IPMBlight2.0 :
using pathogen population information to improve late blight control

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INTRODUCTION

Controlling Potato Late Blight (PLB), caused by the pathogenic Oomycete *Phytophthora infestans,* remains a major challenge in Europe and worldwide. Recent estimates indeed rate the total cost of late blight at some 900 M€ a year in Europe alone, including the cost of losses to the disease and that of control measures enforced by growers and the whole potato industry (Haverkort et al., 2008). Several features in the biology and epidemiology of *P. infestans* qualify it as a re-emerging pathogen in many important potato growing regions of the world (Fry, 2015) and make late blight a definite threat to food security in many developing countries and to farmer income in developed regions.

Currently, late blight control is primarily based on numerous fungicide applications (Schepers et al., this volume). However, this strategy faces increasing concerns. The legislative pressure is strong to limit or ban access to some popular active ingredients, and pesticide use in general (Directive 2009/128/EC on the sustainable use of pesticides). Furthermore, reports of reduced efficacy and/or resistance to some active ingredients, including fluazinam, have been made during the past few years (Nielsen, 2014).

Some of these changes are correlative to large scale, and sometimes rapid genetic changes within European *P. infestans* populations, which prompted the set-up of Europe wide population surveys using FTA cards for sampling and SSR typing to analyse the genetic composition of local samples (Meier-Runge et al., 2014). Although this survey allows to gather rapidly detailed information on the structure of *P. infestans* populations, this information is not currently used to

estimate late blight risk, or exploited in late blight control DSSs. This is due in part to a major shortcoming, namely that the link between SSR genotypes and the phenotypes of the corresponding isolates/populations for biologically important traits, such as virulence to major R genes in potato cultivars, aggressiveness on susceptible hosts, or fungicide sensitivity, remains elusive. This is why the EuroBlight statement from the workshop in Brasov, 2015, recommended i) to continue and expand the monitoring of *P. infestans*, ii) to intensify the phenotyping of important genotypes and iii) that EuroBlight offer to participate in the development of new DSSs, and in the work for adaptation of existing DSSs to IPM2.0 (EuroBlight statement 2015, Brasov).

These recommendations lead to the IPMBlight2.0 project, funded by the C-IPM ERANET funded over the period 2016-2019. This paper will briefly present the objectives, structure and first achievements of this project. Other papers in these proceedings (e.g Hansen et al., this volume) will detail specific aspects of the activities.

IPMBLIGHT 2.0 - OBJECTIVES

The primary goal of IPMBlight 2.0 is to validate the IPM 2.0 concept, with potato late blight as a case study. IPM2.0 is a concept introduced and defined by Kessel et al. (2012) and tested in the DuRPh project (Haverkort et al., 2016). It relies on the fact that the use of resistant varieties are one of the most effective IPM measure (http://euroblight.net/control-strategies/best-practice/), and on the observation that it is as yet underexploited, in part because host resistance is often not stable across many years (Naerstad et al., 2007; Cooke et al., 2011). Although and increasing number of resistant cultivars are now released and made available in all market segments of the potato industry, and despite the existence of modern DSS operated from web platforms or mobile apps, late blight management is still often restricted to a repeated fungicide applications (up to 25 per season in some regions). Developing truly integrated strategies, that will take full advantage of all available options while providing better fungicide, but also host resistance stewardship, are thus needed more than ever. However, simply designing such strategies is not enough: to be sustainable and adopted, they must be tailored to the variability of *P. infestans* populations and their rapid evolution – which is the core of the IPM 2.0 concept. This in turn supposes that pathogen populations be monitored for both genotypes and phenotypes, including virulence, aggressiveness and fungicide sensitivity.

