluazinam use, are apparent with EU_37_A2 still comprising 25% of samples in France and Belgium in 2019 compared to falls to 4% and 10% in the Netherlands and England, respectively.

Fungicide sensitivity testing in laboratories in Wageningen University and The James Hutton Institute with a range of actives from different FRAG groups does not indicate any insensitivity issues with fungicide active ingredients other than fluazinam and phenylamides. However, it did show that EU_36_A2 and EU_37_A2 isolates formed consistently larger foliar lesions than those of the older lineages at very low dose rates of several key fungicide active ingredients. This supports aggressiveness testing conducted at INRAE, as part of the IPMBlight2.0 project that revealed that EU_36_A2 isolates tested formed larger average lesion sizes with abundant sporulation. Such properties are likely to make these lineages more difficult to manage and would explain the way they are displacing other clones across many European crops.

Lastly, the genetically diverse 'Other' samples comprised 26.2% of the sampled population in 2019, a frequency that has remained similar since 2014. These diverse types are always more prevalent in crops in the north and east of Europe and are consistent with a soil-borne source of oospores. Although there are epidemiological threats of earlier primary inoculum and theoretical evolutionary advantages to sexual recombination generating new pathogen phenotypes, we do not yet fully understand the practical threats

posed by 'Other' strains of the pathogen compared to the clones. As part of the IPMBlight2.0 project the aggressiveness and virulence traits of a sample of these 'Other' isolates was tested, but did not highlight any clear trends.

The genetic diversity of the 2019 population has been visualised (Fig. 2) using an analysis tool (*poppr 2.0*) linked to the EuroBlight pathogen database. The minimum spanning network shows sub-clonal diversity within each of the clonal lineages. The clonal and within-clone variation is being used to track the evolution and spread of these pathogen populations across Europe and beyond. 'Other' isolates (not shown) are genetically diverse and distributed across the whole network. Detailed analysis is underway to examine population change using these tools.
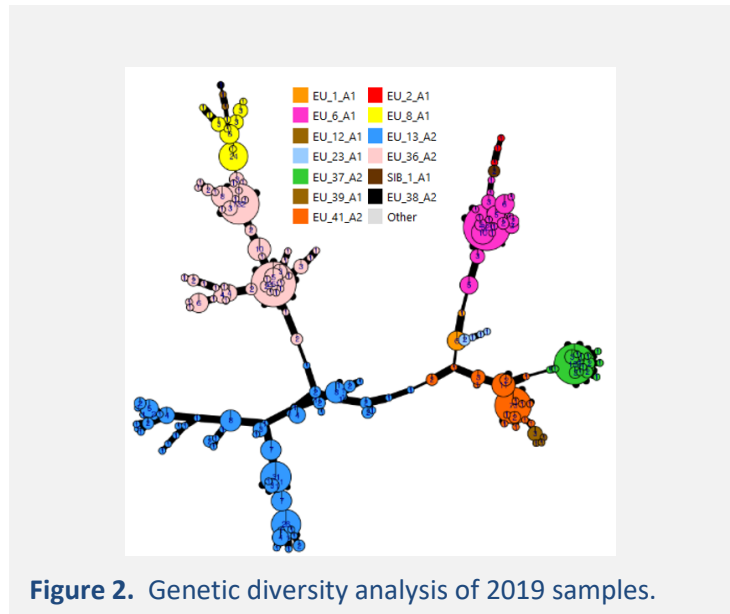
Figure 2. Genetic diversity analysis of 2019 samples.

The EuroBlight model of pathogen tracking is a rapid, cost-effective and co-ordinated approach to understanding pathogen evolution on a European scale. Data on the dominant clones have been passed to growers, advisors, breeders and agrochemical companies to provide practical management advice and shape longer-term strategies. The data provide an early warning of the incidence and spread of novel clones and the case of EU_37_A2 demonstrates such a timely response.

The EuroBlight network continues to harmonise methods with other networks in the Americas, Asia and Africa and encourages continued co-operation between groups involved in managing late blight to exploit the database and tools for improved awareness and blight management on a global scale. We will continue the project in 2020, so please contact the project team if you would like more information or if you would like to contribute. We thank all the partners who have contributed samples and supported the project.

Companies and institutions that participated in the sampling and sponsored the project (2013-2019)
Aarhus University, ACVNPT, ADAMA, AFBI, Agrifirm, Agricultural Institute of Slovenia, Agriphar, AHDB Potatoes, ARVALIS-Institut du Végétal, BASF SE, Bayer CropScience AG, Bayerische Landesanstalt für Landwirtschaft, Belchim Crop Protection, BSV Network (France), Centre Wallon de Recherches Agronomiques, Certis, Cheminova, Corteva CropSolutions, CUConsulting, CZAV, Delphi, Emsland Group, Estonian University of Life Sciences, Eurofins, Germicopa SAS, Hochschule Osnabrück, HZPC Holland B.V., INRAE, Institute of Plant Protection and Environment in Serbia, The James Hutton Institute, Neiker, Nordisk Alkali, NIBIO, PCA, The Plant Breeding and Acclimatization Institute (IHAR), Profytodsd, Swedish University of Agricultural Sciences, Syngenta Agro GmbH, SynTech Research, Staphyt, TEAGASC, Technical University of Munich, and Wageningen University.

Contacts
- Jens G. Hansen & Poul Lassen, Aarhus University. Contact: jensg.hansen@agro.au.dk
- David Cooke & Alison Lees: James Hutton Institute, Dundee. Contact: david.cooke@hutton.ac.uk
- Geert Kessel & Huub Schepers, Wageningen University and Research Centre. Contact: geert.kessel@wur.nl
- Didier Andrivon & Roselyne Corbiere, INRAE. Contact: Didier.Andrivon@inrae.fr