Miljøministeriet
Miljøstyrelsen

IPM2.0 til bæredygtig bekæmpelse af kartoffelskimmel

Udnyttelse af patogen-data til beslutningsstøtte systemer

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Preface and acknowledgement

This report presents result from a C-IPM ERA-Net project funded by the Danish EPA (MST-667- 00174). Eight partners contributed to the results: INRA (France), Aarhus University (Denmark), Estonian University of Life Sciences (Estonia), ARVALIS Institut du Végétal (France), Association des Créateurs de Variétés Nouvelles de Pomme de terre (France), Norwegian Agricultural Extension Service (Norway), NIBIO (Norway) and James Hutton Institute (Scotland). Only activities where the Danish partner (Aarhus University) were actively involved are reported with detailed information. For parts where AU was not involved, key findings are only described briefly.

The project has been followed by an expert group consisting of Jens Erik Ørum (Department of Food and Resource Economics (IFRO), University of Copenhagen), Jens Erik Jensen (SEGES), Ghita Cordsen Nielsen (SEGES), Nis Schmidt (Dow AgroSciences Denmark A/S), Thomas Secher Jensen (Natural History Museum, Aarhus), Signe Anthon (Environmental Economics, Danish EPA), Ilse Ankjær Rasmussen (International Centre for Research in Organic Food Systems), Niels Holst (Department of Agroecology, Aarhus University), Lise Nistrup Jørgensen (Department of Agroecology, Aarhus University), Johannes Michelsen (Department of Political Science and Public Management, University of Southern Denmark), Rune Vesterager Asmussen (Danish Christmas Tree Association), Helga Hjort (Danish EPA) and Henrik Frølich Brødsgaard (Danish EPA).

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Dansk sammendrag

Kartoffelskimmel, forårsaget af *Phytophthora infestans* er et alvorligt problem for kartoffelproduktionen i Europa og sygdommen koster ca. 1 milliard kroner om året i tab og omkostning til bekæmpelse. Et netværk af forskere, rådgivere, forædlere og aktører fra industrien som via nationale projekter arbejder sammen i EuroBlight – a potato late bligt network for Europe, har i en årrække overvåget udviklingen af genotyper (DNA undersøgelse), dels for at forstå udvikling og spredning af skimmeltyper i Europa og dels for at overvåge risikoen for udvikling af resistens mod de fungicider, som anvendes i bekæmpelsen. IPMBlight2.0 projektet er et ERA-Net projekt, hvor de enkelte lande bidrager med penge til en fælles pulje. Landene prioriterer udvalgte indsatsområder, og baseret på disse rammebetingelser, blev der samlet en gruppe af universiteter og private aktører inden for rådgivning og forædling for at gå et skridt videre end det EuroBlight har haft mulighed for. De planlagte undersøgelser tog udgangspunkt i anbefalinger fra EuroBlight workshop i Brasov, 2015 (https://agro.au.dk/fileadmin/EuroBlight_Statement_Brasov_25_6.pdf). Man skal således se projektet både som en koordineret indsats med EurBlight partnere og som en videreførelse af allerede eksisterende aktiviteter baseret på en kombination af nationale projekter og fælles samarbejde via EuroBlight netværket. De otte partnere, INRA (Frankrig), Aarhus Universitet (Danmark), NIBIO (Norge), Estonian University of Life Sciences (Estland), ARVALIS Institut du Végétal, Association des Créateurs de Variétés Nouvelles de Pomme de terre (Frankrig), Norwegian Agricultural Extension Service (Norge) og James Hutton Institute (Scotland) er alle aktive partnere i EuroBlight.

Målet med projektet var at:

- Videreudvikle og intensivere overvågning af *P. infestans* genotyper i Europa
- Undersøge de fænotypiske karakteristika (aggressivitet, virulensegenskaber, fungicidresistens) af navngivne genotyper, men også af genotyper som stammer fra kønnet formering
- Undersøge hvordan vi kan forbedre eksisterende beslutningsstøttesystemer med viden om patogenernes karakteristika, udbredelse og evolution.

Med hensyn til genotyper af *P. infestans*, omtales også resultater fra 2020, som er året efter IPMBlight2.0 sluttede.

Resultater:

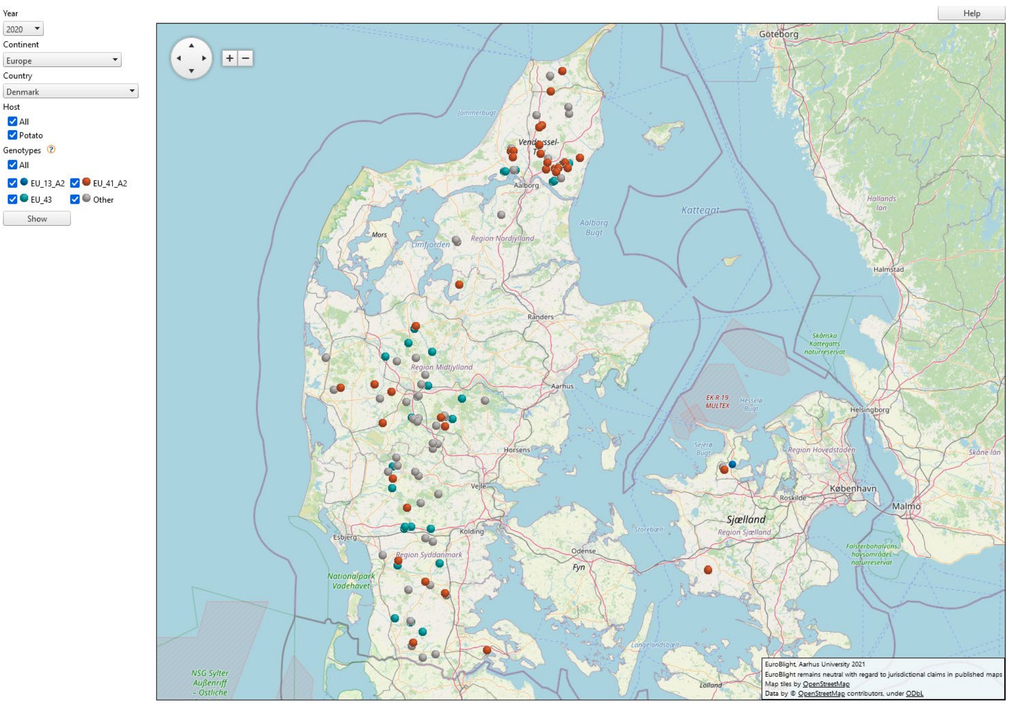
1. **Hvilke skimmeltyper har vi i Danmark og i Europa?:** Via indsamlingen af *P. infestans* isolater fra partner lande og en central SSR genotypning ved James Hutton Institute, blev der identificeret tre nye og betydende kloner af *P. infestans*. Den ene EU_37_A2 (EU37) var fundet tidligere i flere lande (Frankrig, UK, og Benelux). De fænotypiske undersøgelser fra nærværende undersøgelse viser, at denne genotype er mindre følsom overfor fluazinam, som er aktivstoffet i Shirlan i Danmark. Fluazinam har sporedræbende effekt, og det anvendes typisk midt på sæsonen og i slutningen af sæsonen for at udgå angreb på knoldene. De andre to kloner som breder sig nu i Europa er er EU_36_A2 (EU36), en meget aggressive genotype (vokser hurtigt, og danner meget smitstof) og EU_41_A2 (EU41), en genotype som først blev fundet i Danmark, men som nu findes a alle Skandinaviske lande, samt Polen og Tyskland. Alle data blev lagt ind i EuroBlight databasen og præsenteret på kort og grafik på EuroBlight hjemmesiden. EU41 blev observeret første gang i Danmark i 2013. Denne klon er nu den dominerende klon i Danmark, blandet med en population af kønnet formering. EU37 er ikke fundet i Danmark endnu, men den er registreret i Nordtyskland. Der blev registreret tre isolater af EU36 i det

sydlige Danmark i 2017, den var fraværende i 2018, men den er fundet igen i 2019 i Midt- og Sydjylland.

I 2020, blev der konstateret en ny genotype af *P. infestans* i Danmark, EU43, og den blev identificeret ved at analysere genetiske data fra 2020 sammen med data fra tidligere år. Navngivning af nye genotyper følger reglen om at en genotype skal findes udbredt i et område, skal genfindes de efterfølgende år og i flere lande. Hvis det sker, så indikerer det at en sådan type have en fordel frem for andre typer. Dens karakteristika bør derfor undersøges hurtigst muligt, og erhvervet skal opdateres om evt. ændringer i relation til ændringer i sorternes resistens eller i relation til forebyggelse og bekæmpelsesstrategier. I Danmark, er der over perioden 2017-2020 identificeret 2 betydende kloner samt en stor gruppe af ”Andre”, som også indeholder unikke genotyper bl.a. fra kønnet formering (Tabel 1 og Fig. 1). Du kan læse mere om de nye og mere aggressive skimmeltyper i Danmark i bilaget: ”Nye skimmeltyper i Danmark betyder at vi skal ændre praksis”. Her konkluderes at vi kan minimere risikoen for alvorlige angreb ved at reducere tidlige smittekilder, bruge mere resistente sorter og ved at anvende fungiciderne klogt.

TABEL 1. Frekvensen af genotyper i Danmark 2017-2020. Der blev fundet ét isolat af EU13 i hhv. 2017 og 2020 (hhv. 0,6% og 0,7%)

Genotype navn	2017	2018	2019	2020
EU13	0,6%	0	0	0,7%
EU36	1,9%	0	3,9%	0
EU41	34,2%	36,4%	34,1%	26,9%
EU43	0	7,5%	5,2	22,8%
Andre	63,3%	56,1%	56,8	49,7%
Antal isolater testet	158	107	229	145



FIGUR 1. Udbredelsen af genotyper i Danmark i 2020. Der blev fundet ét isolat af EU13 (blå) på en spildkartoffel på den Nordvestlige side af Lammefjorden. I kartoffelområderne i

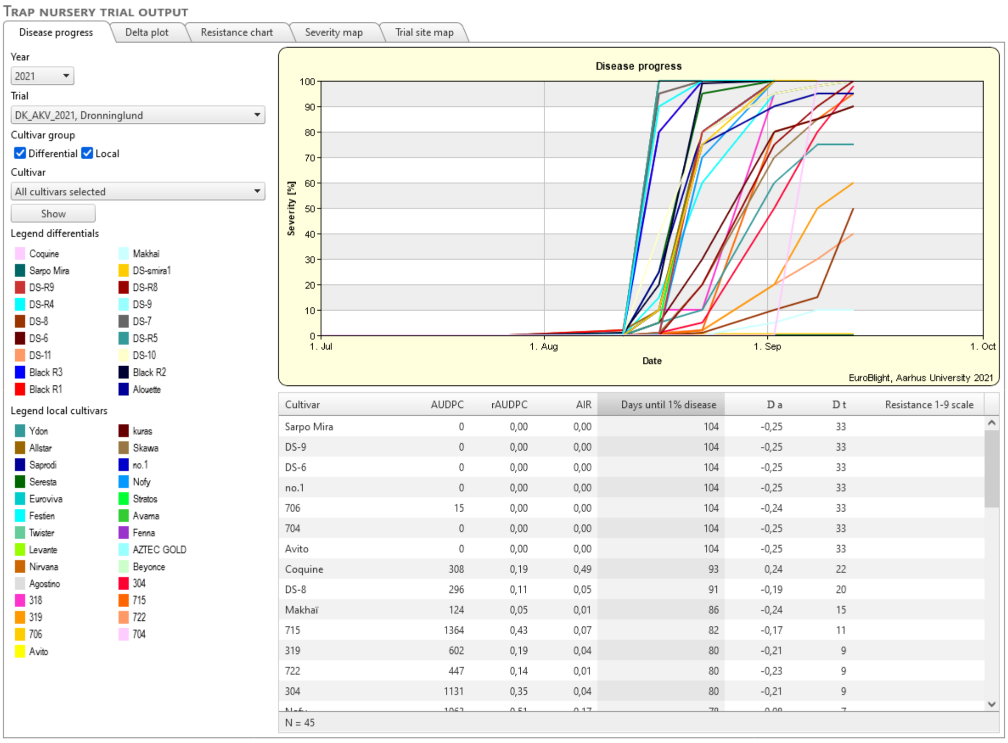
Jylland blev der registreret en kombination af EU41, EU43 og ”andre gruppen”. Kort applikationen laves i Potato Late Blight Toolbox, som er udviklet af AU. Kort er frit tilgængelige på EuroBlight hjemmesiden.

2. **Hvilke karakteristika har de forskellige genetiske typer af skimmel?:** For test af fænotypiske karakterer, blev ca. 40-50 levende reference isolater sendt fra alle lande til NIBIO i Norge. Her blev de opformeret, rengjort og distribueret til test for både fænotypiske (aggressivitet, virulens og fungicid resistens test) og genotypiske karakterer (SSR genotypning). NIBIO har desuden gemt reference isolater i flydende kvælstof (-80°C), hvis der skal laves yderligere analyse på de historiske isolater. Partnere fra Estland og Norge har lavet fungicid resistens testene og INRA har haft hovedansvaret for at teste for aggressivitet og virulens. Virulens betyder at man tester for, hvilke kendte resistensgener et givet isolate eller en genotype kan overkomme. James Hutton Institute lavede SSR genotypning på alle reference isolater. Undersøgelserne af isolaterne fra 2016 og 2017 viser, at der er en relativ stor variation for alle fænotypiske karakteristika – både imellem og indenfor de identificerede genotypiske grupper. Fordelingen af fænotyper gør det muligt at identificere fænotypiske profiler baseret på SSR genotype resultater, men ikke en nøjagtig bestemmelse af et bestemt isolats individuelle karakterer. Resultaterne for Danmark indikerer at isolater tilhørende den genetiske gruppe kaldet ”Andre” var mere aggressive end tilsvarende isolater fra gruppen ”Andre” fra Norge og Estland. Isolater af genotypen EU41 kunne overkommer flest forskellige resistensgener sammenlignet med isolater fra andre testede genotyper. I laboratoriet blev sorten Bintje smittet med isolater af forskellige genotyper. For danske isolater var størrelsen af læsioner efter 5 dage den samme for EU41 og isolater fra gruppe ”Other” – samme størrelse som for EU13 gruppen fra andre lande, men signifikant mindre end for isolater fra EU6 gruppen fra UK. Til gengæld var sporangie produktionen for EU41 isolater - målt efter fem dage på Bintje - den samme som for EU6 isolater, et niveau som er signifikant højere end for isolater fra EU13 gruppen. Når sammenligningen mellem EU41 og EU13 og EU6 er interessant, er det fordi EU6 og EU13 er dominerende kloner i England, Scotland og Wales, og de er begge meget aggressive. EU13 var tilstede i Danmark op til 2014 og den er kendetegnet ved at være resistent overfor aktivstoffet metalaxyl (i produknavnet Ridomil). Da man forbød Ridomil i Danmark fra 2014 forsvandt EU13. Alle reference isolater blev testet for evt. nedsat følsomhed overfor aktivstofferne mandipropamid (i Revus), Cyaxofamid (i Ranman), Propamocarb (i Proxanil) og fluazinam (i Shirlan). Der blev fundet mindre følsomhed for EU37 overfor fluazinam. Ellers blev der ikke fundet nogen vigende effekt af nogen genotyper overfor de fire testede aktivstoffer. For EU36 og EU37 viste en laboratorie test dog, at isolater fra genotypen EU36 og EU37 konsekvent gav relativt højere sygdomsudvikling ved meget lave doser sammenlignet med isolater fra andre genetiske grupper – for alle fungicider testet. Det konkluderes at den eneste klon vi har i Danmark, EU41A2, er en multivirulent og aggressiv genotype. Den har ekspanderet fra 4,7 % i 2013 til 37,1 % i 2018 (105 isolater testet i 2018), og den kan konkurrere med en relativ aggressiv gruppe af ”other” isolater (62,9 % i 2018), som sandsynligvis er baseret på en population med kønnet formering. Vi har endnu ikke undersøgt den fænotypiske profil af EU43, men det vil ske i løbet af 2021 og 2022.

   Kombinationen af en langsom udskiftning af betydende kartoffelsorter, udbredt anstrængte sædskifter, ekspanderende aggressive genotyper som EU41 og EU43, en diversitetsskabende kønnet population af *P. infestans* og en relativt begrænset adgang til fungicider med forskellige virkemekanismer (mode of action) er en trussel for en bæredygtig kartoffelproduktionen i Danmark.