IPMBLIGHT2.0 – PROJECT ORGANISATION

IPMBlight 2.0 was designed around four WP, each dedicated to a specific goal but tightly interconnected (Figure 1).
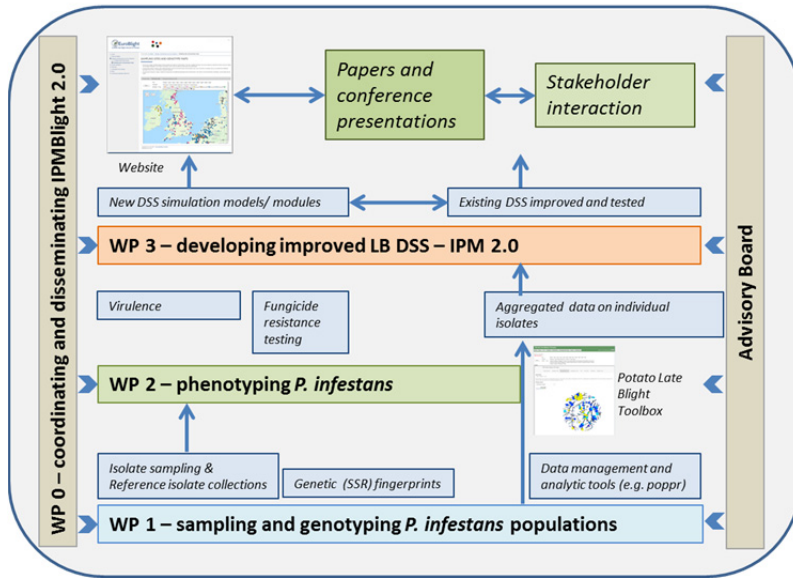
Figure 1. *IPMBlight 2.0 project structure.*

The project sets to analyze genotypic (WP1) and phenotypic (WP2) variation in reference collections of the pathogen sampled from sexual and clonal populations collected in partner countries, and to develop new DSS models while adjusting existing ones to offer risk assessment based on both epidemiological, weather-driven infection likelihood and pathogen phenotypes (WP3). The new DSS modules will therefore be able to best inform tactical choices ('should I spray now?') and strategic decisions ('can I trust this resistant cultivar? how can I adjust my spraying schedule accordingly?) for improved late blight control. WP 0 is dedicated to the administrative tasks, as well as the logistics of the project (meetings, etc.) and dissemination activities.

Confronting data from WP1 and 2 will allow in particular to answer the key question 'are genotypes reliable predictors of phenotypes?'. This is extremely important, since genotyping can now be done quickly and at a rather cheap price, whereas phenotyping biotests are much longer to perform, require the isolations of strains, and are quite costly. Finding a strong connection between genotypes and phenotypes would therefore allow to make rapid assumptions on population composition and characteristics, and hence to adjust in real time the DSS modules or parameters. The fact that many *P. infestans* populations, in particular from Western and Southern Europe, are structured as clones makes this hope plausible. However, IPMBlight 2.0 will also work with presumably sexual populations from Northern and northeastern Europe.

All protocols, data and information will be implemented in the EuroBlight information system, consisting of a Website (euroblight.net) databases and document repositories (for instance for collecting and storing reference protocols). The project therefore complements the annual

Euroblight survey, and provides extra reference material (live isolate collections, phenotypic data, new open-source DSS modules). It will also constitute a platform of reference European laboratories for *P. infestans* epidemiosurveillance and population analysis.

EARLY ACHIEVEMENTS...

Since the project started in the spring of 2016, only data from the first year are available, and not all of these have been processed entirely at the time of writing. Despite this, early achievements include:

