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Results of the EuroBlight potato late blight monitoring in 2022

EuroBlight now reports on the 2022 results. Approximately 1100 samples from 22 countries genotyped.

- Late blight pressure in 2022 was lower than average across many parts of Europe. Disease outbreaks from 22 countries were sampled by 23 teams in 2022 resulting in 1098 genotyped samples
- The frequency of genotype EU_43_A1 (EU43) increased from 2 % in 2021 to 15.8 % of the population in 2022, mainly sampled in Denmark, the Netherlands and Belgium. EU43 was also found in Norway, Sweden, Germany and Portugal
- Isolates of EU43 from several regions in Denmark were resistant to mandipropamid at doses of up to 100ppm. Other genotypes (EU_36_A2, EU_37_A2 & EU_41_A2) were all sensitive.
- Reduced sensitivity of EU37 to fluazinam has reduced its use, prevented management failures & driven a decline of this genotype to 2.6% of the sampled population
- Comprising 36% of the samples, EU36 was the most frequently sampled genotype which suggests it remains fitter than other clones but conclusive evidence of a specific fitness trait is challenging to demonstrate *in vitro*
- Primary inoculum is locally generated and spread. Better management of all inoculum sources is required
- The proportion of 'other' genotypes generated from sexual oospore inoculum remained stable between 20-30%

How did we do it?

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

Co-ordinated and continuous pathogen monitoring was thus proposed by the EuroBlight consortium in 2013 and has since been implemented as an EU-wide monitoring activity supported by many stakeholders. Such monitoring and characterisation of the population changes and invasive genotypes helps to optimise IPM strategies, as required by EU Directive 2009/128/EC on the sustainable use of plant protection products.

FTA sampling cards onto which lesions had been pressed were returned to laboratories in Scotland and France for pathogen DNA fingerprinting using simple sequence repeat markers. Samples were assigned to existing genotypes or defined as new genotypes and all results uploaded to the EuroBlight database. Support from international groups is generating similar data for parts of Asia, South America and Africa, allowing for a more global understanding of pathogen population changes.

What did we find?

The hot dry weather across much of Europe in 2022 reduced late blight pressure, resulting in the second lowest annual sample size since 2013. Reduced inoculum levels may have impacted the pattern of pathogen population change. Nonetheless, results for almost 1100 samples are mapped (Figure 1) and the genotype data from 2013-2022 now comprises over 16,000 samples from 37 European countries and is a valuable dataset.

The transition to relatively new genotypes such as EU36, EU37, EU41 and EU43 continued in 2022 with 60% of the samples being of genotypes that were unknown eight years ago. Conversely, the older genotypes EU1, EU6 and EU13 only represented 17% of the population compared to 68% in 2014.

The most marked change in 2022 was the increased proportion of samples of genotype EU43, increasing from 2% of the sampled European population in 2021 to 16% in 2022. While much of this expansion was in Denmark, it also increased in the Netherlands and in Belgium. In addition, its range also expanded, being sampled for the first time in Germany, Norway, Sweden and Portugal in 2022. Such a sharp increase prompted investigations in Denmark, where the EU43 clone was first reported in 2018. A [press release](#) from Seges (Landbrugsinfo) at the end of August 2022 flagged concerns about the efficacy of mandipropamid in some Danish crops. This was followed by a [press release from Aarhus University](#) in January 2023 in which resistance to mandipropamid in isolates of genotype EU43 was reported. Further information from Syngenta confirmed this finding and reported cross resistance of isolates of EU43 to mandipropamid and the other fungicides of the Carboxylic Acid Amides (CAA) group used for blight control (benthiavalicarb and dimethomorph). Given the importance of CAA fungicides in blight management, the spread of this genotype is a cause for concern. The Fungicide Resistance Action Committee (FRAC) have [updated their guidance](#) to help mitigate concerns on CAA efficacy in 2023. The guidance is dependent on whether CAA resistant strains of *P. infestans* are locally present which will focus attention on the population monitoring for the 2023 season.

