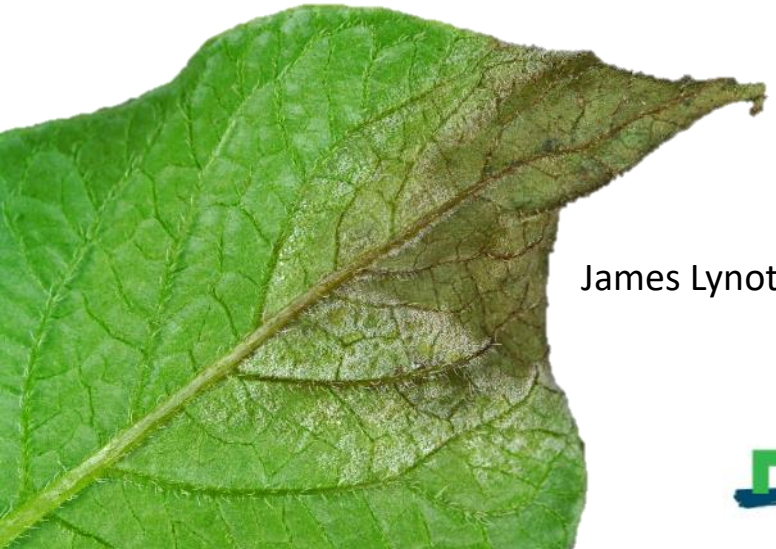
EuroBlight

A potato late blight network for Europe

Update on the population of *Phytophthora infestans* across Europe via EuroBlight monitoring



David Cooke, Geert Kessel, Jens G Hansen, Alison Lees

James Lynott, Beatrix Keillor, Isaac Abuley, Trudy van den Bosch, Romain Mabon

WAGENINGEN UR
For quality of life

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AARHUS UNIVERSITY

Thanks: sponsors/contributors/collaborators

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71 Contributors 2013-2025

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EuroBlight objectives

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- **understand the composition of pathogen populations,** their evolution and the biological, climatic and anthropogenic drivers behind their invasive success

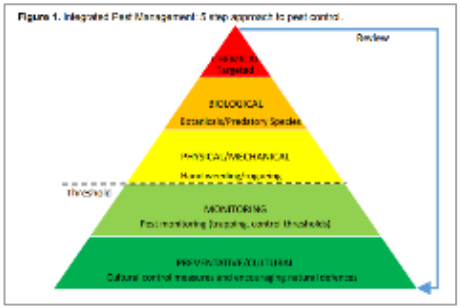
- **develop innovative, effective and sustainable Integrated Pest/Crop Management strategies** which consolidate and exploit population information, climate predictions, available management tools (conventional crop protection products, resistant cultivars, biocontrol options, early detection and warning) and cutting-edge information technologies

- **support optimal deployment and stewardship of effective control methods** to maximize their benefits whilst mitigating the risk of reduced efficacy due to evolving pathogen populations

Foster co-operation, capacity building & shared infrastructure

Potato Late Blight – *Phytophthora infestans*

- Rapid reproduction – ~ 1.5 B spores ha^{-1} at 1% disease
- Fungicide and varietal resistance key to management