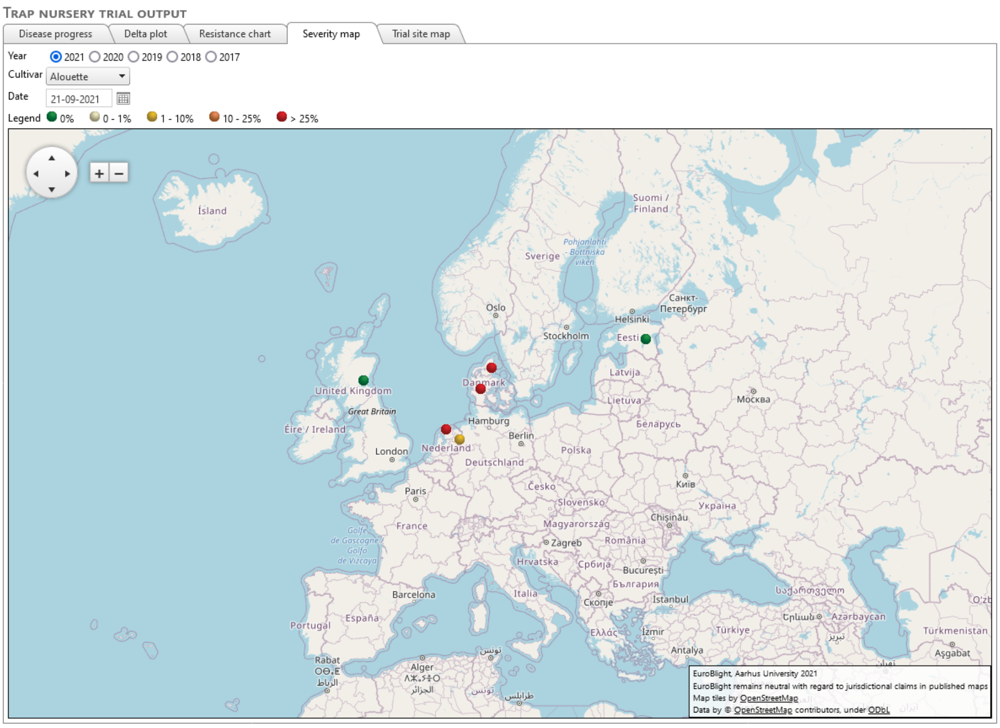
3. **Det er vigtigt at teste for sorternes type, niveau og stabilitet af resistens.**

Ifølge EuroBlight er den vigtigste IPM komponent resistensen i sorterne, men der kan være usikkerhed om, hvordan man skal forebygge og bekæmpe skimmelangreb i nye og mere resistente sorter, som er på vej i disse, bl.a. på grund af forbedrede og hurtigere forædlingsteknikker. Der er også behov for at kvantificere sorternes resistens og overvåge stabiliteten af resistensen så den information kan indarbejdes i bekæmpelsesstrategier. I IPMBligt2.0 projektet udviklede AU et fælles ”Trap Nursery Data Management System” (TNDMS), hvor 21 differential sorter blev udplantet i alle partner lande (tre steder i Danmark: AKV-Langholdt i Nordjylland, KMC i Midtjylland og ved AU-Flakkebjerg på Sjælland). Af disse sorter indeholder de 11 hver ét kendt resistensgen (R1 til R11) og resten indeholder et til flere R gener. Ved at registrere sygdomsudviklingen i differentialsorterne og ved at kombinere dette med genotypning af isolater indsamlet i forsøget, så kan man monitere lokale patogen populationers virulens (dvs. hvilke og hvor mange resistens gener enkeltvis og i kombinationer populationen kan overkomme). Hvis man kender sammensætningen af resistens i kommercielle sorter, så kan man i nogen grad forudsige hvilke sorter som vil være lidt - meget modtagelige med den aktuelle population af *P.infestans* og dermed graduere forebyggelse og bekæmpelsen af kartoffelskimmel. Ved at analysere sygdomsudviklingen for en given kartoffelsort i forhold til tilsvarende i differential sorter med statistiske metoder (Area under the disease progress curve (AUDPC), Apparent infection rate (AIR, hældning), days until 1% disease osv.) kan man også karakterisere typen og graden af resistens. I de danske forsøg med differential sorter har industrien yderligere inddraget eksisterende og nye sorter undervejs og brugt Trap Nursery Data Management Systemet til automatisk beregning af disse statistiske indeks for resistens. Resultaterne viser, at nye sorter undervejs, f.eks. stivelsessorterne no.1, Avito og mange ”nummersorter” har god til 100% resistens mod angreb af kartoffelskimmel (Fig. 2). Målet er at fortsætte og udvide dette TNDMS system til mange lande i Europa, koblet med patogen monitering. Dermed har man et godt samlet system, som kan supplere nationale markspecifikke beslutningsstøttesystemer (DSS) om interaktioner mellem patogenet (som angriber) og sorterne (som forsvarer sig med resistens), og hvordan resistensen udnyttes optimalt sammen med de mange andre IPM metoder, herunder anvendelse af fungicider.



FIGUR 2. Trap Nursery Trial Output fra AKV-Langholdt. Data er baseret på sygdomsbedømmelser gennem sæsonen fra 18 ubehandlede differential sorter og 27 sorter som de selv har valgt at teste. Man kan vælge at se et udpluk af sorter via det interaktive brugerinterface. Baseret på data fra sygdomskurverne kan man beregne en lang række epidemiologiske variable som fortæller noget om typen og niveauet af resistens (se tekst ovenfor). I eksemplet er tabellen sorteret efter dage fra 1. juni og indtil 1% angreb i sorten. Data manipulation, statistik og kort laves i Potato Late Blight Toolbox som er udviklet af AU.

I systemet kan man også se et kort (Severity map fanebladet) over registreringerne i specifikke sorter som testes i netværket af forsøg over Europa (Fig. 3). Når de samme sorter testes i forsøg forskellige steder i Europa, så udsættes de for de lokale populationer af *P. infestans*. Dermed testes de samme sorter over for de skimmeltyper som findes i forskellige regioner af Europa. Nogle typer, kan blive en trussel i andre dele af Europa på et senere tidspunkt. Kartoffelskimmel kan spredes med vinden >50 km og de kan spredes med inficerede læggekartofler. Det er kun tilladt at anvende typer af skimmel til udendørs forsøg, hvis de allerede findes i landet i forvejen. Derfor er netværket af Trap nurseries en god måde til, dels at "opfange det nye" (fordi vi eksponerer nyt genetisk materiale), og dels til at teste nye og mere resistente kommercielle sorter op mod de typer af skimmel som findes i forskellige regioner af Europa. Når vi så tester de samme sorter over flere år i netværket af forsøg, så kan vi beskrive typen, niveauet, og stabiliteten af sorternes resistens – og advare, hvis en sort viser vigende resistens i et eller flere af forsøgene.



FIGUR 3. Severity map, 2021. Sorten Alouette er valgt. Resultaterne vises for datoen 21. september. Prikkerne på kortet indikerer steder hvor denne sort har indgået i forsøget og farven indikerer niveauet af angreb på det givne tidspunkt. Brugeren kan vælge år, sort og dato til visning på kortet. Ved valg af dato vælges resultat for den tætteste observation på den pågældende lokalitet. De fleste steder observeres ugentligt, men ofte to gange ugentligt.

4. **Hvordan kan vi udnytte viden om sorternes resistens i beslutningsstøttesystemer?:**
Det blev dernæst undersøgt hvordan eksisterende beslutningsstøttesystemer (DSSs) i Europa kan forbedres ved i højere grad at udnytte data om lokale patogen populationer.

Indledningsvis blev seks DSS beskrevet og ”motoren” om beregning af skimmelvejr blev taget ud af hvert enkelt system og omprogrammeret, først i Matlab og senere på EuroBlight IT platformen som en Web løsning. De seks DSSere var: Skimmelstyring fra Danmark, Nærsted Model fra Norge, Irish rules fra Irland, WUR blight fra Holland, Hutton criteria fra UK og Mileos fra Frankrig. Beskrivelse af systemerne blev implementeret i på EuroBlight hjemmesiden: http://agro.au.dk/forskning/internationale-platforme/euroblight/research-projects/ipmblight20/decision-support-systems-overview/. Alle seks delmodeller (sub-models) kunne effektivt udpege perioder med hhv. høj og lav risiko for udvikling af kartoffelskimmel, men der var forskelle mellem modellerne i perioder ind imellem. De 5 af de seks modeller plus en reference model blev nu anvendt til at teste fire forskningsspørgsmål: i) er risikoen for skimmeludvikling generelt stigende gennemsæsonen fra maj til september? ii) er der forskel i skimmelrisikoen mellem regioner i Europa? iii) Er der forskel i skimmelrisikoen mellem årene, og iv) er beregningen af skimmelrisiko forskellig mellem modellerne. Der blev anvendt vejrdata (timedata for temperatur relativ luftfugtighed, stråling, nedbør og bladfugt) fra 6 lande, to stationer, og årene 2014-2017. Resultaterne viste, at den vejrbetingede risiko generelt er stigende gennem sæsonen. Der var forskel i skimmelrisikoen mellem årene. Risikoen i 2015 var signifikant lavere end årene 2014, 2016 og 2017, hvor forskellen ikke blev fundet signifikant. Den højeste risiko for skimmeludvikling blev fundet for Viller Saint Christophe, i Frankrig. Den laveste risiko for skimmeludvikling blev fundet ved Apelsvoll i Norge. Der var generelt sammenlignelige vejrbetingede betingelser for skimmeludvikling ved stationer i Holland, UK og Danmark. Der var forskelle i beregningen af skimmelvejr mellem modellerne, men alle modeller beregner de samme højrisiko og lav risiko perioder. Læs mere her (Hansen et al. 2017) og her (Hjelkrem et al., 2019). Ved at teste hypoteser som eksempelvis de ovennævnte opnås mere robuste resultater end hvis man blot anvendte en enkelt af modellerne. Denne tilgang er anvendt i en årrække inden for forskning i klimaændringer. Analysen af de forskellige delmodeller for udvikling af kartoffelskimmel antyder at forskellen mellem de fulde systemer mere er baseret på fortolkningen af skimmelvejr til en egentlig vejledning om forebyggelse og bekæmpelse. I praksis anvender ingen af de testede systemer data om patogen populationer og resistens anvendes kun i ringe grad, og ofte blot som en ekstra forsikring. Det skyldes netop at resistens ikke er en fast størrelse, men at den kan ændres eller nedbrydes af patogen populationer som udvikler ”våben” som kan nedbryde det forsvar som resistensen er udtryk for. Inden for forædlingen har man kaldt det et våbenkapløb. For at teste IPM2.0 konceptet (inddrage patogen information i DSS) blev der anlagt et KAF finansieret forsøg ved Flakkebjerg i 2018, med anvendelse af sorterne Kuras (modtagelig), Novano (middel modtagelig) og Nofy (mere resistent). Man kunne i dette forsøg reducere fungicidforbruget med 28% i forhold til ugentlige behandlinger med 50% dosis fungicid. I Novano og Nofy var den tilsvarende reduktion 35%. I Nofy blev der observeret under 1% sygdom ved sidste bedømmelse. Skal man så slet ikke behandle Nofy? I IPMBligt2.0 konceptet arbejder man med begreberne ”Gene Stewardship” og ”Active ingredient Stewardship”. Det betyder at man skal beskytte resistensgenerne men også aktivstofferne. Man anvender fungicid i meget resistente sorter, hvor de er mest ”presset” og under højt infektionstryk. Samtidig bruger man kun aktivstofferne efter behov samtidig med at anvendelsen af resistente sorter holder smittetrykket lavt. Dermed reduceres risikoen for at *P. infestans* udvikler resistens over for aktivstofferne såvel som tilpasser sig sorternes resistens. Aktivstofferne og resistensen passer så at sige på hinanden i et partnerskab.

I Danmark har vi en relativ aggressiv og divers population af skimmel på grund af kønnet formering. Det resulterer i en risiko for udvikling af mindre følsomhed overfor visse fungicider og også risiko for tilpasning til sorternes resistens. For de vigtigste nye genotyper anbefales det, at undersøge epidemiologiske forhold under markforhold og sammenligne disse resultater med nærværende resultater fra IPMBlight2.0, som er opnået under kontrollerede forhold i laboratoriet. For at vurdere truslen fra EU41, EU43 - og andre ekspanderende genotyper, vil det være relevant at fortsætte monitering af genotyper i Danmark, at holde nøje øje med indikationer fra praksis på vigende effekt af fungicider samt at overvåge niveauet og stabiliteten af resistensen i anvendte sorter. Det er vigtigt, fordi fokus på betydningen af primære inokulum kilder, anvendelse af mere resistente sorter, udvikling af robuste bekæmpelsesstrategier med inddragelse af teknologier fra præcisionsjordbrug er helt afgørende for udvikling af en bæredygtig kartoffelproduktion.

Summary

- **Monitoring of the European *P. infestans* metapopulation:** The sampling of populations of *P. infestans* in partner countries allowed to detect three new and emerging clonal lineages, among which one (EU_37_A2) was already present in several countries (France, UK, and Benelux). The phenotypic characterisation of isolates of this genotype, suggests that it is less sensitive to fluazinam. The other two emerging clones were EU_36_A2, a highly aggressive lineage, and EU_41_A2, a genotype invading sexual populations of the pathogen in Scandinavia, with the ability to overcome most race-specific resistance genes present in current European cultivars and high aggressiveness to susceptible potato breeds. All data were uploaded to the Potato Late Blight Toolbox and presented on maps and charts via the EuroBlight website. EU_41_A2 was first identified as a clone in Denmark 2014, most probably from the North of Jutland. This is now the dominating clone in Denmark, mixed with a sexual recombining population. EU_37_A2 has not yet been identified in Denmark, but it is present in the North of Germany. EU_36_A2 was found at low level in the south of Denmark in 2017, it was absent in 2018, but identified again in Mid / South Denmark in 2019.
- **Linking phenotypic traits to genotypes:** The typing of the reference collection of isolates established from the 2016 to 2018 samples shows a large variation for all phenotypic traits analysed (virulence, aggressiveness to reference cultivars and sensitivity to major late blight fungicides), occurring both between and within pathogen lineages. This particular distribution of phenotypes makes it possible to identify broad phenotypic profiles from SSR genotyping, but not an accurate prediction of isolate individual traits based on their SSR fingerprints. Results indicate that the group of ”Others” (probably from sexual recombination) from Denmark was more aggressive than the group of ”Others” from Norway and Estonia. The EU_41_A2 could overcome most resistance genes compared to all other known genotypes. For lesion size (after five days on Bintje) EU_41_A2 and «other» group isolates from DK, NO and ES was similar to EU_13_A2 isolates. For sporangia production, EU_41_A2 and Danish «other» isolates showed no significant difference to results for the EU_6_A1 isolates. In conclusion EU_41_A2 is a highly virulent and aggressive clonal genotype. It has a potential to compete with aggressive sexual combining populations in Denmark and Norway. Concerning potential for dispersion and expansion, more investigations are needed regarding other ecological processes i.e. seed tuber latent infection, overwinter survival in the fields in the context of climate change and field fitness versus fitness results in the laboratory.
- **Virulence monitoring:** A Trap nursery data management system was implemented in the Potato late Blight Toolbox for the monitoring of virulences in trap nurseries (21 differential cultivars) across Europe and for the evaluation of the type and stability of resistance in local cultivars tested in the same nursery. The obtained results of host resistance evaluation is considered as important input to European national decision support systems for the chemical control of potato late blight.
- **Improve national DSSs with pathogen information:** Major modules from six existing European DSSs was reprogrammed on the same IT platform, allowing for analysis of sensitivity and output comparisons with identical weather data sets as well as test of hypothesis of variation in late blight during the growing season, between regions in Europe, between years and between the models tested. This analysis has shown an overall match between prediction of risk periods by the various models, but also consistent variations that can be of strong local importance for early season warnings and accurate risk forecast. The data from trap nurseries for epidemic monitoring, established across partner countries, proved valuable for input late blight management during the season. The Danish DSS, Skimmelstyring was improved by including the IPM2.0 approach – e.g. utilizing information from trap nurseries, and a test in 2018 indicated a great potential of saving fungicides in

more resistant cultivars in years less favorable regarding weather conditions for late blight development.

The project has been an important contributor of communications to the EuroBlight workshops held in Aarhus, Denmark in May 2017, in York, UK in May 2019 and at the online zoom workshop in 2021, as well as to the EAPR Triennial Conference held in Versailles, France in July 2017. Interactions with the Scientific Advisory Board during the four project meetings have been very fruitful and open ideas for a more accurate dissemination of scientific results to stakeholders as they become available.

Bilag 1. Supplerende materiale

Nedenfor er inkluderet to artikler fra Danske Kartofler om den praktiske betydning af nye skimmeltyper i Danmark. De to artikler introducerer det nye BlightManager projekt, men data og erfaringer som omtales i artiklerne stammer fra IPMBlight2.0 projektet, som derfor burde være omtalt som kilde. Der var ikke afsat budget i IPMBlight2.0 til test af bekæmpelsesstrategier i Danmark, men der blev søgt og bevilliget penge fra Kartoffelafgiftsfonden til et sådant forsøg. Resultaterne fra test af IPMBlight bekæmpelses strategi ved Flakkebjerg, 2018 er vedlagt som supplerende materiale. Yderligere udvikling af IPMBlight strategien er fortsat i tre opfølgende projekter og nye data for *P. infestans* genotyper publiceres løbende på EuroBlight hjemmesiden:

- H2020 EU projekt, OrganicPlus: Pathways to phase-out contentious inputs from organic agriculture in Europe (2018-2022)
- GUDP projekt, BlightManager: Beslutningsstøtte om forebyggelse og bekæmpelse af kartoffelskimmel og bladplet i kartofler (2019-2021)
- Era-Net, Ecosol: Eco-friendly solutions for the integrated management of late and early blight of potatoes (2021-2023)
- EuroBlight, a potato late light network for Europe (2007 -)

Om Blightmanager

Formålet med projektet er at udvikle grundlaget for at kunne reducere brugen af pesticider i kartofler med op til 30%. Det skal være med til at sikre en langsigtet, bæredygtig og konkurrencedygtig kartoffelsektor i Danmark. For at nå målene vil projektet udvikle BlightManager, et beslutningsstøttesystem om bekæmpelse af kartoffelskimmel og bladplet som gør brug af nye lokale vejrstationer og satellit data til beregning af sygdomsrisiko og sprøjtevejr, robotteknologi til genkendelse af sygdomme, mobile platforme til data indsamling, varsling og rådgivning, og bedre karakterisering og udnyttelse af sorternes resistens i kombination med nye fungicider. Projektet er et samarbejde mellem KMC, AKV Langholdt, BJ-AGRO, SAGRO, SEGES, Aarhus Universitet, AgroIntelli og FieldSense. AU koordinerer dette projekt.

Om Ecosol

ECOSOL integrates biological control into IPM programs to manage late and early blight. To reach this goal, the efficacy of various BCAs and PRIs to control disease development are tested in planta and work is carried out to understand their mode of activity in order to secure stewardship into the future. The importance of factors including timing of application and level of host resistance on their efficacy is investigated. The most promising pesticide alternatives are tested under field conditions in a range of participating countries to ensure transferability. Host Resistance is a critical component in any IPM strategy for the sustainable control of late blight but is often quickly overcome due to the genetic diversity in pathogen populations. The project will therefore optimise the deployment of existing and new sources of host resistance through understanding and monitoring pathogen characteristics that cause host resistance to be overcome in practice, testing the durability of key resistances across time and location and mitigating against new pathogen strains that threaten such resistance.

