



## Potato blight mapped in Europe

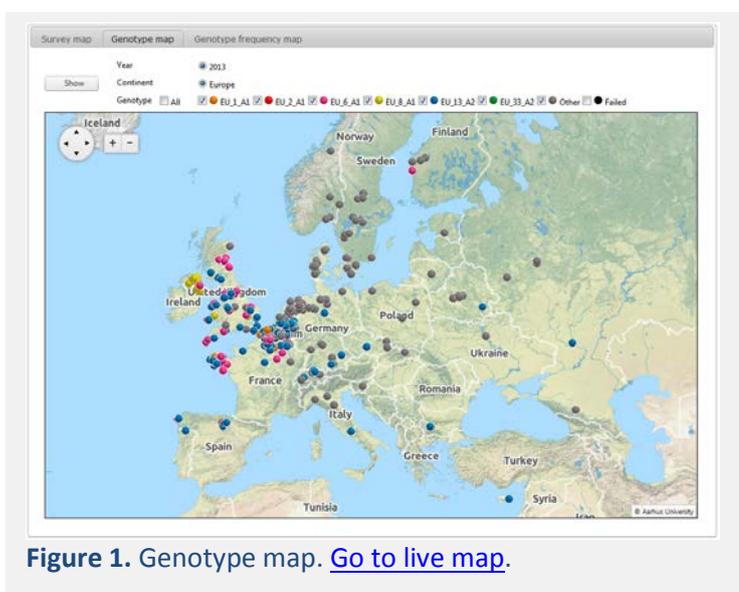
A team of researchers tracking the 2013 population of the potato late blight pathogen have, for the first time, spatially plotted its diversity and shown areas dominated by clones contrasting with novel genetically diverse isolates in other regions.

[www.EuroBlight.net](http://www.EuroBlight.net), 25 April 2014

Since its arrival in the nineteenth century, *Phytophthora infestans*, the cause of late blight has remained a serious threat to potato crops. Although we are now better equipped to control the disease than in the past, an evolving pathogen population continues to challenge our management practices. Rapid changes in *P. infestans* populations causing late blight in Europe, America and Asia, including the emergence of strains with altered pathogenicity or reduced fungicide sensitivity have been observed. Constant monitoring of populations and characterization of invasive genotypes is a prerequisite for the deployment of IPM strategies, as required by EU Directive 2009/128/EC on the sustainable use of plant protection products. The changes in *P. infestans* populations directly influence the development and deployment of resistant cultivars, the performance of disease warning systems and the efficacy of plant protection products. Coordinated and continuous pathogen monitoring was proposed by the EuroBlight consortium at its meeting in 2013. Here, researchers in the Netherlands, Scotland and Denmark, working with partners from research labs and industry, present the first report on its pathogen monitoring in potato crops in 2013.

The project hinged on the distribution of 'FTA cards' to hundreds of disease 'scouts' from across the industry who, in the course of their work, visited blight-infected crops. Disease lesions were pressed on the cards and returned to the laboratories where the pathogen DNA was analysed at Wageningen University and the James Hutton Institute, Dundee using the technology used in criminal forensics. Despite low disease pressure in 2013 over 795 samples were returned. This data also includes that from the Potato Council 'Fight Against Blight' campaign monitoring the pathogen in British crops. The fingerprint patterns of all the *P. infestans* samples were combined and compared to those found previously. In an exciting development, the data is being processed and, for the first time, mapped using tools developed by a team at Aarhus University.

A structure within the population is apparent with a distribution of dominant clones to the west of Europe and a scatter of novel, genetically diverse isolates defined in a category termed 'other' to the east (Figure 1). The aggressive clone EU\_13\_A2 (blue-13) was the most prevalent. It is resistant to phenylamide fungicides and has been dominant in Dutch and British populations for some years. The data indicates a broad distribution of this clone from Spain to Russia and Scotland to Cyprus. Growers should be aware that this clone is more difficult to manage than others. Another aggressive clone termed EU\_6\_A1 (pink-6) was found mainly in France and Great Britain with a single new record in Finland. The EU\_33\_A2 (green-33) clone linked with reduced sensitivity to fluazinam, was found only once in Europe. This marked decrease from its 20% incidence in the Netherlands in 2011 suggests that

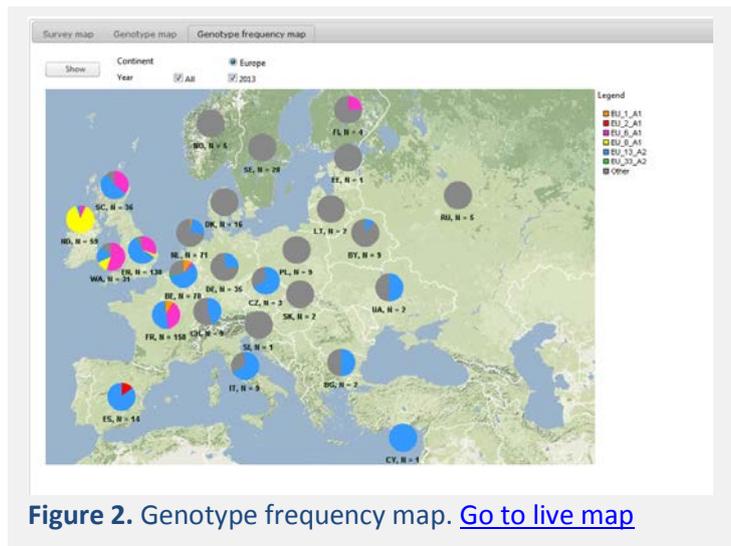


**Figure 1.** Genotype map. [Go to live map.](#)



changing the pattern of fluazinam use has been an effective strategy to reduce risk. Interestingly the only other find of this clone was in Mauritius, 900 km's east of Madagascar in the Indian Ocean. Other older clones (EU\_1\_A1, EU\_8\_A1 and EU\_2\_A1) were found at a low frequency and predominantly in the west of Europe. There is a clear east-west trend with the genetically diverse 'Other' samples found primarily in the east and north-east regions (Figure 2). In contrast to the clonal types, each of these isolates has unknown novel traits and has probably originated from soil-borne oospore inoculum. Longer rotations may help reduce this source of primary inoculum.

This model of pathogen tracking offers a rapid, cost-effective and co-ordinated approach to understanding pathogen change on a European scale. Data on the dominant clones has been passed to growers, advisors, breeders and agrochemical companies to provide practical management advice and shape longer-term strategies. Furthermore, early warning of newly evolved clones will enable a timely response from the industry. Further samples will be added in time to add to the resolution. More detailed genetic analysis of the population and tools to display this information on the web site are also planned.



We will continue the project in 2014 so please make contact with the project team if you would like more information. We thank all the partners who have contributed to the funding and data collection.

### Companies and institutions that participated in the sampling and sponsored the project

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