Pathogen genotyping
EuroBlight

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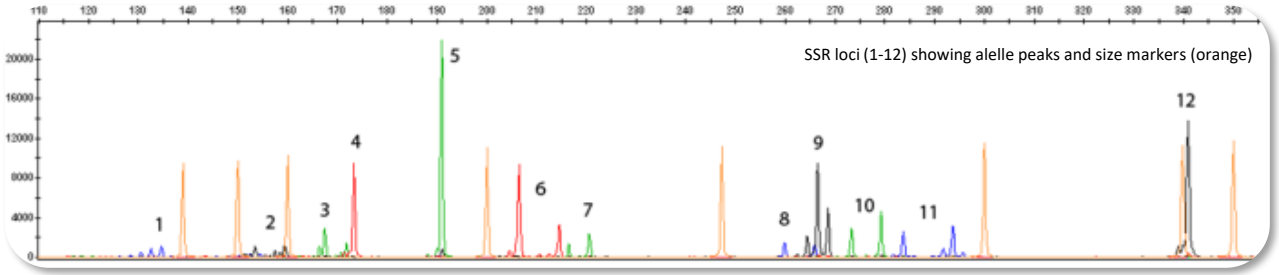
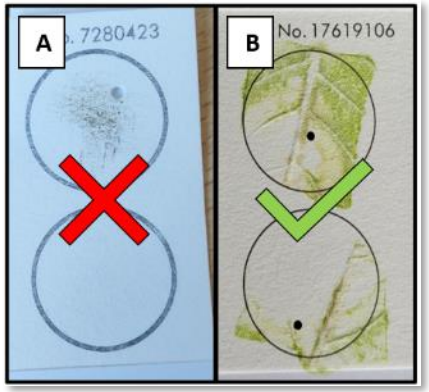
- Scouts collect samples (FTA cards + some isolates)
- Metadata recorded (location, date, crop type, cultivar)
- DNA fingerprinted - 12-plex SSRs (Li et al. 2013)
- Genotypes defined & data stored in EuroBlight database
- Data publicly mapped on www.euroblight.net
- Sponsorship €38 per sample – covers costs



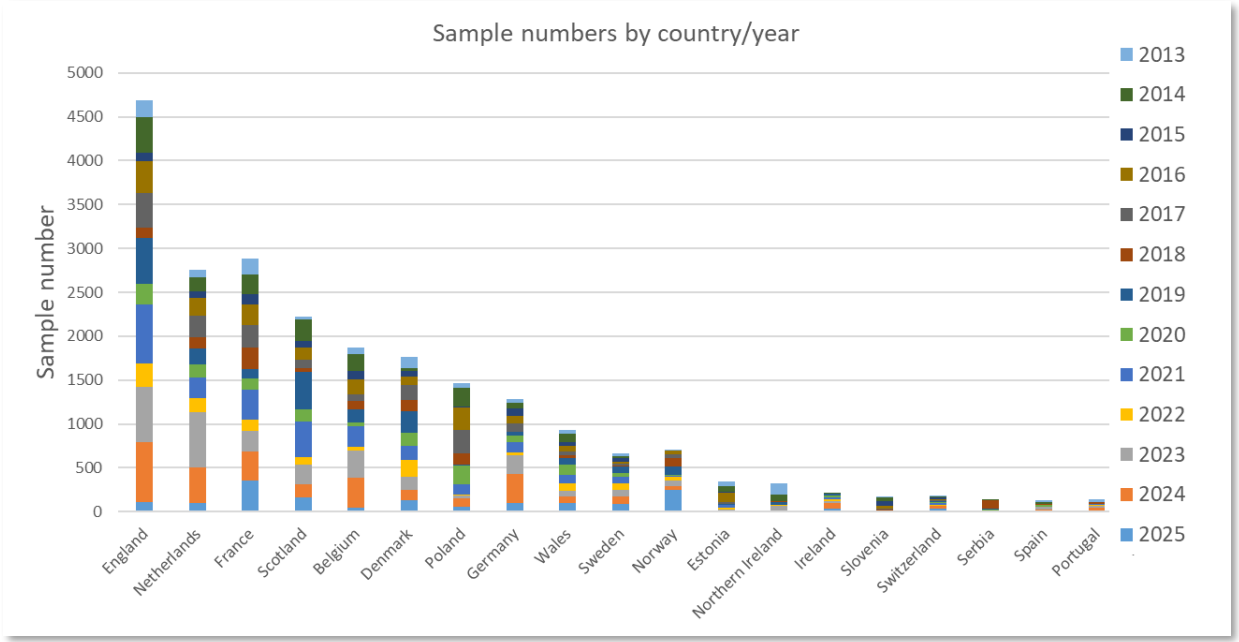
Scottish Government
Riaghaltas na h-Alba
gov.scot