ECOSOL adapts decision support systems to tailor them for the integration of biocontrol agents and for both early blight and late blight management decision making. IPM strategies are developed which include the most effective biological control agents with optimal timing of application, host resistance and reduced fungicide inputs. These strategies will be tested across a wide range of locations and by industry partners to ensure practical applicability. The success of the strategies will be measured in terms of early and late blight disease control with reduced pesticide usage compared with national conventional approaches.

The project encompasses strong stakeholder engagement to ensure alignment of experimentation, validation and demonstration aspects with industry requirements. This is supported by links to the established EuroBlight infrastructure which brings complementarity through unparalleled access to late and early blight expertise, industry contacts and dissemination activities.

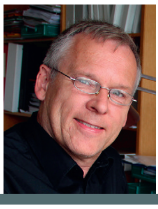
AU deltager i ledelse af projektet og bl.a. ansvaret for data management plan og plan for explotation and dissemination of results. AU er med til at teste nye biologiske midler mod skimmel og bladplet i kartofler. Resultaterne bruges til at videreudvikle BlightManager, et beslutningsstøttesystem til forebyggelse og bekæmpelse af skimmel og bladplet. AU er også ansvarlig for data management af alle data fra projektet, herunder at udvikle nye web baserede tools og services som oprindeligt blev udviklet i EuroBlight, og senere IPMBlight2.0 projekterne.

Om Organic-PLUS (O+)

The Organic-PLUS (O+) project has the overall aim of providing high quality, trans-disciplinary, scientifically informed decision support to help all actors in the organic sector, including national and regional policy makers, to reach the next level of the organic success story in Europe. By doing so, organic food systems can be more true to organic principles but equally to the EU Bio-economy agenda.

Organic-PLUS has four objectives: 1) to identify and evaluate contentious inputs currently used in European agriculture 2) to provide specific technical solutions to minimise or phase-out their use 3) to provide environmental, social and economic assessments of phase-out scenarios 4) to disseminate and broker knowledge, ideas and results to maximise impact.

AU participate in WP PLANT that researches alternatives to copper and mineral oils used for plant protection, working on potatoes, glasshouse crops and perennial Mediterranean crops. The Danish DSS is adapted for use of biological control agents and plant resistance inducers.



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Nyt projekt vil videre-udvikle varslingssystemet Skimmelstyring

Baggrunden for at videreudvikle Skimmelstyring er blandt andet at kunne modvirke effekten af nye skimmeltyper og samtidig at kunne reducere brugen af fungicider i kartofler

I januar begyndte et nyt GUDP finansieret projekt, som skal videreudvikle og forbedre varslingssystemet Skimmelstyring. Det nye system hedder *BlightManager*.

Baggrunden for det nye projekt er, at kartoffelskimmel er blevet vanskeligere at bekæmpe med fungicider, og der ses i gennemsnit hvert andet år tidlige angreb af kartoffelskimmel fra jordsmitte. Vigtige stivelsessorter som før var resistente, får nu angreb som nogen af de første i registreringsnettet. Oven i det er kartoffelbladplet blevet et større problem end tidligere i Danmark, og der er fundet fungicidresistens hos både skimmel og bladplet.

Skimmelstyring er udviklet i samarbejde mellem forskningen, rådgivningen og industrien. Systemet anvendes direkte eller indirekte af stort set alle avlere i Danmark og 20 procent af stivelsesavlerne i Sverige

BlightManager

Formålet med projektet er at udvikle nye metoder, som kan medvirke til at reducere brugen af fungicider i kartofler, og som samtidig understøtter en langsigtet, bæredygtig og konkurrencedygtig kartoffelsektor i Danmark.

Vi har brug for mere viden om betydningen af nye skimmeltyper, og vi skal kunne udnytte de nye sorters bedre resistens i bekæmpelsesstrategierne. Vi skal undersøge, hvordan vi kan udnytte lokale vejrstationer, robotter og satellitdata til lokal og målrettet vejledning om bekæmpelse osv.

I 2019 skal vi undersøge, hvilke skimmeltyper vi har i Danmark og deres betydning. Vi vil også undersøge betydningen af primære smittekilder samt hvordan vi skal bruge de nye vejrstationer i varslingen for skimmel og bladplet. Derudover skal AgroIntelli "træne" deres robot i forsøgsmarken til at genkende skimmel og bladplet, og vi skal afprøve innovative bekæmpelsesstrategier i nye resistente sorter i forsøg på tre forsøgslokaliteter.

FOTO: AGROINTELLI

Som et led i det nye projekt skal AgroIntelli træne deres robot i at genkende skimmel og bladplet i forsøgsmarken.

Aggressive skimmeltyper

Årsagerne til, at alvorlige angreb af skimmel og bladplet er mere udbredt nu end tidligere, er en kombination af flere forhold, men ikke mindst på grund af en helt basal ændring i kartoffelskimmelens biologi.

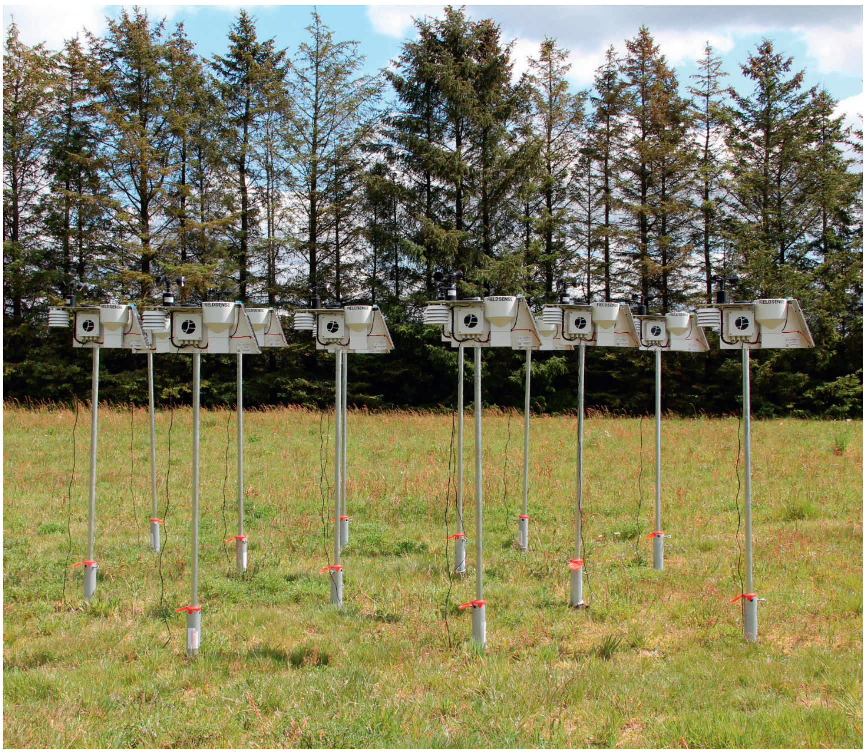
Fra 1845 til 1997 var der kun det ene køn (A1) af skimmel i Danmark. I 1997 oplevede vi for første gang i Danmark effekterne af, at der var kommet en ny bestand af skimmel med begge køn (A1 og A2) til Europa. Det er først i de senere år, at vi har set den fulde effekt af disse ændringer. Den kønnede forme-

Figur 1. *Genotyper i Danmark i hhv. (fra venstre) 2012, 2014 og 2018. Blå prikker er EU_13_A2, , Orange prikker er EU_41_A2 og Grå prikker er Andre.*

ring giver tidligere angreb fra svampens hvilelegemer (oosporer), som kan overleve cirka fire-fem år i jorden og smitte planterne allerede ved fremspiring. Den kønnede formering giver mere variation i afkommet, og hermed øges risikoen for at der udvikles nye racer, som kan overvinde sorternes resistens eller har nedsat følsomhed for fungiciderne.

I Danmark brugte vi tidligere Ridomil, som havde en effektiv og systemisk effekt over for skimmel. I 2012 var den dominerende skimmeltype i Danmark EU_13_A2. Vi ved nu, at EU_13_A2 var resistent overfor aktivstoffet i Ridomil. Derfor havde EU_13_A2 en fordel frem for andre skimmeltyper. Da Ridomil blev taget af markedet fra 2014,

FOTO: JENS GRØNBECH HANSEN



Figur 2. *Tolv klimastationer opsat ved forsøgsarealet ved Arnborg.*

» forsvandt denne type fra Danmark. I stedet er en nu fremkommet ny type EU_41_A2, som ser ud til at have sit udspring i Danmark, og den ser ud til at være meget aggressiv og breder sig hurtigt (fig. 1.).

På det netop afholdte EuroBlight møde i York i England blev der talt meget om tre nye genotyper (DNA) som lige nu spreder sig i Europa – EU_36_A2, EU_37_A2 og EU_41_A2.

Genotypen EU_36_A2 er kendetegnet ved at være meget aggressiv – blandt andet danner den mange sporer og vokser hurtigt).

EU_37_A2 er kendetegnet ved at være mindre følsom overfor fluazinam, aktivstoffet i Shirlan – også ved fuld dosering. EU_41_A2 er kendetegnet ved at være meget virulent, dvs. den kan angribe mange forskellige sorter med god resistens. EU_36_A2 og EU_37_A2 breder sig fra Holland både mod øst og mod vest. EU_36_A2 blev fundet i det sydlige Danmark i 2017 men ikke i 2018 og EU_37_A2 er fundet i Nordtyskland men endnu ikke i Danmark eller de andre Skandinaviske lande. EU_41_A2 er opstået i Danmark i 2014. Herfra har den spredt sig til Sverige, Norge og Polen siden 2016.

I 2019 vil vi analysere skimmelisolater så hurtigt som muligt, så vi allerede efter 2-3 uger kan give besked om, hvad der er fundet, og om der er en sandsynlig vigende effekt af at bruge Shirlan. Man kan tænke sig, at vi måske kan undgå en invasion af EU_37_A2, hvis fluazinam kun anvendes til forebyggelse af knoldskimmel sidst i sæsonen. Hypotesen er at EU_37_A2 kun har en fordel frem for andre typer, hvis der anvendes fluazinam.

BlightManager

Projektet er et samarbejde mellem kartoffelindustrien (AKV og KMC), rådgivere (SEGES, Agri Nord og BJ-Agro), kartoffelavlere, Aarhus Universitet samt FieldSense og Agrointelli. Du kan læse mere om projektet på hjemmesiden: http://projects.au.dk/blightmanager/

Anvendelse af nye vejrstationer

I projektet vil vi arbejde med 45 vejrstationer fra FieldSense (fig 2.). Vi vil først undersøge kvaliteten af stationerne, og hvordan de skal placeres korrekt. Senere skal de bruges til at undersøge, om der er områder i marken, som er mere favorabelt for udvikling af skimmel og bladplet end andre samt til demonstration hos avlere. Det er planen, at vi i sidste halvdel af projektet skal bruge data fra stationerne, så man kan beregne sprøjtevejr og få en skimmelvarsling med helt lokale vejrdata.

Kan en robot lære at kende skimmel og bladplet?

Agrointelli skal undersøge om deres robot kan "trænes op" til at genkende skimmel, bladplet, virus, fysiske skader m.m. i marken. Målet er, at en robot på en sprøjtebom i fremtiden kan finde skimmel tidligere end man finder det med øjet.

Det er dyrt i kemikalier at bekæmpe et etableret angreb. Bladplet er vanskelig at genkende i marken, og hvis robotten kan sige, hvornår det er og hvornår det ikke er bladplet, så kan man udgå at starte bekæmpelse af bladplet for tidligt. Tidlige symptomer af bladplet vil blive indsendt til AU Flakkebjerg, hvor der vil blive udviklet en hurtig PCR test for, om det er bladplet eller ej.

Overblik over bekæmpelsesbehov i alle marker lige ved hånden

Når de nye modeller og beslutningsstøtte komponenter er færdige, vil de blive integreret i CropManager fra Seges. Hermed sikres, at der for den enkelte avler er direkte adgang til egne data i Dansk Markdatabase, som skal føde ind til et GIS baseret, markspecifikt beslutningsstøttesystem. Der vil kunne anvendes vejrdata fra DMI eller Fieldsense vejrstationer, og man kan se sine varslinger på alle marker på mobiltelefonen. BlightManager udvikles, så det kan anvende data fra andre systemer, som lagrer grunddata for landmænd. ■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Nye skimmeltyper i Danmark betyder at vi skal ændre praksis

Nye skimmeltyper i Danmark er meget aggressive, men vi kan minimere risikoen for alvorlige angreb ved at reducere tidlige smittekilder, bruge mere resistente sorter og anvende fungiciderne klogt

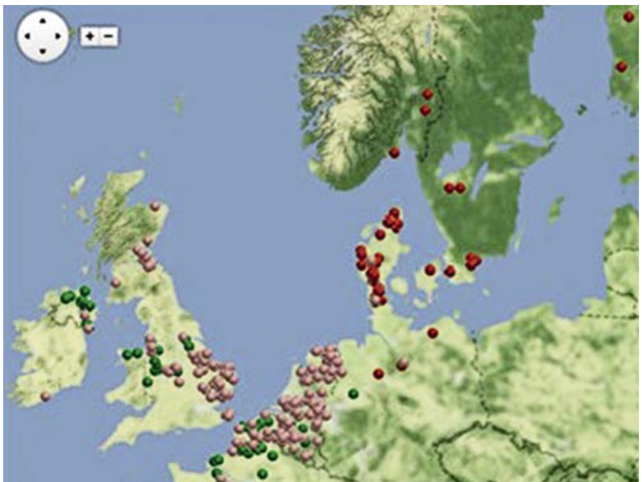
Kartoffelskimmel er blevet vanskeligere at forebygge og bekæmpe med fungicider. Det så vi med al tydelighed i 2019, hvor skimmelen var udbredt og vanskelig at bekæmpe i mange marker.

Det er sandsynligvis først nu, at vi har set den fulde effekt af, at der er i midten af 1990'erne kom en ny bestand af skimmel til Danmark. Indtil da havde vi en bestand af skimmel med kun én parringstype (A1). Den nye bestand havde både A1 og A2, og når en A1 og en A2 type mødes på det samme blad, kan der ske en parring. Afkommet er oosporer – hvilelegemer – som kan overleve i jorden og give anledning til smitte i op til fem år under gunstige betingelser.

Den kønnede formering giver mere variation i afkommet og dermed en øget risiko for, at der udvikles nye typer, som kan overvinde sorternes resistens eller har nedsat følsomhed overfor for fungiciderne. Men har vi allerede set indikationer på sådanne tilpasninger? Og hvad kan vi gøre for at undgå det værste?

EuroBlight overvåger bestanden

EuroBlight er et netværk af forskere, forædlere, rådgivere og partnere fra industrien, som har det fælles mål at forstå biologien af skimmel og bladplet og samtidig at udvikle ny viden om forebyggelse og bekæmpelse af de to sygdomme.

Figur 1. *Resultat af genotypning i Europa 2014 (øverst) og 2019 (nederst), hvor der kun er valgt at kortlægge EU37 (Grøn); EU36 (rosa) og EU41 (mørk orange). I 2014 blev der indsamlet ca 1700 prøver og i 2019 ca 1800 prøver fra ca. de samme områder. Udbredelsen af de tre nye genotyper er på bekostning af EU13 og EU6 i Holland og Belgien og EU13 og "andre" i Danmark*

Et væsentligt element er at overvåge bestanden af skimmeltyper i Europa. Kartoffelskimmel er symptomet, som skyldes en svampelignende organisme som hedder *Phytophthora infestans*. Ligesom halsbetændelse i de allerfleste tilfælde skyldes en bestemt virus. Det er således *P. infestans*, man laver DNA profil på i laboratoriet. En bestemt DNA profil kaldes en genotype, og hvis en genotype findes i flere lande eller over flere år, så får den et navn. Den må altså have en klar fordel over for andre, siden den kan brede sig.

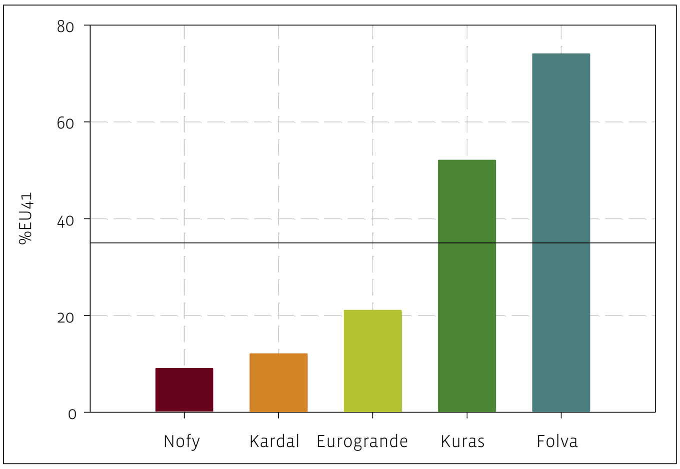
Nye skimmeltyper i Europa

I 2019 blev der indsamlet ca. 1.800 prøver fra 27 lande heraf 245 fra Danmark. Tre nye genotyper af *P. infestans* (EU36, EU37 og EU41) breder sig i Europa lige nu, fra en hyppighed for disse tre på 0,8 procent i 2014 til 40 procent i 2019 (Figur 1), og avlerne spørger naturligvis, hvad det betyder for dem. "Skal jeg ændre bekæmpelsesstrategi eller skal jeg vælge en anden sort?"