- The collection of samples from all five partner countries (France, Denmark, Norway, Estonia, and the UK) confirm that western European populations of *P. infestans* (FR and UK) retain a clonal genetic structure, whereas Nordic populations (DK, EE and NO) appear sexually reproducing, with almost exclusively unique SSR genotypes.
- They also pointed out the presence within clonal populations of a new, apparently emerging clone, designated as 37_A2. The compilation of IPMBlight 2.0 and Euroblight survey data allowed to recognized that this clone, first spotted as an isolated outbreak in the Netherlands in 2013, has now spread to the whole Benelux, Northern France, UK, and some isolated locations in Germany, Switzerland and Adriatic countries.
- The comparison of aggressiveness between major clonal lineages collected within the IPMBlight survey suggest that there is extensive variability within lineages, but that 37_A2 tend to be among the most aggressive isolates present within the sampled populations (Fig 2)
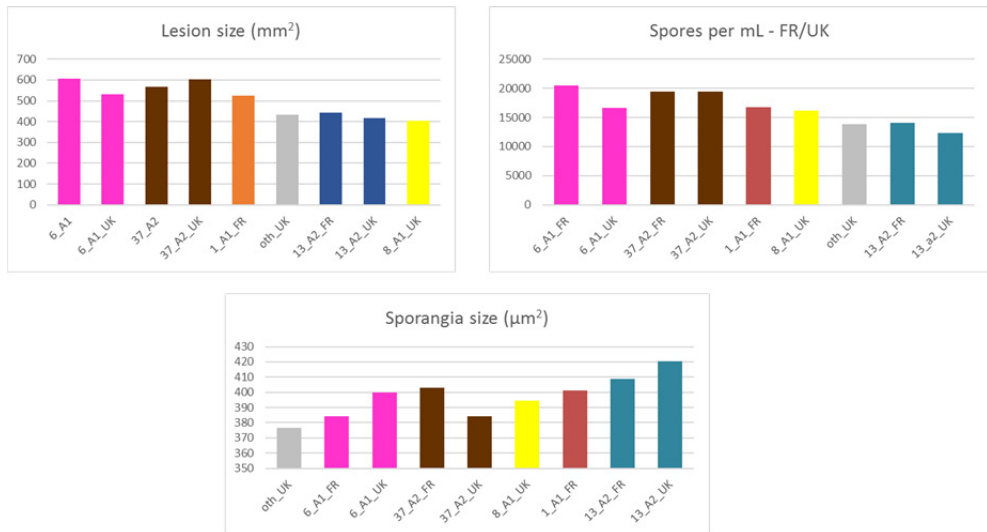
Figure 2. *Comparison of aggressiveness traits in current EU clonal lineages. The emerging 37_A2 clone appears to be highly aggressive.*

- The fungicide sensitivity assays carried out on IPMBlight 2.0 samples provide evidence that fluazinam insensitivity is developing within European populations of *P. infestans*. The data now need to be fully consolidated and matched with genotypic analyses.

- Trap nurseries were established in all partner countries in 2017, and in some of them in 2016, with a new differential host set including both 'historical' R genes from *Solanum demissum* and new resistance sources more recently introduced into breeding lines and cultivars. Again, the data are not fully analysed yet, but they reveal marked variation between hosts and locations.
- Finally, a re-coding of late blight DSSs in MatLab and in depth comparison of their performance with standard weather datasets has been made. A detailed account of this part of the work is given in another paper (Hansen et al., this volume).

… AND PRELIMINARY CONCLUSIONS

One year into the project is of course too early to decide to which extent it has been successful in reaching its objectives. However, the activities and results obtained this far are quite encouraging for the IPM 2.0 approach, on two main grounds:

- They demonstrate the value of an epidemiosurveillance scheme coupling fast genotyping and targeted phenotyping. This was evident in the ability of the network of labs involved in the project to i) spot the emergence of 37_A2 in its first year of real expansion outside its initial cradle, and ii) to generate the first comparative phenotypic data on this emerging lineage, relative to other major European clones. The fact that 37_A2 was identified as a highly aggressive lineage is worrisome. Recent evidence (Schepers et al., 2017) show that this genotype is most likely quite insensitive to fluazinam, which remains one of the staple pesticide used against late blight in Europe and elsewhere in the world. We now have to check whether our own data on the 37_A2 isolates in our collection confirm this insensitivity, and also what is the virulence profile of this lineage. The fast reaction to the discovery of this emerging threat is proof positive that a network of coordinated labs is essential for timely monitoring, but also controlling *P. infestans*.
- They also are instrumental in the development of improved management tools for better risk assessment. The comparison of existing DSS modules serves as the first step to design new software exploiting both the meteorological, but also the population composition data. This will make use of the EuroBlight IT platform, which plays a dual role: data storing and processing on one hand, result dissemination to scientists and end-users on the other hand.

This makes us confident that by the end of the project, this IT platform with enriched functionalities will further contribute to a better, more sustainable control of the late blight disease.

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