Optimum sampling for 2026



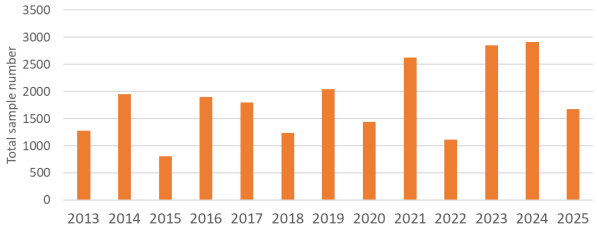
- Sample early in day
- Fresh sporulation – underside of leaf
- If lesion dry – reactivate
- Maximise disk cutting ‘hit-rate’ for optimal DNA extraction

Sample statistics (2013-2025)



- Total 23.6K samples from 38 countries
- NW Europe most sampled
- Long ‘tail’ of countries with relatively few samples
- 33% of samples from Great Britain (EN, SC, WA) – sampling bias

Top 20 countries by sample number



Sample distribution 2024 & 2025

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2024 record breaking year 2.9K

2025 1.7K

Clones vs 'Other' phylogeny
poppr analysis 2025 SSR data (577 MLGs)

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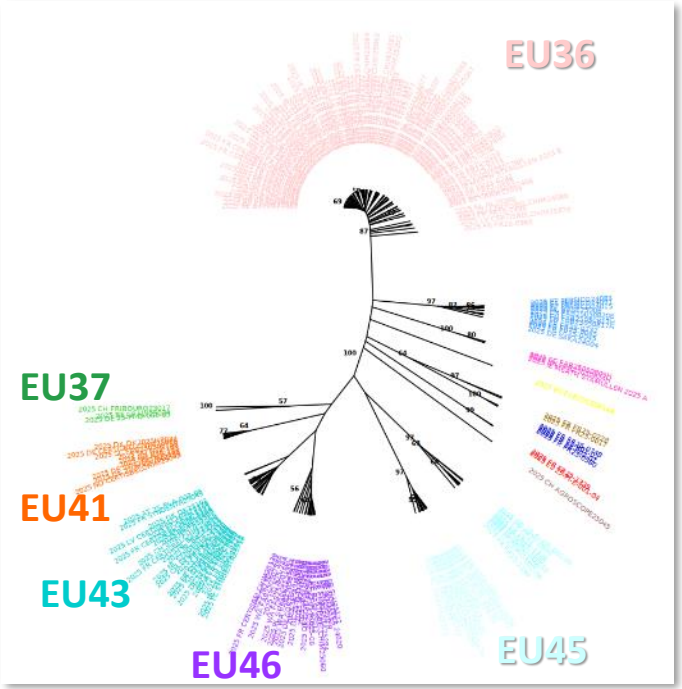
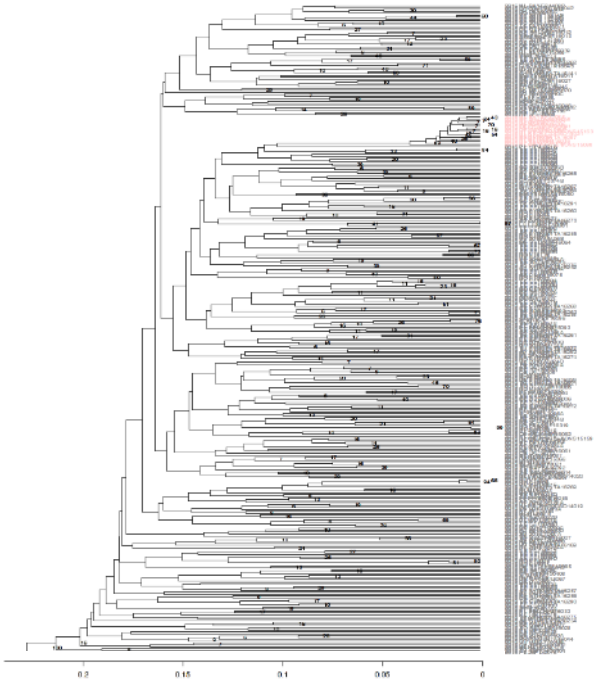