Tabel 1. *Hyppigheden [%] af kendte kloner og "Andre" for tre indsamlinger af skimmelisolater i 2019. Første indsamling var 13. juni til 4. juli. Anden indsamling 5. juli til 2. august og tredje indsamling 3. august til 11. september. Resultaterne fra 2019 sammenlignes med gennemsnit 2017-2019*

Genotype	Jun 2019	Jul 2019	Aug – sept 2019	Gennemsnit 2017-2019
EU37	0	0	0	0
EU36	7	0	0	2
EU41	23	50	37	35
Andre	69	50	63	63

»



Figur 2. *Søjlerne angiver hvor stor procentdel af undersøgte skimmelisolater som var af typen EU41 indsamlet på fem forskellige sorter: Nofy, Kardal, Eurogrande, Kuras og Folva. Totalt blev der undersøgt 449 isolater, 2017-2019. Den vandrette linje viser 35 procent, som er den gennemsnitlige hyppighed af EU41 i Danmark 2017-2019.*

» Udover at lave DNA profil har man derfor også undersøgt, hvordan de opfører sig på planter i drivhus og laboratorier og deres følsomhed overfor forskellige fungicider. Det viser sig, at EU36 danner flere sporer og vokser hurtigere på bladene end andre typer. EU37 er som den eneste mindre følsom overfor fluazinam, aktivstoffet i Shirlan – også ved fuld dosering.

EU41 er også aggressiv, og den kan angribe mange sorter med god resistens. Situationen i Danmark er, at 35 procent af bestanden er EU41 og stort set resten er "andre", som overvejende stammer fra kønnet formering. EU41 blev første gang fundet i Danmark i 2013, og siden 2016 er den spredt til resten af Skandinavien samt i 2019 også til Finland og Tyskland. EU36 og EU37 har bredt sig fra Holland ind i Belgien, Frankrig og videre til Storbritannien og Irland. I Danmark blev der i 2019 fundet to marker med EU36, men ingen med EU37 i de ca. 200 undersøgte marker (Figur 1).

BlightManager – resultater af indsamling 2019

I Danmark har vi et GUDP projekt (BlightManager, 2020) om udvikling af beslutningsstøtte til forebyggelse og bekæmpelse af skimmel og bladplet. Da vi i 2018 så, at EU37 var fundet i Nordtyskland men endnu ikke i Danmark, besluttede vi at indsamle skimmel tidligt i sæsonen 2019 og håbede at kunne få et hurtigt svar på DNA undersøgelsen.

Vi sendte ca. 100 isolater til Skotland den 25. juni for at undersøge om EU37 var tilstede eller ej. Målet var, at vi så tidligt som muligt kunne svare på, om det var hensigtsmæssigt at anvende fluazinam eller ej senere på sæsonen. Den 5. juli kunne vi give besked til erhvervet, at EU37 ikke var fundet i den første indsamling. Resultatet af to yderligere indsamlinger gennem sæsonen viste, at EU37 slet ikke blev fundet i 2019 (Tabel 1). EU36 blev kun fundet i to marker tidligt på sæsonen. I 2019 var der ved den tredje indsamling 37 procent EU41, og 63 procent var af typen "Andre".

Kuras og Folva er nu mere modtagelige

Vi har vidst længe, at resistensen i Kuras har været vigende, og det samme er sandsynligvis gældende for andre sorter, som vi har dyrket længe som for eksempel Folva. Der er altså udviklet genotyper, som kan overkomme den resistens, der er i sorterne.

For at undersøge om det er sandsynligt, har vi analyseret de data, vi har indsamlet i de seneste tre år, 2017-2019. Andelen af EU41 har været nogenlunde stabil på cirka 35 procent i alle tre år. Hvis man kigger på et udvalg af sorter, hvor der oftest er taget prøver fra i 2019, så viser resultaterne, at 9 procent af isolater, samlet på Nofy, var EU41 (91 procent var typen "other"). Tilsvarende er henholdsvis 52 procent og 74 procent af isolater samlet på Kuras og Folva af typen EU41 (Figur 2).

Forsøg ved AKV-Langholdt og ved Flakkebjerg i 2019 viser også, at Kuras og Avarna nu er ligeså modtagelige som Bintje, når EU41 er tilstede (Figur 4). Ved Flakkebjerg, hvor ingen af de nye genotyper er fundet, er Kuras og Avarna mere resistente sammenlignet med Bintje.

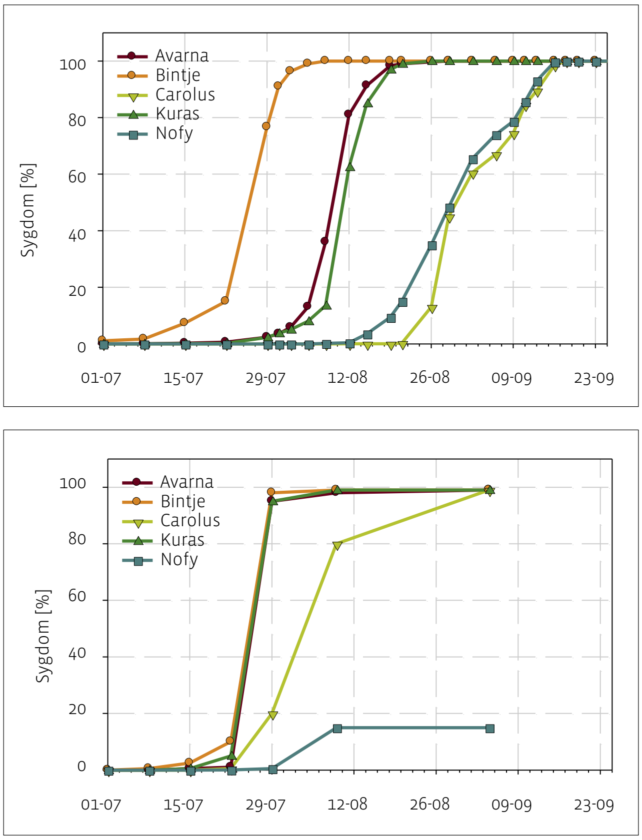
Ved AKV Langholdt, hvor de indsamlede isolater var EU41, udvikler skimmelen sig ligeså hurtigt i Kuras og Avarna som i Bintje (Figur 3). Dette er også i overensstemmelse med erfaringerne fra praksis, fordi AKV skrev allerede for nogle år siden i deres nyhedsbrev, at Kuras nu må betragtes som en modtagelig sort.

Data i figur 2 og figur 3 er ikke beviser i sig selv, men de bidrager til et samlet billede af, at sorternes resistens ændrer sig, fordi patogenerne ændrer sig.

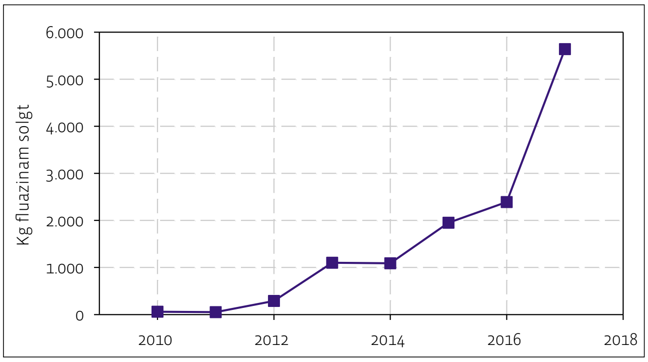
Reducer brugen af fluazinam – hold EU37 ude af Danmark

Følsomhedstest af de mest anvendte aktivstoffer viser, at der lige nu i Europa kun er påvist resistens mod fluazinam (Shirlan og Banjo Forte) og phenylamider (Ridomil). Sidstnævnte er ikke længere tilladt i Danmark. Men resultaterne viser også, at isolater af EU36 and EU37 laver større læsioner end nogle af de ældre genotyper ved meget lave doser af flere af aktivstofferne (EuroBlight, 2020).

I et EU projekt (IPMBlight2.0) blev det også påvist, at EU36 isolater i gennemsnit laver større læsioner og producerer mere smitstof i form af sporangier. Det betyder, at den type skimmel sandsynligvis er mere vanskelig at bekæmpe. Større aggressivitet og mindre følsomhed overfor fungiciderne, det kan være en medvirkende årsag til at de to nye genotyper breder sig i Europa på bekostning af andre (EuroBlight, 2020). I Danmark er brugen af fluazinam igen stigende efter at have været lav i en årrække (Figur 4). Derfor bør man



Figur 3. *Udvikling af kartoffelskimmel på fem kartoffelsorter (Avarna, Bintje, Carolus, Kuras og Nofy) ved Flakkebjerg (øverst) og Dronninglund (nederst) i 2019.*



Figur 4. *Solgt mængde fluazinam [kg] i Danmark, 2010-2017. I 2019 blev 77 procent af de angivne mængder anvendet i kartofler og 23 procent i grøntsager (MST Bekæmpelsesmiddel-statistik, 2019)*

diskutere og anbefale strategier, som minimerer risikoen for at EU37 bliver et problem i Danmark.

Hvad skal vi gøre?

Udbredelsen af nye aggressive genotyper i Danmark betyder, at vi skal være på vagt og opføre os klogt.

For det første skal vi minimere betydningen af tidlige smittekilder, det vil sige flere år imellem kartoflerne for at reducere risikoen for tidlige angreb fra jordsmitte, bekæmpe spildkartofler, overdække affaldsdynger med sort plastik, bruge sundt læggemateriale og bidrage aktivt til registreringsnettet for tidlige angreb.

For det andet skal vi bruge fluazinam-baserede produkter på en måde, så vi undgår, at EU37 etablerer sig og spreder sig i Danmark. Hvis det sker, mister vi sandsynligvis et meget vigtigt aktivstof, som kan reducere sporedannelse og dermed beskytte mod skimmel i knoldene. Vi kan lære fra Storbritannien og Holland, hvor de har set et markant fald i EU37 efter de reducerede anvendelsen af fluazinam.

For der tredje skal vi undersøge og overvåge typen, niveauet og stabiliteten af resistensen i de gamle og nye sorter overfor de genotyper, vi allerede har (EU41, EU36 og "Andre"), men også overfor de genotyper, som måske kommer (EU37).

Da Kuras blev markedsført for ca. 20 år siden, havde den en skimmel resistens-karakter på 7-8, mens den i dag er 4. Derfor er det vigtigt, at der laves strategier, så man relativt hurtigt kan skifte til nye og mere resistente sorter. Forsøg med nye sorter som Nofy og Carolus viser, at de har en meget god resistens over for de genotyper, vi har i Danmark.

Hvis udbredte sorter ikke bevarer deres resistens, skal der bruges flere fungicider for at undgå epidemiske angreb, og så stiger risikoen for fungicidresistens. Dette er samlet set en trussel for bæredygtigheden af den økonomisk meget attraktive kartoffelproduktionen i Danmark. ■

Kartoffelafgiftsfonden

Kilde: AKV Langholdt

Titel

Bekæmpelse af skimmel i nye resistente stivelsessorter

Projektansvarlig og deltagere

Ansvarlig: Jens G. Hansen, Forskningscenter Foulum, Institut for Agroøkologi, Aarhus Universitet, Blichers Allé 20, Postboks 50, DK-8830 Tjele

Deltagere: Bent J. Nielsen og Hans Hansen, Forskningscenter Flakkebjerg, Institut for Agroøkologi, Aarhus Universitet

Resume

Sortsresistens er et af de vigtigste elementer i IPM. Derfor er behov for at undersøge hvordan og hvor meget kan vi reducere bekæmpelsesindsatsen i mere resistente sorter uden at det går ud over dyrkningssikkerheden. IPM2.0 er et koncept som forsøger at udnytte viden om sorternes resistens ovefor forskellige skimmelracer. Princippet er at man starter behandling i de mere resistente sorter når skimmel findes i en gruppe af differential sorter (kendte resistensgener), som modsvarer den restens, som er i den sort som undersøges. Hermed kan man udskyde den indledende forebyggende bekæmpelse. Efter start af behandling bekæmpes efter et beslutningsstøttesystem som på basis af smittetryk, sortsresistens og vejrbaseret infektionstryk beregner dosis af kendte forebyggende fungicider. For at teste dette princip blev der anlagt et KAF finansieret forsøg ved Flakkebjerg i 2018, med anvendelse af sorterne Kuras (modtagelig), Novano (middel modtagelig) og Nofy (mere resistent). Første behandling efter IPM2.0 blev foretaget den 13. August (54 dage efter start af rutine behandling). Sygdomsniveauet i ubehandlet var ved forsøgets afslutning (17 September) 85% i Kuras, 91% i Novano og ca. 1% i Nofy. I behandlede led var angrebet 4-6% i Kuras og under 1% for Novano og Nofy. I Kuras blev der efter IPM2.0 behandlet 6 gange heraf en gang stopsprøjtning med Proxanil. Dosis af de øvrige behandlinger varierende afhængig af infektionstrykket. Totalt BH var 5.75. Man kunne i dette forsøg reducere fungicidforbruget med 28% i forhold til ugentlige behandlinger med 50% dosis fungicid. I Novano og Nofy var den tilsvarende reduktion 35%. I Nofy blev der observeret under 1% sygdom ved sidste bedømmelse. I behandlede led var angrebsgraden ca 0,5%. Skal man så slet ikke behandle Nofy? I IPMBligt2.0 konceptet arbejder man med begreberne ”Gene Stewardship” og ”Active ingredient Stewardship”. Det betyder at skal beskytte resistens generne men også aktivstofferne. Man anvender fungicid i meget resistente sorter hvor de er mest ”presset” og under højt infektionstryk. Samtidig bruger man kun aktivstofferne efter behov samtidig med at anvendelsen af resistente sorter holder smittetrykket lavt. Dermed reduceres risikoen for at *P. infestans* udvikler resistens overfor aktivstofferne såvel som tilpasser sig sorternes resistens. Aktivstofferne og resistensen passer så at sige på hinanden i et partnerskab.

Projekts formål, baggrund samt faglige forløb.

I stivelses produktionen er der nye og mere resistente sorter på vej ind på markedet. De nye sorter er mere resistente mod skimmel og giver potentielt mulighed for at reducere bekæmpelsesindsatsen. Der er behov for at undersøge forskellige bekæmpelsesstrategier i mere resistente sorter dvs. hvordan og hvor meget kan vi reducere bekæmpelsesindsatsen uden at det går ud over dyrkningssikkerheden. IPMBlight2.0 er et ERA-NET projekt som AU deltager i. Målet er netop at give anvisninger om nye måder at reducere pesticidforbruget ved brug af IPM. IPM2.0 er et koncept som forsøger at udnytte mere viden om interaktionen mellem patogenet og værten. I forsøgssammenhæng betyder det at strategiforsøget anlægges sammen med eller tæt på et ubehandlet sæt af ca. 20 differential-sorter, hvor resistensen er kendt for de fleste af sorterne. Behandling i de mere resistente sorter skal først starte når skimmel findes i en gruppe af differential sorter som modsvarer den restens som er den eller de sorter som er i forsøget. Hermed spares kemi ved at udskyde indledende bekæmpelse. Efter start af behandling bekæmpes efter Skimmelstyring, et beslutningsstøttesystem som på basis af smittetryk, sortsresistens og vejrbaseret infektionstryk beregner dosis af kendte forebyggende fungicider (typisk en kombination af Revus og Ranman). Der blev anlagt et KAF finansieret forsøg ved Flakkebjerg i 2018.

Metode

I forsøget indgik tre sorter – Kuras, Novano og Nofy, og der blev udført tre behandlinger – 1) ubehandlet, 2) efter rutine med ugentlige behandlinger med halv dosis Ranman eller Revus og 3) efter IPMBlight2.0 konceptet.

Start af behandling var ved rækkelukning for Rutinebehandling og når skimmel blev fundet i differential-sorterne i IPMBligt2.0 leddet. Dosis er beregnet med Dosis modellen som er en delmodel i Skimmelstyring, som omformer vejrbetinget infektionstryk til en anbefalet dosis afhængig af bl.a. smittetryk og sortsresistens.

Resultater

Vejret var i 2018 ekstremt tørt og varmt. Den vejrbetingede risiko for sygdomsudvikling beregnet med Skimmelstyring (infektionstrykket) var generelt meget lavt indtil ca. 10. August (fig. 3). Skimmel blev observeret i Trap nursery den 8. August. I forsøget blev skimmel først observeret i ubehandlede parceller den 20. og 21. August Tabel 1. De sidste bedømmelse er den 14-17. september. Der blev lavet en ekstra sygdomsbedømmelse, 24 September, men da planterne samtidig var i kraftig afmodning er denne bedømmelse ikke taget med. Første behandling blev foretaget efter rutine ved rækkelukning den 20 Juni. Der blev observeret skimmel i modtagelige og mere resistente sorter i trap nursery den 8 August (Black R3; Black R6; Black R7; Alouette og Coquine) og IPMBlight leddet skulle være behandlet denne dag. Første behandling efter IPMBlight2.0 blev foretaget den 13. August (54 dage efter start af rutine). Da IPMBligt2.0 blev behandlet første gang 5 dage for sent blev der foretaget en stopsprøjtning med Proxanil 2.0 (Tabel 2). Der blev foretaget en stopsprøjtning i Kuras den 12 September fordi der blev observeret aktiv, sporulerende skimmel her (ikke i de andre to sorter).

Sygdomsniveauet i ubehandlet var ved forsøgets afslutning (17 September) 85% i Kuras, 91% i Novano og ca. 1% i Nofy. I behandlede led var angrebet 4-6% i Kuras og under 1% for Novano og Nofy. Der er ingen statistisk forskel mellem resultaterne for IPMBlight2.0 og Rutine. I Kuras er der behandlet 13 gange primært med 50% Revus og Ranman, en stopsprøjtning med Proxanil. Total BH er 8,0. I Kuras blev der efter IPMBlight2.0 behandlet 6 gange heraf en gang stopsprøjtning med Proxanil. Dosis af de øvrige behandlinger varierede afhængig af infektionstrykket. Totalt BH er 5.75. Man kan i dette forsøg reducere fungicidforbruget med 28% i forhold til ugentlige behandlinger med 50% dosis fungicid. I Novano og Nofy er den tilsvarende reduktion 100 – (4,25/6,5) *100 = 35%. Det skal bemærkes at kun de færreste avlere bruger 50% dosis i ugentlige intervaller som standard behandling. Derfor er reduktionspotentialet i 2018 sandsynligvis større.
I Nofy blev observeret under 1% sygdom ved sidste bedømmelse. I behandlede led var angrebsgraden ca 0,5%. Skal man så slet ikke behandle Nofy? I IPMBligt2.0 konceptet arbejder man med begreberne ”Gene Stewardship” og ”Active ingredient Stewardship”. Det betyder at vi skal beskytte resistens generne men også aktivstofferne. Man anvender fungicid i meget resistente sorter hvor de er mest ”presset” – sidst på sæsonen (resistensen er vigende) og under højt infektionstryk. Samtidig bruger man kun aktivstofferne efter behov samtidig med at anvendelsen af resistente sorter holder smittetrykket lavt. Dermed reduceres risikoen for at *P. infestans* udvikler resistens overfor aktivstofferne såvel som tilpasser sig sorternes resistens. Aktivstofferne og resistensen passer så at sige på hinanden i et partnerskab.