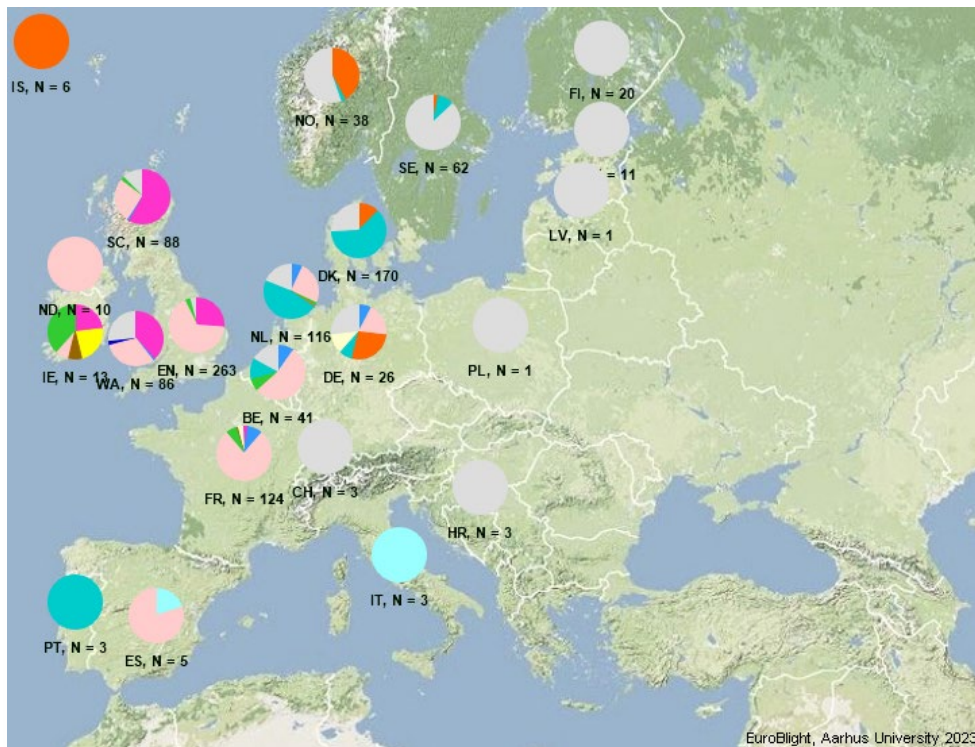


Figure 1. Distribution of genotypes in 2022 season.

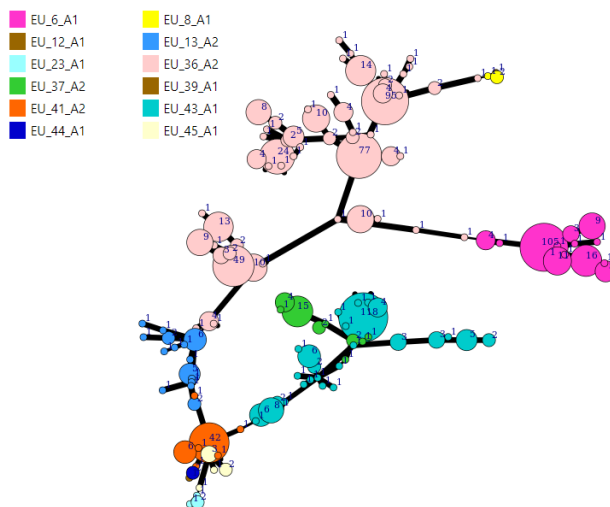


Figure 2. Minimum spanning network showing the genetic relatedness of genotypes sampled in 2022.

The single most prevalent genotype sampled in 2022 was EU36 which comprised 36% of the genotyped samples with a dominance across sampled crops in the low countries, France and the United Kingdom. Since its appearance in 2015 it has spread across 21 countries and displaced other older genotypes. This spread, plus evidence from laboratory studies, and anecdotal evidence of it being challenging to manage, suggest it has an increased fitness over other genotypes. For example, in 2022 it comprised 54, 67 and 77% of the samples in Belgium, England and France, respectively. There is no evidence of any shifts in its sensitivity

to current fungicide active ingredients. Genotype EU37 continues to decline in prevalence. From an incidence of 14% of the sampled populations in 2017 and 2018 it has reduced to 7-8% over the past three seasons and in 2022 made up only 2.5% of samples. It was detected in the UK, Ireland, France, Belgium and the Netherlands. Since 2018, fluazinam usage has declined which has reduced the positive selection pressure on EU37 isolates in the population. Initial reports suggested it was aggressive and competitive, even in the absence of fluazinam exposure, but the decline of EU37 in the population suggests otherwise. Its reduced incidence supports a continued role for fluazinam in late blight spray programmes when used in accordance with FRAC guidelines. This demonstrates the value of the EuroBlight monitoring approach which has driven a change in best practice, prevented disease control failures and constrained increases in fluazinam resistance that may have resulted in the withdrawal of this fungicide from future use.

EU41 is another relatively recent genotype of concern that originated in Denmark in 2013 and has since spread to 13 countries. In 2022 it only represented 4.9% of the samples, up slightly from 3.3% in 2021. In 2022 it was sampled in six countries but 2021 findings in France, Scotland, Estonia and Poland were not repeated in 2022. Once again it was the cause of serious blight outbreaks in Icelandic potato crops.

As mentioned above, older genotypes such as EU13 and EU6 have continued to decline and are confined to countries in the west of Europe. From around one quarter of the population in 2014, EU13 has now declined to only 2.4% of the 2022 sample. Although EU6 remains at 14.7% of the sampled population in 2022, most of these samples were from the UK population.

No new genotypes were defined in Europe in 2022 and other recent genotypes such as EU44 and EU45 remained localised and rare at less than 1% of the population. This may have been due to the overall restricted population size. Lastly, the genetically diverse 'Other' samples comprised 22% of the sampled population in 2022 which was slightly lower than the 26% average since 2017. These diverse range of genotypes are most prevalent in crops in the north and east of Europe and are consistent with a soil-borne source of sexual oospores. There are ongoing epidemiological threats of earlier primary inoculum and evolutionary advantages to sexual recombination generating pathogen phenotypes within these oospore-borne populations.

The genetic diversity of the 2022 population has been visualised (Figure 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 genotypes (also known as 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.

The EuroBlight model of pathogen tracking provides a cost-effective and co-ordinated approach to understanding pathogen evolution on a European scale. Data on the dominant genotypes have been passed to growers, advisors, breeders and agrochemical companies to provide practical management advice and help shape longer-term strategies. Given the ongoing drive to more integrated pest management (IPM) approaches and the specific

threats posed by CAA resistance we proposed to monitor the population of *P. infestans* more intensively in 2023. We will endeavour to provide the industry with timely feedback that includes within-season updates whenever possible.

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 monitoring in 2023, 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.

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