- Distinct clusters of genetically similar MLGs = major clones and their sub-clonal variants (212 MLGs)
- Long branches between clones reflect greater Bruvo distances
- Multiple identical samples (max single EU43 of 120 samples)



EU_36_A2

- Highly diverse
- Branches join deep in tree with no clear pattern
- Few identical samples (largest MLGs 17 samples in NO)

Fungicide resistance reports

- EU43 & EU46 CAA & OSBP
- Details reported
- Mechanisms investigated
- Management changed
- Looking forward to hearing more details…

Europe genotype change

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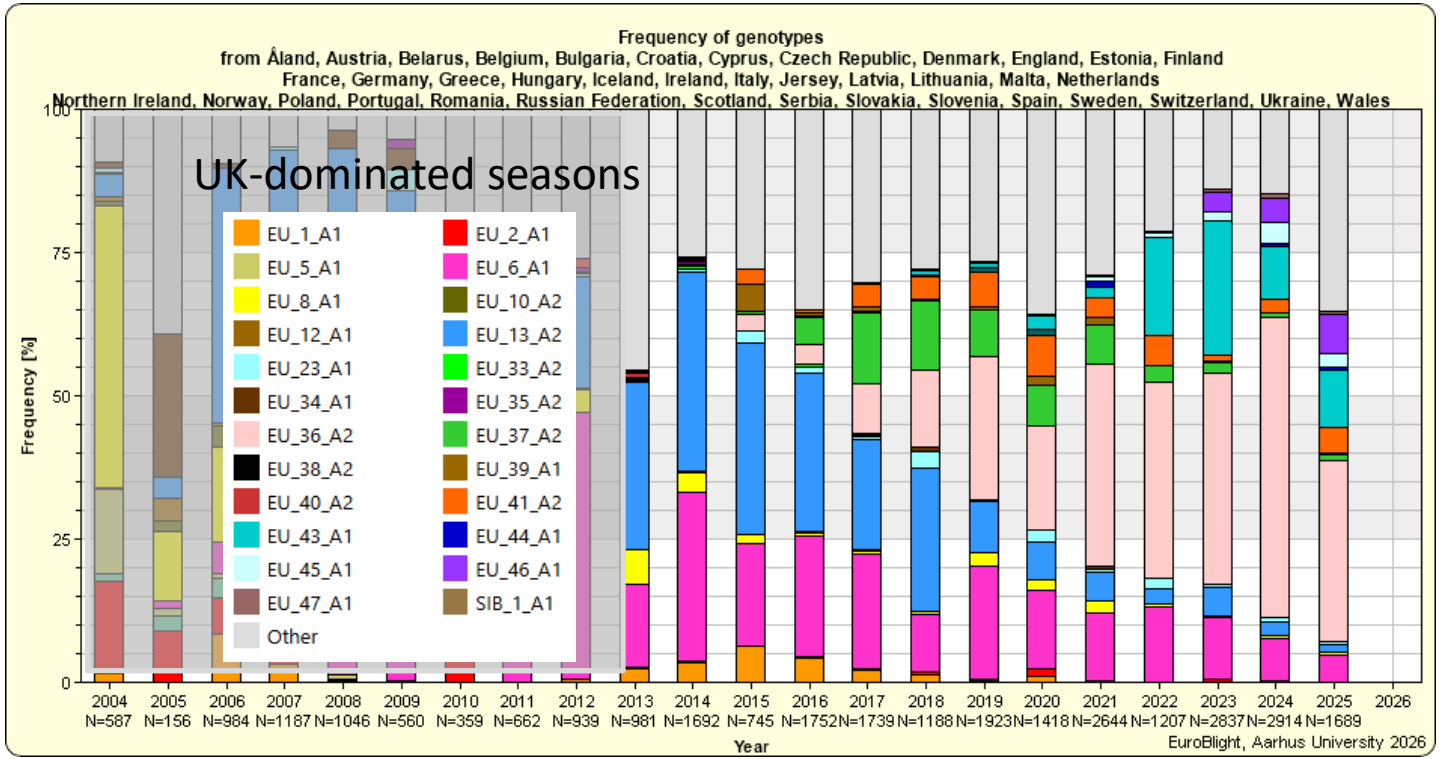
A potato late blight network for Europe