Tabel 1. Dato for hvornår skimmel er observeret første gang i tre sorter i ubehandlet led. Sidste bedømmelse er 17 September. Herefter er soterne gået ind i afmodningsfasen og forsøget er standset.

Sort	Første skimmel observeret			Sidste bedømmelse
	Ubehandlet	IPMBlight2.0	Rutine	
Kuras	21 August	21 August	28 August	17 September
Novano	21 August	21 August	21 August	17 September
Nofy	20 August	29 August	29 August	14 September

Tabel 2. Første og sidste behandling i tre led, Ubehandlet, efter rutine med ugentlige behandlinger fra rækkelukning samt efter IPMBlight2.0 hvor behandling starter når skimmel findes i Trap Nursery i tilsvarende sæt af differential sorter som sorterne i forsøget. BH = Behandlings Hyppighed

Behandling	1. behandling	Sidste behandling	BH		
			Kuras	**Novano**	**Nofy**
Ubehandlet	-	-	0	0	0
IPMBligt2.0	13 August	12 September	5,75*	4,25*	4,25*
Rutine 0,5	20 Juni	12 September	8	6,5	6,5

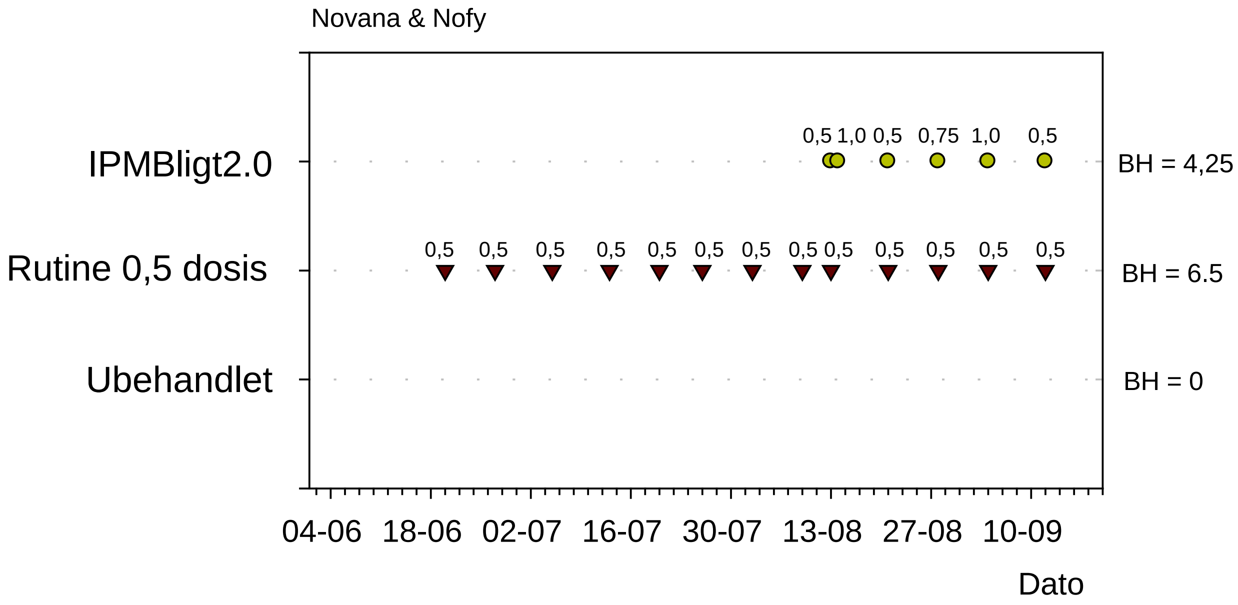
*ekstra stop behandling i alle tre sorter med Proxanil 2,0 den 14 August fordi skimmel var fundet i Trap nursery den 8. August (indikerer start af behandling)

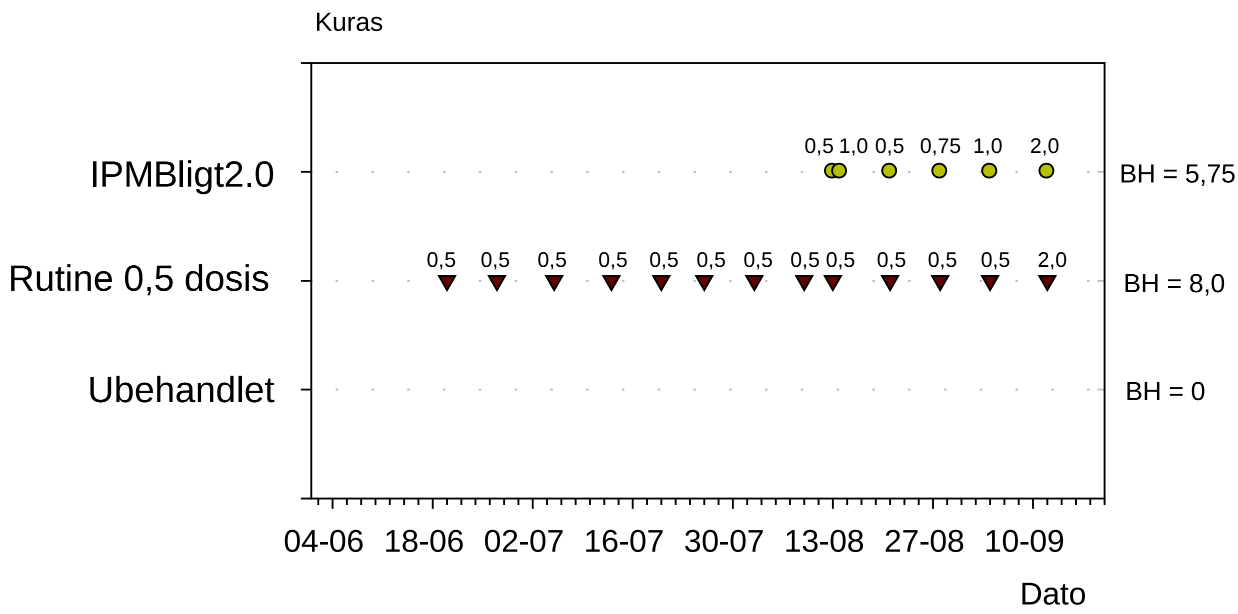
Tabel 3. Knoldskimmel [%]

Behandling	Knoldskimmel		
	Kuras	**Novano**	**Nofy**
Ubehandlet	2,3	7,5	0,3
IPMBligt2.0	0,3	0	0
Rutine 0,5	0,5	0	0
LSD	*2,29*	*0,58*	*0,5*

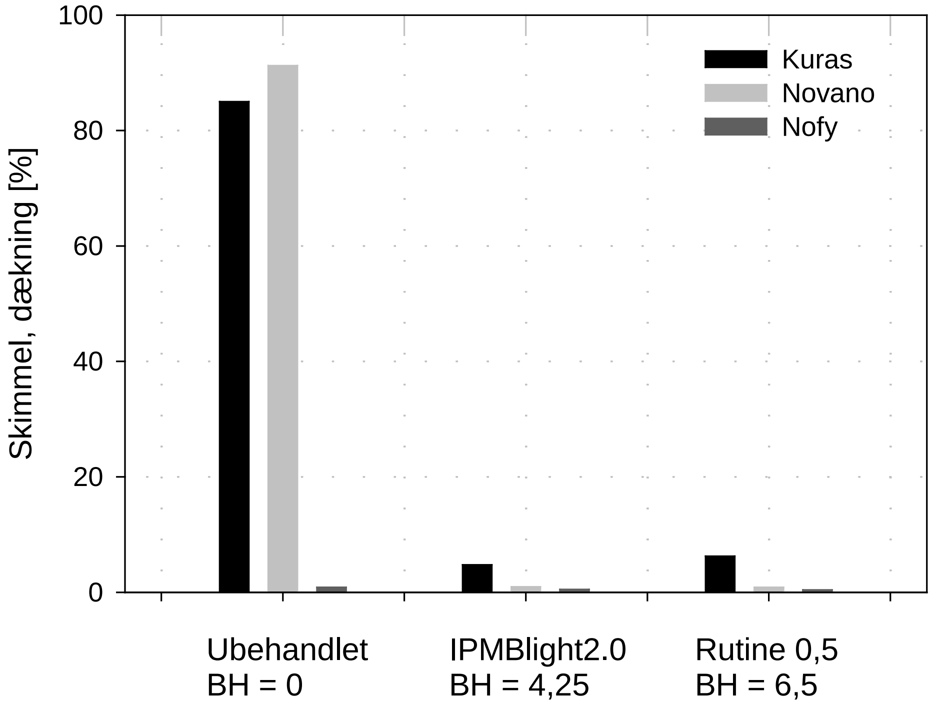
Tabel 4. Udbytte [hkg/ha]

Behandling	Knoldskimmel		
	Kuras	**Novano**	**Nofy**
Ubehandlet	561	416	843
IPMBligt2.0	615	455	863
Rutine 0,5	634	462	850
LSD	*60*	*47*	*31*

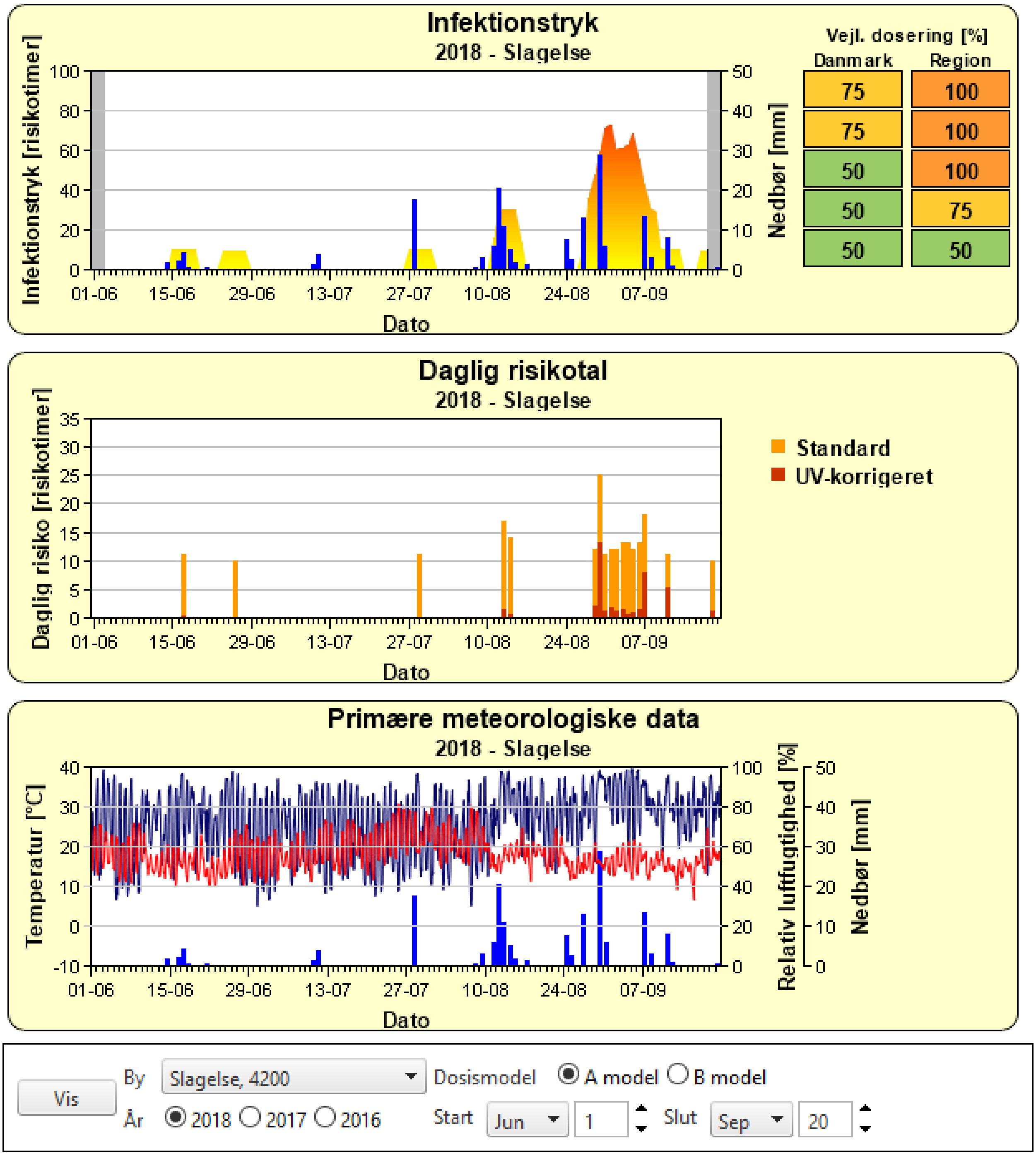




Figur 1. Øverst: Dato og dosis for sprøjtning med Revus/Ranman i sorterne Novano og Nofy. Stopbehandling med Proxanil den 14 August fordi behandling skulle være startet den 8. August. Nederst tilsvarende for Kuras.



Figur 2. Skimmel [% dækning] den 17. September i sorterne Kuras, Novano og Nofy behandlet efter hhv. Ubehandlet, IPMBlight2.0 og Rutine med ugentlige behandlinger, afveksling mellem Revus og Ranman i halv dosis (50%)



Figur 3. Infektionstrykket ved Slagelse fra 1 Juni til 20 September 2018. Infektionstryk, Lavt: 0-20, Moderat: 20-40 og Højt: >40

Konklusion

Forsøget viser at der er et stort potentiale i at udnytte sorternes resistens i den forebyggende bekæmpelse af kartoffelskimmel. Sorternes resistens er ikke stabil, fordi *P. infestans* som er årsagen til kartoffelskimmel kan tilpasse sig sorternes resistens (som det er sket i Kuras). Derfor er man nødt til at overvåge stabiliteten af nye sorters resistens og ændre bekæmpelsesstrategi når resistensen er vigende. Danmark samarbejder med mange lande via EuroBlight om at videreudvikle disse strategier, men også at medvirke til de overvågningssystemer som er vigtige elementer af IPM.

Formidling

Resultaterne er formidler via diverse møder, og resultaterne har indgået i ansøgning til GIDP om udvikling af BlightManager. Dette projekt blev bevilliget 13 mill Dkr.

- Kartoffelworkshop, december 2018
- Indlæg på avlermøder mv., vinter 2018-2019
- Rapport på AU hjemmeside
- EuroBlight Workshop York 12-15 May 2019

Funded by the
European Union

C-IPM

Coordinated Integrated Pest Management in Europe

Grant agreement no.: 618110

Final report

IPMBlight 2.0

April 2016- March 2019

9 November 2021

C-IPM

Funded by the European Union

Project information

Project acronym:	IPMBlight 2.0	Project ID:	28
Project title:	IPM2.0 for sustainable control of potato late blight - exploiting pathogen population data for optimized Decisions Support Systems		
Project website (if existing):	http://euroblight.net/research-projects/ipmblight20/		
Start of project: Duration in months:	April 2016 36	End of project:	March 2019

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1) University, Public research centre, Private research centre, Company, Other

2) PC = Project coordinator, WPL = Work package leader, WPCL = Work package co-leader, TL: task leader; P = Participant

Short description on the elaboration of the proposal (earlier projects this project is based on, involvement of end users/farmers/other stakeholders in the design of the project)

Late blight, caused by *Phytophthora infestans*, remains the major threat to potato crops in Europe, and a main reason for pesticide use. Despite the release of resistant cultivars and the implementation of modern DSS operated from web platforms or mobile apps, integrated management of late blight still relies heavily on many fungicide applications (up to 25 per season in some regions). The need is thus obvious to develop strategies that take full advantage of alternative options for more sustainable crop protection and better fungicide stewardship.

To be sustainable and implemented efficiently, such strategies must be tailored to the variability of *P. infestans* populations and their rapid evolution – 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. IPMBlight 2.0 aims at validating the IPM 2.0 concept, with potato late blight as a case study. To this end, it analyzes genotypic (WP1) and phenotypic (WP2) variation in reference collections of the pathogen sampled from partner countries, and 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.

The project arose from the priority setting, issued as Statements from the 2015 Euroblight workshop (http://euroblight.net/fileadmin/euroblight/Workshops/Brasov/EuroBlight_Statement_Brasov_25_6.pdf) and monitoring activities carried out within EuroBlight, and complements them by providing critical, but currently unavailable phenotypic data. EuroBlight is a large collaborative network of scientists, breeders, agrochemical industries, DSS developers and extension specialists dedicated to improved blight control, which has been active for over 20 years. IPMBlight 2.0 uses the IT platforms and population typing protocols, developed and validated within EuroBlight, to generate and disseminate original data and analyses on pathogen evolution, improved open-source DSS models and to establish a reference network of laboratories able to track new emergences within European *P. infestans* populations. Through its international links, IPMBlight 2.0 will also provide updated information regarding the connections between European and global populations of the late blight pathogen.