Clone	2024	2025
'Other'	15	35 %
EU46	4	7 %
EU43	9	10 %
EU41	3	5 %
EU37	1	1 %
EU36	52	32 %
EU13	2	1 %
EU6	7	5 %

https://www.euroblight.net/

Europe (minus UK) genotype change

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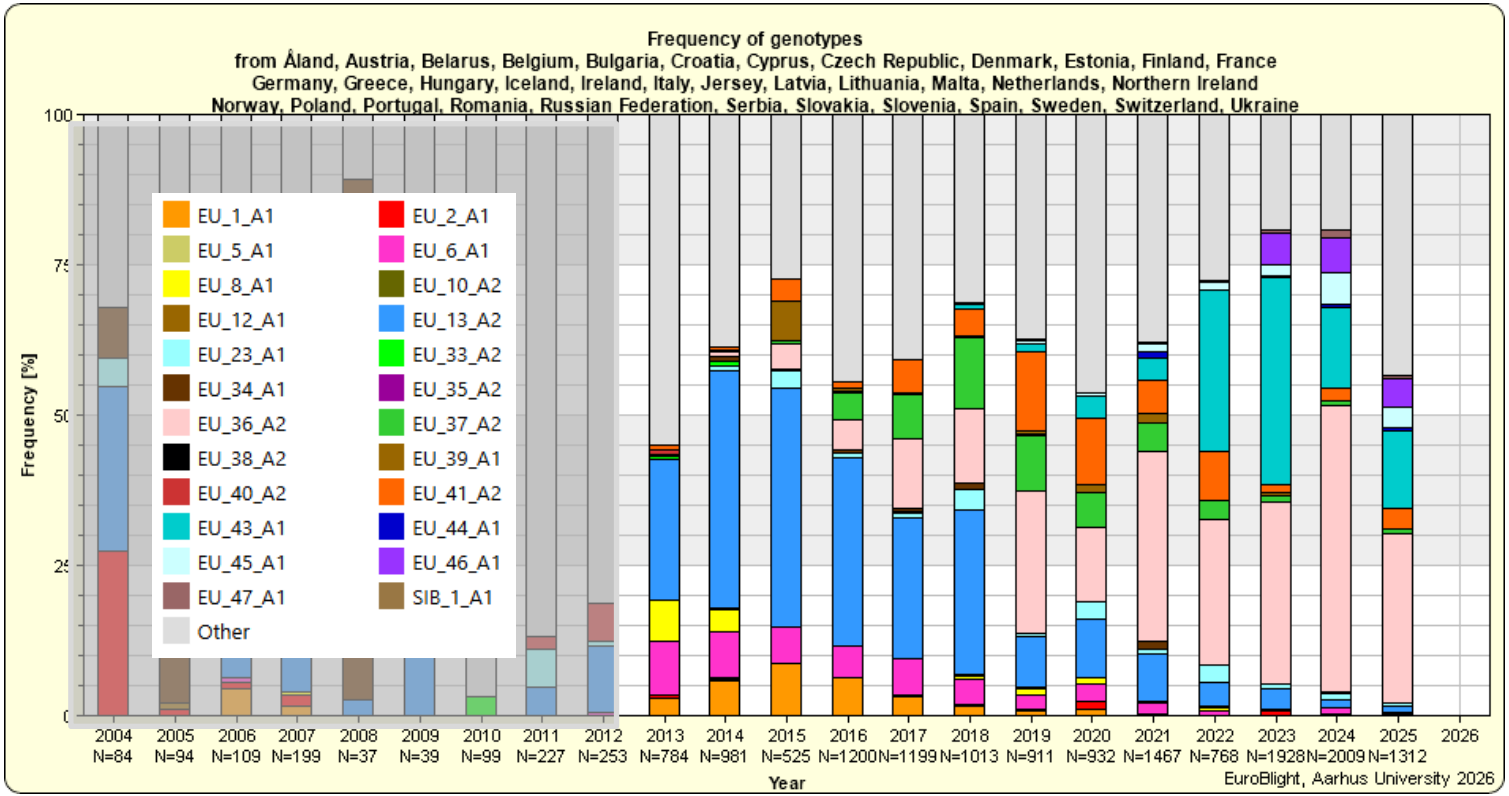
A potato late blight network for Europe