Outputs - results of the activities undertaken in the project

IPMBlight 2.0 started in April 2016, and yielded some major results:

- The sampling of populations of *P. infestans* in partner countries allowed to detect three new and emerging clonal lineages, among which one (EU_37_A2) was already present in several countries (France, UK, and Benelux). The phenotypic characterisation of some isolates from this lineage suggests that it is less sensitive than earlier clones to fluazinam. The other two emerging clones were EU_36_A2, a highly aggressive lineage, and EU_41_A2, invading sexual populations of the pathogen in Scandinavia, with the ability to overcome most race-specific resistance genes present in current European cultivars and high aggressiveness to susceptible potato breeds.
- The typing of the reference collection of isolates established from the 2016 and 2017 samples shows a large variation for all phenotypic traits analysed (virulence, aggressiveness to reference cultivars and sensitivity to major late blight fungicides);, occurring both between and within pathogen lineages. This particular distribution of phenotypes makes it possible to identify broad phenotypic profiles from SSR genotyping, but not an accurate prediction of isolate individual traits based on their SSR fingerprints.
- Major modules from existing DSS have been coded into MatLab, allowing for analysis of sensitivity and output comparisons with identical weather data sets. This analysis has shown on overall match between prediction of risk periods by the various models, but also consistent variations that can be of strong local importance for early season warnings and accurate risk forecast. The data from trap nurseries for epidemic monitoring, established across partner countries, proved valuable for late blight management during the season.

Technical workshop were held on phenotyping methods, and on modelling. Training periods of Ph.D students in partners' labs were also repeatedly carried out.

The project has been an important contributor of communications to the EuroBlight workshops held in Aarhus, Denmark in May 2017 and in York, UK in May 2019, as well as to the EAPR Triennial Conference held in Versailles, France in July 2017. Interactions with the Scientific Advisory Board during the four project meetings have been very fruitful, and open ideas for a more accurate dissemination of the project outputs to stakeholders as they become available.

Main results, conclusions and fulfilment of objectives by Work Package

<u>Note</u> : Since IPMBlight 2.0 has been designed from the start as a fully collaborative project, it is difficult (and probably inaccurate) to describe activities and achievements per individual partner. In this report, we will therefore mention the main achievements and deviations from original plan as collective activities of partners involved, and simply identify contributing partners by their respective project numbers.

WP0	**Coordinating and disseminating IPMBlight 2.0**
WPL: D. Andrivon (P1)	
Overall summary of main results and conclusions WP0 WP0 aimed at running the project from administrative, logistic and dissemination standpoints.	

The project was successfully launched in April 2016. Contracts with all national funding bodies were signed, although some were late due to delays and difficulties in establishing a Consortium Agreement accepted and signed by all partners.

Four project meetings were held: a kick –off meeting in Paris France, hosted by INRA (April 2016), a first-year general meeting in Foulum, (Denmark) just after the Euroblight workshop in Aarhus, hosted by Aarhus University (May 2017), a second-year general meeting in Oslo, hosted by NIBIO (May 2018), and a project final meeting next to the Euroblight workshop in York (May 2019). Many web meetings were held between WP leaders or project participants, thanks to the IT platform made available by Aarhus University.

A web site was established by Aarhus University (AU) as soon as the project started. It consists of both an Internet public interface, accessible through the EuroBlight platform for extra visibility, and an Intranet, accessible through login and password to all project members, and containing both a project management tool and document repository. This website is very efficient, and regularly updated.

An Advisory Board was established, and met with project members during each project meeting. The AB issued written recommendations that were used by the project leaders to assist in the project management.

Task by task report

Task 0.1: Project operation
Lead partner: P1; Contributing: all

A- Results obtained:

The project was successfully launched in April 2016, during a 1.5 day kick –off meeting attended by all partners in Paris, France. Two interim project meetings, one and two years after the project started, were held in Foulum, Denmark in May 2017, immediately following the EuroBlight workshop in Aarhus, and in Oslo in May 2018. Both meetings were dedicated to a review of plans and activities, and decisions /adjustments were made on any specific issue that needed corrective measures. A final meeting was held in York (May 2019), to review the data generated during the project, finalise the dissemination strategy of these results, and prepare the final report.

Overall, the scientific operation of the project was very satisfactory, despite some administrative delays (P3, P7, see Task 0.4 for more details) and staff changes (P4) for some project partners.

B- Comments on deviations from original plan:

Prof. Eve Runno-Paurson, decided, for personal reasons, to resign her position at EULS early in 2017. Prof. Runno-Paurson was the appointed leader of WP2; her resignation prompted several changes in the project operation:

- The transfer of WP2 leadership to Dr Roselyne Corbière (P1) was proposed and accepted during the meeting in Foulum;

- The administrative responsibility of the project at EULS (P4) was transferred to Prof. Marika Mänd (a specialist of pollinator biology, not of plant pathology), of the same Department as Prof. Runno-Paurson.
- The operational responsibility for IPMBlight2.0 activities at EULS rested primarily on Mrs Britt Puidet and Mrs Riinu Kiiker, two PhD students working mainly or partly on this project. The work programme remained unchanged, as well as the distribution of tasks between partners. Several project partners, especially P1, P3 and P8, assisted Mrs Puidet's in the supervision of her Ph.D work.
- During the last year of the project, Isaac K. Abuley replaced Bent J Nielsen after his retirement at Aarhus University.

Task 0.2: Advisory Board
Lead partner: P1

A- Results obtained:

The project Advisory Board, composed of Dr Jadwiga Sliwska (plant breeding, Poland), Dr Ragnhild Naerstad (*P. infestans* epidemiology and management; former researcher at NIBIO, now with Syngenta, Norway), Dr Albert Shirring (plant protection systems and policy; Bayer Crop Science, Germany) and Dr Geert Kessel (*P. infestans* population genetics and management; WUR, The Netherlands) was successfully established between the acceptance and the actual launch of the project (P1). The Advisory Board met, together with the project members, during all project meetings. The role of the Advisory Board was to provide advice and feedback from stakeholders and potential users of the projects outputs, that the project members could exploit throughout the operation of the project.

The Advisory Board issued, after each meeting, a set of written comments and recommendations that project members can use. These documents were made available to all project members through the project intranet.

The help of advisory board members for the validation and confirmation of some of the experimental data is also gratefully acknowledged.

B- Comments on deviations from original plan:

No deviation from original plan.

We are very thankful to Advisory Board members for the time they devoted to helping us asses and manage the project, and for their very insightful and constructive recommendations.

Task 0.3: Internal communication
Lead partner: P2; contributing : all

A- Results obtained:

A project website, containing both an Internet portal and a login/password protected Intranet dedicated to project management, data exchange and storing from and between partners, was established as soon as the project started (April 2016; P2). Both were, and still are, accessible through the EuroBlight web platform, and were regularly updated.

Partner P2 also made available an easy to use, flexible web communication system for informal bilateral or multilateral meetings. This proved very handy for preparation of workshops, seminars and meetings, and is used frequently by project members for bilateral exchanges.

B- Comments on deviations from original plan:

No deviation from original plan.

Task 0.4: IPR and contractual issues
Lead partner: P1; contributing : all

A- Results obtained:
The consortium agreement and all bilateral contracts between partners and their national funding bodies were sign in September, 2017.

B- Comments on deviations from original plan:

The preparation and final signing of the Consortium Agreement took much longer than expected: this task could only be terminated in September 2017, after almost 17 months of iterations between partners on successive versions of the CA draft. The delays were due to differences in appreciation between countries on specific provisions of the CA, as well as by staff movements in some participating institutions which retarded the negotiations.

An unfortunate consequence of this was the late availability of national funds to our Norwegian partners (P3 and P7), since the Norwegian national funding agency requires a Consortium Agreement signed by all partners to liberate the funds. Despite this, partners P3 and P7 fully contributed to the tasks they committed to during the first year of the project – many thanks to them!

Finally, there was a change in the status of partner P7, which was taken into account during the negotiations for the consortium Agreement. P7 is now a subcontractor of P3, rather than a full partner of the project. This change, acted upon request of partner P7, was agreed by P3 and by the national Norwegian funding body.

Task 0.5: Reporting
Lead partner : P1; contributing : all

A- Results obtained:

Minutes /decisions from each project meeting were produced and distributed to all project members through the project Intranet.

The mid-term report requested by C-IPM was produced in due time and sent, as requested, to C-IPM coordinators by P1, and to the national funding bodies. No comments were received regarding this report.

The present document is the final project report.

B- Comments on deviations from original plan:

While we initially proposed to produce annual reports, we later realised that this was not matching C-IPM requests (*i.e.*, one mid-term report after 18 months and one final report at the end of the project). We therefore choose to adjust our reporting scheme to match C-IPM requirements.

The production of the final report was postponed by four months relative to the originally planned date (March 2019), so that this document could reflect also the latest decisions made during the final project meeting, held next to the 17th EuroBlight workshop in York (12-15 May 2019).

WP1	**Monitoring European *P. infestans* populations**
WPL: D. Cooke (P8)	

Overall summary of main results and conclusions WP1

WP1 aimed at sampling, isolating, genotyping and storing reference isolates from partner countries. It was carried out as a complement to the EuroBlight monitoring, which covers extra countries but does not provide phenotyping information (only DNA is collected and used for genotyping within this large survey).

The sampling covered the 2016 and 2017, to allow for the genotyping and phenotyping activities to be carried out within the project. A reference collection with isolates from 2016 and 2017 of 170 isolates from all partner countries was established, genotyped and stored as planned. It was distributed to partners involved in the phenotyping activities (WP2). The genotyping confirmed the clonal structure of *P. infestans* in the UK and France, and the presumably sexual structure of Nordic populations.

Within clonal populations, the SSR genotypes showed the now widespread distribution and rapid increase in frequency of three new lineages (EU_36_A2 and EU_37_A2), suggesting that these emerging genotypes might become invasive. This invasive ability was confirmed through the general EuroBlight survey, as well as additional genotyping conducted in 2018 by project members (P1 and P8). Well established lineages, mainly EU_13_A2 and EU_6_A1, however remained dominant in both countries.

A significant finding was the emergence within Nordic populations of a new clonal lineage, designated EU_41_A2. This lineage proved invasive, and spread from Denmark to Norway and neighbourging Sweden and Poland during the course of the project. The establishment of a clonal lineage in these predominantly sexual populations represents an unexpected and major change in the genetic structure of local *P. infestans* populations in these areas (EU_41_A2 was found in Finland and Germany in 2019, indicating its high invasive potential)

Task by task report

Task 1.1: Sampling isolates in DK, EE, FR, and NO.
Lead partner: P8; contributing : all

A- Results obtained:

Both DNA (as prints on FTA cards) and live samples were obtained from all partner countries, including UK, in 2016 and 2017. The distribution of live isolates retained for phenotypic analysis, according to genotypes and origins, in 2016 and 2017 are indicated in the tables below.

Genotype	France	UK	Norway	Estonia	Denmark	Total
1_A1	9	-				9
8_A1	-	4				4
6_A1	10	12				22
13_A2	14	13	2			29
37_A2	8	2				10
41_A2			6			6
« other »	-	7	29	40	6	82
Total	41	38	37	40	6	162

Genotype	France	UK	Denmark	Estonia	Norway	Total
1_A1	7	-	-	-	-	**7**
6_A1	12	10	-	-	-	**22**
8_A1	-	2	-	-	-	**2**
39_A1	-	3	-	-	-	**3**
13_A2	12	6	-	-	-	**18**
36_A2	-	4	2	-	-	**6**
37_A2	9	10	-	-	-	**19**
41_A2	-	-	8	-	4	**12**
« other »	-	5	31	40	38	**114**
Total	**40**	**40**	**41**	**40**	**42**	**203**

Table 1: Distribution of isolates collected in 2016 (above) and 2017 (below) and selected for phenotyping studies within IPMBlight.

B- <u>Comments on deviations from original plan</u>:

UK samples were collected together with those from ‘full partner’ countries. This addition allowed us to substantially increase the number of populations and genotypes compared and typed within this project. In Denmark, more than 80 isolates were sampled live, to be sent to JHI at a later stage for genotyping. None of those samples did grow in pea agar plates, and still we have no explanation even this is a well-known and documented method.

Task 1.2: SSR genotyping
Lead partner: P8; contributing : P1

A- <u>Results obtained:</u>

The SSR genotypes identified from the live sample collection established by IPMBlight partners, as well as from extra FTA cards collected by the same:

- confirmed the clonal structure in French and UK *P. infestans* populations, and the presumed sexual structure of Nordic populations;
- showed the persistent presence of recent major clones (EU_13_A2 and EU_6_A1) in clonal populations;
- revealed the emergence and expansion of several new clones, most notably EU_36_A2, EU_ 37_A2 and EU_41_A2 (Figure 1). The frequency of these clones, first detected in 2013-2014 but then each restricted to a very limited geographical area, sharply rose since 2016 - in France and UK, as well as in some neighbouring countries (Benelux) for the first 2, in Scandinavia for the third one as shown by the EuroBlight survey.

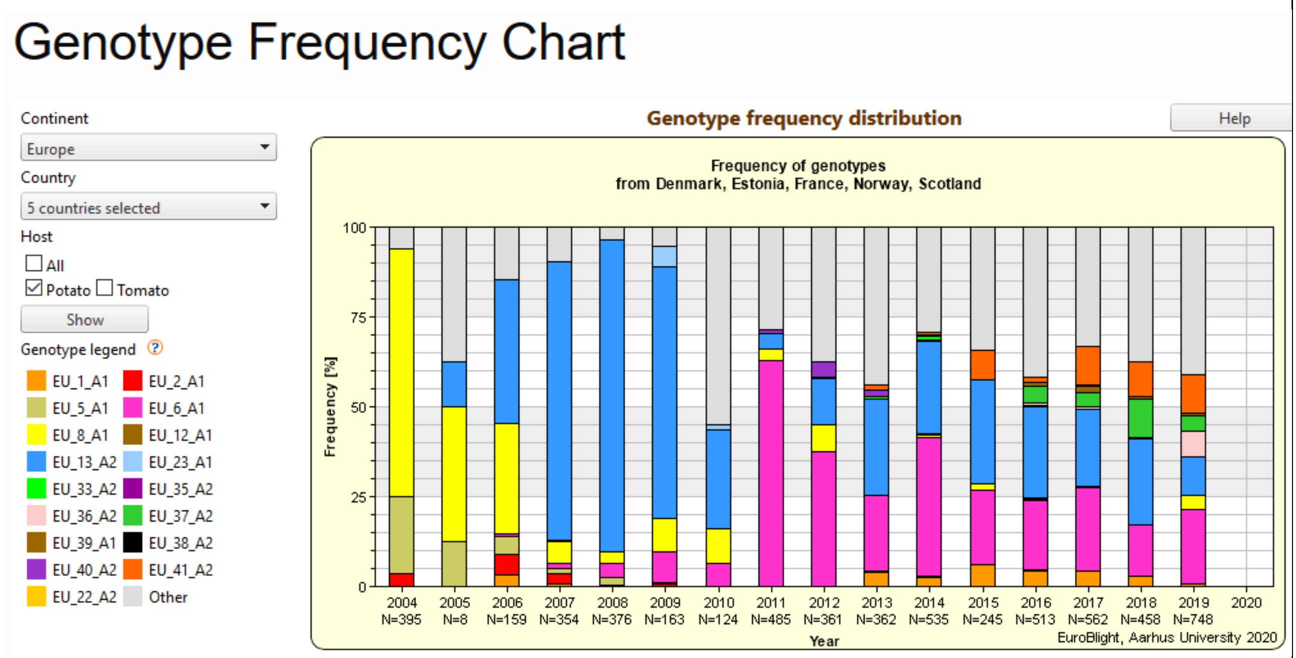

Figure 1. Genotype distribution in European populations of the potato late blight pathogen Phytophthora infestans (data EuroBlight.net). Each colour corresponds to a clonal lineage, except the grey fraction of each bar which corresponds to unique isolates (called 'other'). The frequency of this last group seems to be stable at 25-30% across EuroBlight samples. The frequency of the once dominant EU-13_A2 remained stable at about 20 % of European samples 2013-2018, whereas that of the new clones EU_41_A2, EU_36_A2 and EU_37_A2 sharply rose since 2013 and 2014 respectively.

B- <u>Comments on deviations from original plan:</u>

Although the initial project involved Norway (P3) in the genotyping activities, it was found more practical and efficient to split this task between two partners only, UK (P8) and France (P1); P1 handled the French and Norwegian samples, while P8 genotyped those from the remaining countries.

Task 1.3: Establishing and storing reference collections
Lead partner: P3

A- Results obtained:

Isolates selected based on SSR profiles (task 1.2; table 1) were purified, stored as live cultures on agar slants and liquid nitrogen, as well as spore suspensions. The collection represents 365 live cultures. It was not considered useful to supplement it with extra isolates. All isolates in the collection were distributed to partners engaged in WP 2 for phenotyping.

B- Comments on deviations from original plan:
No deviation, except the additional storing mode as spore suspensions.

Task 1.4: Data storage, management and display tools, EuroBlight database
Lead partner: P2; contributing: P8, P1, P6

A- Results obtained:
Historical data have been transferred and implemented into the new EuroBlight database by Aarhus University.

B- Comments on deviations from original plan:
The display system and management tool for phenotypic data is ready to take the data from WP2. These data are pending due to quality control issues, but they will be added to the database during the autumn of 2019. The visualisation and analysis of the combined genotypic and phenotypic data by tools in the toolbox will be further developed in subsequent projects.

Task 1.5: Population genetics
Lead partner: P8; contributing: P2, P1

A- Results obtained:
Further developments to the POPPr R package have been made and implemented by Aarhus University. They allow a better analysis of polyploid data sets. More specifically, as regards IPMBlight2.0, the package allowed to unambiguously assign new genotypes and variants within clonal populations to new (EU_37_A2) or more ancient lineages (EU_13_A2, EU_6_A1, EU_1_A1; Fig. 2), and to show the limited number of genotypes shared between countries. This is certainly due to the prevalence of 'other' isolates in the Baltic and Nordic countries, and the restriction of EU_41_A2 to Denmark and Norway, and the higher frequency of EU_37_A2 in UK than in French samples collected (Fig. 3).

B- Comments on deviations from original plan:
The use of the improved package to analyse historical data sets has started, but the draft paper planned as Del 1.5.2 is not ready yet, so the production of this deliverable will be delayed relative to the original plan.

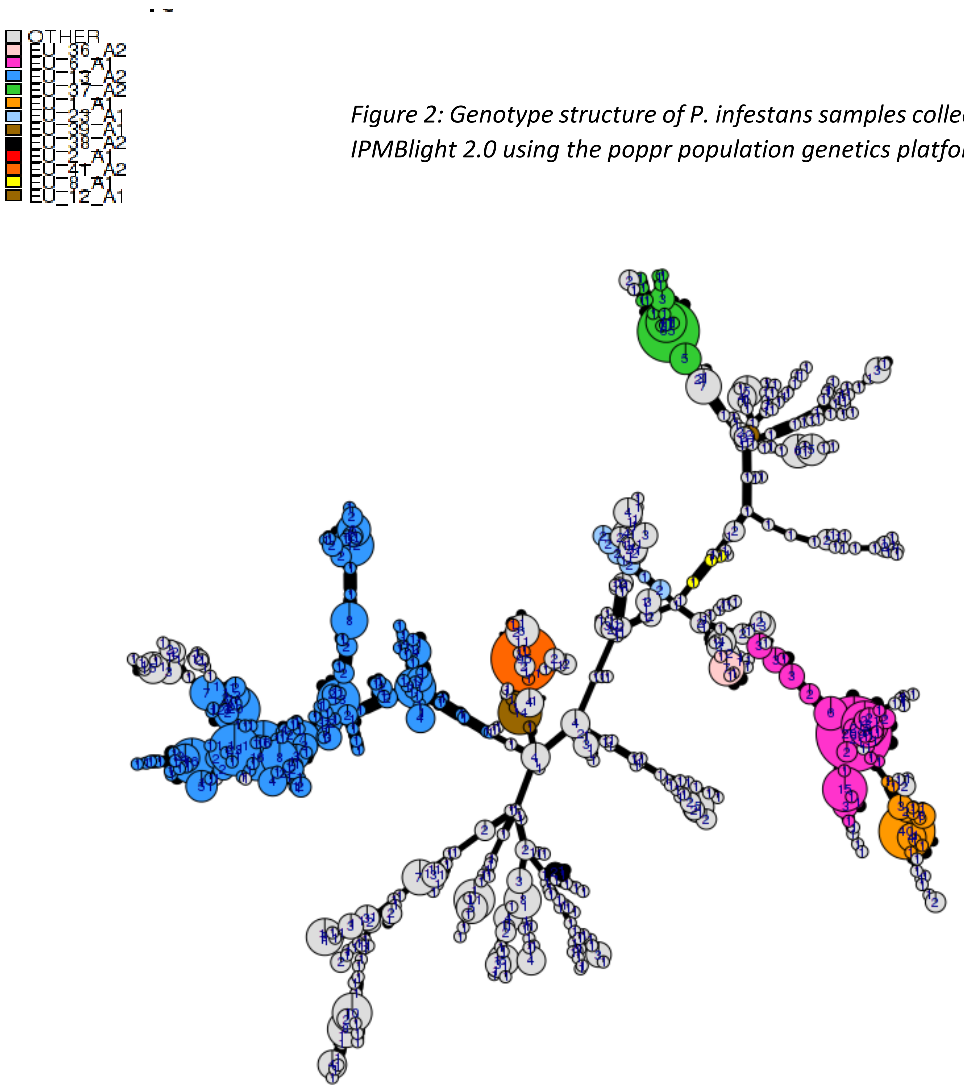

Figure 2: Genotype structure of P. infestans samples collected during IPMBlight 2.0 using the poppr population genetics platform at AU

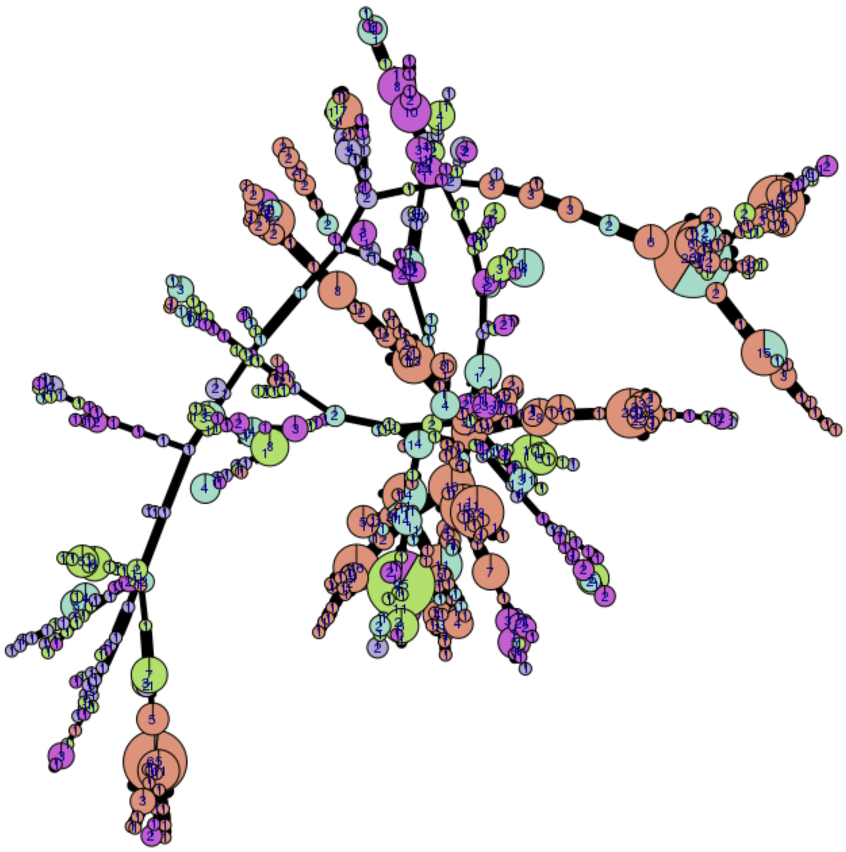

Figure 3. Genotype distribution of IPMBlight 2.0 P. infestans isolates according to countries of origins.

Very seldom MLGs are shared among the five partner countries. A few examples are shared MLGs between Denmark and Norway and between Scotland and France as expected. One example was found that Denmark and France shared one MLG for more than one sample.

WP2	**Linking phenotypes to genotypes**
WPL: E. Runno-Paurson (P4) ; transferred to R. Corbiere (P1) at Foulum meeting	
Overall summary of main results and conclusions WP2 The virulence, aggressiveness and fungicide sensitivity data collected suggest that isolates from sexual populations are less diverse for phenotypes than for genotypes, which may reflect the action of local selection on phenotypic traits but not on SSR (*a priori* neutral) markers. Conversely, substantial phenotypic variation was observed both between and within clonal lineages. Overall, these data tend to indicate that SSR profiles do not correctly predict individual phenotypes, although inter-clonal variation allows some rough estimates of phenotype differences according to molecular profiles. The data also show:	

- The occurrence of fluazinam insensitivity within several populations. This seems to be directly connected to the presence in these populations of the recent clonal lineage EU_ 37_A2 with strong epidemic potential;
- The high aggressiveness of isolates belonging to the EU_36_A2, and to a somewhat lesser extent EU_37_A2 and EU_41_A2 lineages;
- Highly diverse virulence profiles between isolates and genotypes. Lineage EU_41_A2 appears to have a highly complex virulence profile (*i.e.* the ability to overcome most or all resistance genes present in the 'historical' late blight set of differential hosts , as well as the resistance of some recent cultivars such as Kelly). However, the data from in–field trap nurseries do not always match those of detached-leaflet bio-tests, in particular with some highly resistant cultivars in the field such as Sarpo Mira.

Together, these data suggest the existence of rather different biological profiles among the three new clones: a highly aggressive, moderately virulent and fungicide sensitive one (EU_36_A2), a fluazinam –resistant, moderately aggressive and moderately virulent one (EU_37_A2), and a highly virulent, highly aggressive, fungicide sensitive one (EU_41_A2).

Task by task report:

Task 2.1: Intra/interclone variation for aggressiveness
Leader: R Corbière (P1)

A- Results obtained**:**

The 365 isolates selected based on genotypes were tested for aggressiveness on the susceptible cv. Bintje. We measured four traits: latent period, lesion size 5 days after inoculation, spore production 5 days after inoculation and spore size. An internal control was included in all batches for calibration purposes.

The data are not fully analysed yet, but suggest that extensive variation for aggressiveness is present within clones. The dominant clonal lineage EU_13_A2 is among the least aggressive under our test conditions, while the emerging clone EU_36_A2 is among the most aggressive (comparable to EU_6_A1, well established in France and the UK).

Conversely, the distribution of aggressiveness among isolates from sexually reproducing populations is not as large as their genotypic variation. These populations contain however both weakly aggressive and highly aggressive isolates.

Year to year variation in aggressiveness levels within each lineage was also detected, with a trend to a general decrease in aggressiveness in the 2017 samples compared to 2016 ones, without altering the relative ranking of lineages. The reasons for this observation are still unclear.

B- Comments on deviations from original plan:

No deviation.

Task 2.2: Intra/interclone variation for fungicide resistance.
Leader : E Runno- Paurson (P4), transferred to H. Eikemo (P3) at Foulum meeting; contributing: P4.

A- Results obtained**:**

The tests involved the isolates from the reference collection. Cyazofamid and propamocarb were tested in Norway (P3), while fluazinam and mandipropamid were tested in Estonia (P4). The data, presented during the Euroblight workshops in Aarhus and York, confirm the recent publication by a Dutch group that EU_37_A2 isolates had a low sensitivity to fluazinam. fluazinam sensitivity in Europe is shifting towards less sensitive populations. By contrast, no major change in the sensitivity to the other three compounds was detected.

As for aggressiveness, there was a trend towards higher sensitivity to fluazinam in the 2017 than in the 2016 samples. This trend might be related to the development of new genotypes, to intra-clonal selection of more or less sensitive individuals within lineages, or to selective responses to shifts in fungicide pressure. The statistical robustness of this observation however needs additional analyses, currently underway, as each lineage was represented by a different, and sometimes low, number of isolates.

Overall, and although different methodologies were used, the results obtained within IPMBlight2.0 are in line with reports from other research work carried out outside the project over the same period.

B- Comments on deviations from original plan:
No deviation.

Task 2.3: Intra/interclone variation for virulence.
Leader: E Runno- Paurson (P4), transferred to Catherine Chatot (P7) at Foulum meeting; contributing: P4

A- Results obtained**:**

An extended set of differential hosts was successfully designed and used. It contains the 'historical' clones with *S. demissum* genes (R1-R11), susceptible and partially resistant conrols (Bintje and Robijn, respectively), and recently released cultivars with high levels of (presumably) race–specific resistance : Sarpo Mira (complex pyramid if R genes, including at least *Rpi-Smira 1*, *Rpi-Smira 2, R8*, and presumably at least two other R genes), Carolus, Toluca (*Rpi-Blb 2*), Alouette (*Rpi-vnt1*) , Kelly (*R8*) and Makhai.

This set was used to test virulence profiles of the 365 isolates in the reference IPMBlight2.0 collection using the detached leaftest bioassay validated by EuroBlight. The data are still under complete analysis, but show 1) as expected, a widespread breakdown of some 'historical' R genes (R1, R3, R4, R7, R10, R 11), 2) strong differences between and within clones for virulence to the remaining genes, 3) an apparently narrower virulence profile in some new clones (in particular EU_37_A2, which does not seem to overcome R2) compared to some older lineages such as the highly multivirulent EU_13_A2, 4) the ability of EU_41_A2 to overcome most of the genes in the differential set, and 5) the unexpected susceptibility of some new cultivars, including Sarpo Mira, in these biotests.

B- Comments on deviations from original plan:

No deviation.

Task 2.4: Trap nurseries and real-time P. infestans population virulence profiling.

Leader : C. Chatot (P7) ; contributing : all

A- Results obtained**:**

The same set of differential cultivars and clones was established in all partner countries in 2017 and 2018. Severity scores on all cultivars were recorded throughout the season (until end of September in some cases). All datasets are not entirely analysed yet, but a quick examination shows 1) differential expression of some resistances across sites and 2) a trend towards resistance breakdown at the latest dates. The field data do not always match the virulence frequencies from the isolates of the previous year, especially for some clones like Sarpo Mira which keeps a high resistance in the field but seems rather susceptible in virulence biotests on detached leaflets.

In some countries, trap nurseries were also established in 2016. The match (or lack of match) between 2016 and 2017 data will probably yield interesting information as to the stability of resistance within sites and the nature/selection of isolates.

Data management and analytical system was implemented on the Potato Late Blight toolbox. This will enable the estimation of type and level of resistance as well stability of resistance across countries and years. The system developed will be further elaborated to be used in subsequent projects, such as the on-going Danish BlightManager GUDP project. A publication on the system and results are in preparation.

B- Comments on deviations from original plan:

No deviation.

WP3	**Developing innovative DSS integrating epidemiological and population knowledge**
WPL: J.G Hansen (P2)	
Overall summary of main results and conclusions WP3 A comparative description of existing Late blight DSS operated in Europe was produced, and six of them were selected for further work. The algorithms were re-coded in MatLab, and tested with actual historical datasets for sensitivity analyses. These algorithms were made available as web tools for analysis with weather data from any weather station in Europe. The results of the analysis of the weather based sub-models for blight risk indicate that all models calculate high and low infection pressure at the same times during the season. There are differences especially during medium blight risk periods. It is concluded that differences among the complete DSSs are not the calculation of blight weather, but more the interpretation of blight weather into decision rules for spray or not spray, and choice of fungicide type and dosage.	
Task by task report: *Task 3.1 Develop a suite of simulation models for the integration of new data on pathogen information, host resistance and weather* *Leader: P3; contributing: P2, P1, P6, P7, P8;* A. Results obtained**:**	

Current European DSS were described and compared. The underlying equations were re-coded in MatLab to allow an in depth comparison using standard weather datasets provided by partners.

The test of weather data files showed that the quality of especially relative humidity is very variable. A quality routine was developed to analyse and conclude on quality of weather data.

By using data from two weather stations from six countries acroos 2014-2017 the project tested four hypotheses:

- Is there a seasonal effect of Blight risk?
- Is the Blight risk is different between regions?
- Is the Blight risk is different between years?
- does the estimation of Blight risk differs between models?

The results of these analyses was reported at the EuroBlight workshop in York and a peer-reviewed publication is in preparation.

B- Comments on deviations from original plan:

No deviation.

Task 3.2: Implement the simulation model (from task 3.1) as a web tool that can be used by all partners on the EuroBlight platform.
Leader: P3; contributing: P2

A- Results obtained**:**

The Matlab coded submodels were implemented on the Potato Late Blight Toolbox, and can be freely tested with own meteorological datasets by any interested users.

B- Comments on deviations from original plan:

No deviation.

Task 3.3: Adapt existing DSSs based on results from the simulation model.
Leader: P3; Contributing : P2, P8; P5, P6

A- Results obtained**:**

The Danish DSS was adapted to the IPMBlight2.0 approach and tested in a field experiment in 2018. The results were presented at the EuroBlight workshop in York, 2018.

B- Comments on deviations from original plan:

Original plan was also to change parameters in some of the models based on results from WP2 and make some simulations. Quality controlled data were not available early enough to make this part. Instead all phenotypic data are stored in the EuroBlight database for such analysis later.

Status of milestones and deliverables

These are shown in the screen captures from the respective tables, present as of July 2019 in the project intranet.

Milestones

All milestones have been reached in time.

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Milestones

= Completed = To be completed within next 6 months = Completion date expired

No.	Title	Completion date
M0.2.1	Advisory Board established	February 2016
M0.1.1	Kick Off meeting	April 2016
M0.2.2	Advisory Board meeting (together with kick-Off meeting)	April 2016
M1.1.1	Sampling protocol validated and distributed	May 2016
M1.2.1	Genotyping scheme decided and validated	June 2016
M2.2.1	Technical workshop : differential set and protocols for virulence, fungicide and trap nurseries	July 2016
M2.4.1	Differential host set obtained from Wageningen University Research and multiplied	October 2016
M3.1.1	Existing models and applications relevant for the IPMBligt 2.0 identified and evaluated	October 2016
M1.5.1	Technical workshop on data management analysis and display of genotypic & phenotypic data	November 2016
M0.2.3	Advisory Board meeting (with Euroblight Workshop)	May 2017
M0.1.2	Intermediate meeting (with Euroblight Workshop) Aarhus	May 2017
M0.3.1	IPMBlight 2.0 Presentations at Euroblight workshop	May 2017
M3.2.1	Technical workshop: Simulation model implemented as a web tool	October 2017
M3.2.2	Simulation model updated based on new data from the project	February 2018
M0.1.3	Final meeting	October 2018
M0.2.4	Advisory Board meeting (with final meeting)	October 2018

Milestone details

No.	M0.1.1
Title	Kick Off meeting
Completion date	April 2016
Responsibility	Didier Andrivon (Institut National de la Recherche Agronomique,)

Description	File	File size	Owner
Participant list		13135	Didier Andrivon (INRA)
Agenda and logistics		262494	Didier Andrivon (INRA)
Overview and coordination		2149347	Didier Andrivon (INRA)
Wrap-UP session		21449	Jens Grønbech Hansen (AU)

Deliverables

Funded by the European Union

IPMBLIGHT2.0

Intranet

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Deliverables

🟢 = Completed 🟡 = To be completed within next 6 months 🔴 = Completion date expired

	No.	Title (*Responsibility*)	Completion date
🟢	D0.3.1	Project web page established (*Didier Andrivon,Jens Grønbech Hansen*)	April 2016
🟢	D1.1.1	2016 sample collections on FTA cards and live samples complete (*David Cooke*)	September 2016
🟢	D1.4.1	Historical SSR data 2004-2012 quality controlled and imported into EuroBlight Database (*Jens Grønbech Hansen*)	September 2016
🟢	D1.4.2	Isolate information and SSR fingerprints 2016 inserted into Euroblight database (*Jens Grønbech Hansen*)	December 2016
🟢	D1.4.5	Virulence trap nursery data mananagement and display system in place for use in task 2.4 (*Jens Grønbech Hansen*)	December 2016
🟢	D1.5.1	Upgraded version of PoPPR platform (*David Cooke*)	December 2016
🟢	D3.1.1	System description of models and applications to be implemented on the EuroBlight platform (*Anne-Grete Roer Hjelkrem*)	February 2017
🔴	D2.2.1	2016 Fungicide sensitivity and virulence phenotypes determined and in Euroblight database (*Catherine Chatot,Roselyne Corbière,Britt Puidet*)	April 2017
🟢	D1.3.1	Reference collection established and stored (*Vinh Hong Le*)	April 2017
🟢	D1.3.2	Reference collection supplemented with additionnal isolates -if relevant (*Vinh Hong Le*)	April 2017
🟢	D2.1.1	Agressiveness measured for reference isolates from 2016 collections (*Roselyne Corbière*)	April 2017
🟢	D1.1.2	2017 sample collections on FTA cards and live samples complete (*David Cooke*)	September 2017
🟢	D0.3.2	Books of contributions to Euroblight workshop issued (*Didier Andrivon*)	October 2017
🟢	D0.4.1	Midterm Status Report to C-IPM (*Didier Andrivon*)	October 2017
🟢	D1.4.3	Isolate information and SSR fingerprints 2017 inserted into Euroblight database (*Jens Grønbech Hansen*)	December 2017
🔴	D1.5.2	Population genetic analysis of the European metapopulation 2004-2016 - peer reviewed paper (*David Cooke*)	January 2018
🟢	D2.4.1	2017 Virulence trap nursery data implemented and analysed (*Catherine Chatot*)	January 2018
🟢	D3.2.1	Simulation model implemented as a web tool incl. integration with all data from WP1 and WP2 (*Jens Grønbech Hansen*)	January 2018
🔴	D2.2.2	2017 Fungicide sensitivity and virulence phenotypes determined and in Euroblight database (*Catherine Chatot,Roselyne Corbière,Britt Puidet*)	April 2018
🟢	D2.1.2	Agressiveness measured for reference isolates from 2017 collections (*Roselyne Corbière*)	April 2018
🟢	D3.3.1	Existing national DSSs adjusted for IPM 2.0 approach (*Håvard Eikemo*)	April 2018
🟢	D1.1.3	2018 sample collections on FTA cards and live samples complete (*David Cooke*)	September 2018
🟢	D2.4.2	2018 Virulence trap nursery data implemented and analysed (*Catherine Chatot*)	October 2018
🟢	D2.1.3	Draft paper on phenotype/genotype comparison. (*Didier Andrivon*)	November 2018
🟢	D3.2.2	Draft paper about BlightIPM 2.0 modelling approach (*Jens Grønbech Hansen*)	November 2018
🟢	D1.4.4	Isolate information and SSR fingerprints 2018 inserted into Euroblight database (*Jens Grønbech Hansen*)	December 2018
🟢	D3.3.2	Draft paper on test of adjusted DSSs in national field experiments (*Håvard Eikemo*)	January 2019
🔴	D2.2.3	2018 Fungicide sensitivity and virulence phenotypes determined and in Euroblight database (*Catherine Chatot,Roselyne Corbière,Britt Puidet*)	March 2019
🔴	D0.4.3	Final Report to C-IPM (*Didier Andrivon*)	March 2019

Deliverable details

No.:	D0.3.1
Title:	Project web page established
Completion date:	April 2016
Responsibility:	Didier Andrivon (Institut National de la Recherche Agronomique), Jens Grønbech Hansen (Aarhus University)

The deliverables currently late concern primarily the inclusion of phenotypic data in the EuroBlight database, and are being completed now (see report above). Another late deliverable is the peer-reviewed paper on the EU population, which is currently being drafted following most recent analyses with the improved PoPPR tools. The final late deliverable is the submission of this report, which was postponed due to uneven official project starting/funding dates among partner countries.

Outputs of the consortium

Publications

- List of published scientific papers in peer-reviewed journals. Please indicate accessibility of the publication (Open Access, Thomson Reuters Web of Science, SCOPUS etc.)

  None yet (several in preparation for submission)

  - *Total number of items at this level*: 0

- List of non-peer-reviewed scientific publications, proceedings and books:

International conferences

20th Triennal Conference of European Association for Potato Research (EAPR), 9-14 July 2017, Versailles, France.

Andrivon D., Hansen J.G., Runno-Paurson E., Eikemo H., Cooke D. E., Lees A. K., Gaucher D., Glorvigen B., Barbary A., Aurousseau F., Corbière R., Mabon R., Le Hong V., Chatot C., 2017. IMPBlight 2.0 : Using pathogen population information to improve late blight control (Oral presentation ; summary)

Corbière R., Chatot C., Mabon R., Gaucher D., Aurousseau F., Barbary A., Laty P., Andrivon D., 2017. Monitoring French populations of *Phytophthora infestans* 2013-2016 on potato reveals local changes in genotypic structures (Poster)

11th International Congress of Plant Pathology (ICPP) 2018, Boston, Massachusetts, USA, 29 July-3 August 2018

Cooke D., Lees A., Kessel G., Andrivon D., Lassen P., Hansen J.G., 2018. Understanding *Phytophthora infestans* populations at local and global scales. 11th International Congress of Plant Pathology (ICPP) 2018, Session « Potato Late Blight—Global Research and Networking ». *Phytopathology*, **108** (10S), 263.

9th International Agriculture Symposium "AGROSYM 2018", Jahorina, Bosnia and Herzegovina, 4-7 October 2018.

Puidet B., Chatot C., Aurousseau F., Dewagenière P., Corbière R., Andrivon D., 2018. Virulence variation in sexual and asexual populations of *Phytophthora infestans*. Poster

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EuroBlight workshops

16th EuroBlight Workshop, Aarhus, Denmark, 14-17 May 2017.

Andrivon D., 2017. IPMBLIGHT 2.0: Using pathogen population information to improve late blight control (Oral presentation). Paper

Cooke D., Kessel G., Hansen J.G., Lassen P., Sanmohan B., Andrivon D., Corbière R., *et al.*, 2017. Update on European *Phytophthora infestans* population and EuroBlight Toolbox (oral presentation).

Hansen JG & Hjelkrem, 2019. Comparison and evaluation of six European late blight risk models. 17th EuroBlight Workshop, York, UK, 12-15 May 2019. (Oral presentation). Paper

Puidet B., Eikemo H., Le VH, Najdabbasi N., 2017. Fungicide sensitivity in Europe (oral presentation)

Corbière R., Chatot C., Mabon R., Moulin P., Guibert M., Gaucher D., Aurousseau F., Barbary A., Laty P., Andrivon D., 2017. Monitoring French populations of *Phytophthora infestans* 2013-2016 on potato reveals local changes in genotypic structures (Poster)

17th EuroBlight Workshop, York, UK, 12-15 May 2019.

Oral communications

Andrivon D., Puidet B., Kiiker R., Wilk N., Mabon R., Guibert M., Le V., Heikemo H., Hansen J.G., Cooke D.E.L, Lees A.K., Aurousseau F., Corbière R., Deweigenaere P., Saubeau G., Chatot C., 2019. Phenotypic traits of the new *P. infestans* genotypes expanding in Europe. 17th EuroBlight Workshop, York, UK, 12-15 May 2019. (Oral presentation)

Andrivon D., Mabon R., Guibert M., Corbière R., Chatot C., Saubeau G., Puidet B., Aurousseau F., Dewaegeneire P., 2019. Are *Phytophthora infestans* genotypes reliable predictors of pathogenicity phenotypes in Western European clonal lineages? 17th EuroBlight Workshop, York, UK, 12-15 May 2019. (Oral presentations)

Corbière R., Puidet B., Mabon R., Guibert M., Chatot C., Saubeau G., Aurousseau F., Dewaegeneire P., Andrivon D., 2019. Pathogenicity – a driver for the epidemic potential of the clonal lineage EU_41_A2 of *Phytophthora infestans* inside sexually reproducing populations of Nordic European countries? 17th EuroBlight Workshop, York, UK, 12-15 May 2019. (Oral presentation). Paper.

Cooke D., Kessel G., Hansen J.G., Lassen P., Andrivon D., Corbière R., et al., 2019. The European population of *P. infestans* in a global context. 17th EuroBlight Workshop, York, UK, 12-15 May 2019. (Oral presentation). Paper.

Hansen JG & Hjelkrem, 2019. IPM2.0: Test of a DSS including information from a trap nursery. 17th EuroBlight Workshop, York, UK, 12-15 May 2019. (Oral presentation). Paper.

National meetings oral

Hansen JG (2020) Ændringer i kartoffelskimlens biologi i Europa –betydning for bekæmpelse. Danske kartofler: Generalforsamling & Store kartoffeldag, Vingsted hotel & Konferencecenter 28 Januar, 2020

Hansen, JG & Abuley IK. (2019) Genotypes of *P. infestans* in Denmark–changes during the season and implications for practice. Kartoffelworkshop, SEGES, Konference Hotel Horizon, December 2019

Hansen, JG & Nielsen BJ. Kartoffelskimmel – udnyttelse af ny viden om skimmeltyper i bekæmpelsesstrategier. Kartoffelworkshop, SEGES, Konference Hotel Horizon, December 2018

<u>Poster</u>

Guibert M., Mabon R., Wilk N., Corbière R., Chatot C., Aurousseau F., Dewaegeneire P., Barbary A., Gaucher D., Andrivon D., 2019. Genotypic and phenotypic variations within 2017-2018 Phytophthora infestans French clonal populations. 17th EuroBlight Workshop, York, UK, 12-15 May 2019.

Papers in technical journals

Andrivon D., Corbière R., Mabon R., 2016. Projet IPMBlight 2.0 : L'épidémio-surveillance pour une meilleure aide à la décision. *Potato Planet* 50 : 76- 79.

Corbière R., Chatot C., Mabon R., Mariette N., 2016. Mildiou en France *: Phytophthora infestans* sous surveillance. *Phytoma* 690: 30-36.

Andrivon D., Mabon R., Corbière R.**,** Chatot C., 2017. Epidémiosurveillance : Enjeux actuels et acquis récents. *La pomme de terre française/ Hors-série*, avril 2017 : 4-6.

Hansen J.G., Abuley I.K., 2019. Nyt projekt vil videreudvikle varslingssystemet Skimmelstyring (New project will improve the Danish Blight Management DSS). *Danske Kartofler*, June 2019.

Jens G. Hansen & Isaac K. Abuley (2020). Nye skimmeltyper i Danmark betyder at vi skal ændre praksis. Danske kartofler, April 2020, s. 28-31.

Student memoirs

Moulin Pernelle, 2017. Le mildiou de la pomme de terre : le génotype est-il un bon prédicteur du phénotype chez *Phytophthora infestans* ? Double graduation, as Masters student (Master 2 Science Technologie Santé, SV-ECOBIOVALO (Sciences Végétales – ECOproduction et BIOVALOrisation), Université Caen Normandie, 30 pages.) and Agriculture Ingeneer (Mémoire d'Ingénieur en Agriculture, UniLaSalle, Mont Saint Aignan (76), 43 pages).

Rebondy Gabriel, 2017. Knowledge contribution to *Phytophthora infestans*, causal agent of potato late blight. Study of the possible links between genotype and life history traits of the oomycete isolates. *Master 1 Integrative Biology and Physiology (BIP), Cellular Biology Physiology and Pathology (BCPP), Speciality Plant Sciences*, AgroParisTech, Paris-Saclay & Paris-Diderot Universities, 17 pages.

Wilk Nina, 2018. Le pouvoir pathogène de *Phytophthora infestans*, agent responsable du mildiou de la pomme de terre, dépend-il du génotype des isolats des souches ? Conséquences pour l'épidémio-surveillance des populations européennes. Licence 3ème année (*Bachelor thesis*) Mention Sciences de la vie; Parcours BCGMP (Biologie Cellulaire Génétique Microbiologie et Physiologie), Université de Rennes 1, 32 pages.

- Total number of items at this level: 20

- List of <u>non-scientific publications</u>:

- Andrivon D., 2018. A novel approach to potato blight. *Impact*, August 2018, 61-63
- Andrivon D., 2018. The re-emergence of potato late blight: a major reason for pesticide use in arable crops. *Open Access Government*, December 2018. *https://www.openaccessgovernment.org/pesticide-use-in-arable-crops/55271/*
- Andrivon D., 2019. Understanding the potato late blight pathogen: key for sustainable control. *Open Access Government*, July 2019. *https://www.openaccessgovernment.org/potato-late-blight-pathogen-sustainable-control/68847/*

  - Total number of items at this level: 3

- List of <u>press releases, interviews and TV appearances</u>:
- EuroBlight Newsletter:
  - Results of the EuroBlight potato late blight monitoring in 2019
  - Results of the EuroBlight potato late blight monitoring in 2018
  - New, emerging clones of Phytophthora infestans in Europe - what do we know about them?
  - Potato blight tracking in Europe - 2017
  - Potato blight tracking in Europe

  - Total number of items at this level: 5

Events with stakeholders (if applicable)

Event	Aim/ location/ date	Approximate number of attendees
Seminar at Potatoes in Practice Field event for UK potato industry	Dundee, UK/ August 2017	100

AHDB Potatoes Treater Group	Potato advisors forum/Dundee, UK/ Nov 2017	12
COMITE NORD Annual technical meeting	Achicourt, France/ December 2016, December 2017 and December 2018	80
Potato 2017	National/nordic potato meeting in Norway	260
Open Field Day, 2017	Flakkebjerg, Denmark, August 2017	100
Open Field Day, 2018	Flakkebjerg, Denmark, August 2017	100
Potato workshop, 2018	Aarhus, December 2017	80
Potato 2019	National/nordic potato meeting in Norway	300
Potato workshop, 2019	Aarhus, December 2019	80

Training sessions conducted (if applicable)

Description of training course	Approximate number of attendees
Virulence and aggressiveness testing training course – Wageningen UR, July 2016	6

Methods, techniques, tools etc. (if applicable)

Description of methods, techniques, tools etc. developed in the frame of the project:

	Description
New methods, techniques, tools e.g. a method to monitor or attract a specific pest species	
Patent applications, other IP e.g. patent for extraction process of lure/attractant	
Prototypes, pilots e.g. a trap prototype	
Marketable product/service e.g. a trap, lure, pheromone etc.	

Explanation of the use of resources

Funding

*(All requested amounts should be **expressed as thousands** of euros. E.g.: 1.357.900 euro should be written as € 1357.9 in the answer box.)*

Effective funding sources

(NB: I understand this as the amounts available to the partners during the period covered by the report; these are of course less than the total amounts granted for the whole duration of the project)

Partner no.	EU funds (ERA-NET)		Other external public funds		External private funds		Own funds		**Total funds €**
	€	%	€	%	€	%	€	%	
P1	65.0	36.0					74.5	38.0	139.5
P2	194.6	100							194.6
P3	326.1	100							326.1
P4	56.0	56.0							56.0
P5	13.3	30.0					21.0	74.0	34.3
P6	16.5	33.0					34.0	100.0	50.5
P7 (now subcontractor)									
P8 (associate)			*£16.212*						*£16.212*
TOTAL									

List any deviations in participant's use of resources pertinent to the project as a whole, describe corrective actions adopted for any deviations

Effective costs

Partner no.	Personnel	Travelling / meetings	Consumables /Equipment	Subcontracts	Other costs	**Total effective Costs**
P1	74.5	17.0	46.0			137.5
P2	115.9	11.3	1.9	6		135.1
P3	225.0	19.0	11.0	71.1		326.1
P4	15.0	5.0	8.0		13.0	41.0
P5	33.4	3.0				34.3
P6	40.9	7.2	2.4			50.5
P7						
P8						
TOTAL						

Human resources

Total number of people in partner teams

Indicate the number of employees of the following positions that were permanent staff members / that were hired especially for the project *(only include people that were paid by ERA-NET funds):*

Partner no.	Researchers with PhD more than 3 years / experienced scientists		Researchers PhD post-docs / young scientists		PhD students		Master students		Support or technical staff		Other (Ingeneers)	
	Permanent	Hired	Permanent	Hired	Permanent	Hired	Permanent	Hired	Permanent	Hired	Permanent	Hired
P1	2							2	2			
P2	3								3			
P3	2								1			
P4	2				6							
P5												
P6	3							1	6		2	
P7												
P8												
TOTAL												

How many people completed any of the following qualifications through their work on the ERA-NET funded project and/or using funding from the ERA-NET project?

Number of PhDs: 1 (ongoing)
Number of MSc, MEng: 2
Number of BSc: 1

IPM2.0 til bæredygtig bekæmpelse af kartoffelskimmel - Udnyttelse af patogen-data til beslutningsstøttesystemer

Kartoffelskimmel, forårsaget *af Phytophthora infestans* er et alvorligt problem for kartoffelproduktionen i Europa og sygdommen koster ca. 1 milliard kroner om året i tab og omkostning til bekæmpelse. Et netværk af forskere, rådgivere, forædlere og aktører fra industrien som via nationale projekter arbejder sammen i 'EuroBlight – a potato late bligt network for Europe', har i en årrække overvåget udviklingen af genotyper (DNA undersøgelse), dels for at forstå udvikling og spredning af skimmeltyper i Europa og dels for at overvåge risikoen for udvikling af resistens mod de fungicider, som anvendes i bekæmpelsen. IPMBlight2.0 projektet var et projekt initiativet C-IPM under EU's ERA-Net-program.

Målet med projektet var at videreudvikle og intensivere overvågning af *P. infestans* genotyper i Europa , at undersøge de fænotypiske karakteristika (aggressivitet, virulensegenskaber, fungicidresistens) af navngivne genotyper, men også af genotyper som stammer fra kønnet formering og at undersøge, hvordan vi kan forbedre eksisterende beslutningsstøttesystemer med viden om patogenernes karakteristika, udbredelse og evolution.

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