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Europe (tomato) genotype change

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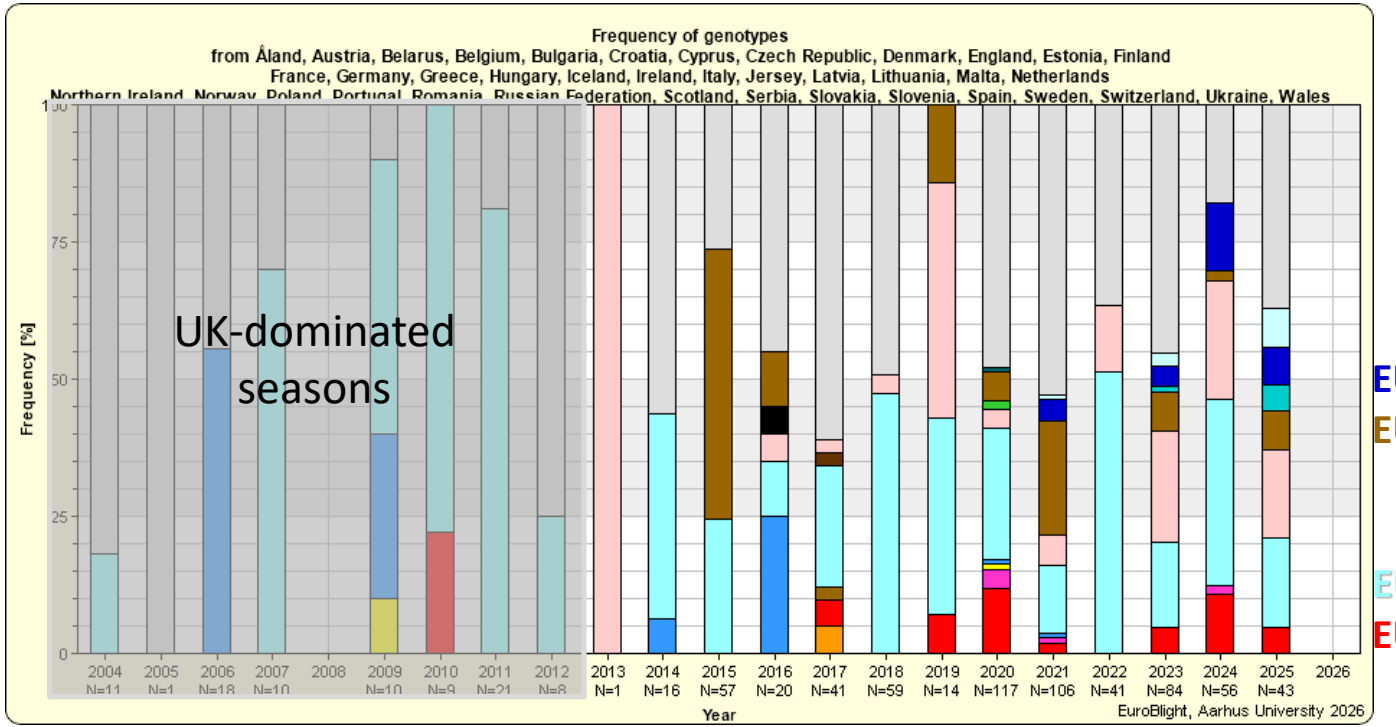


EU44

EU39

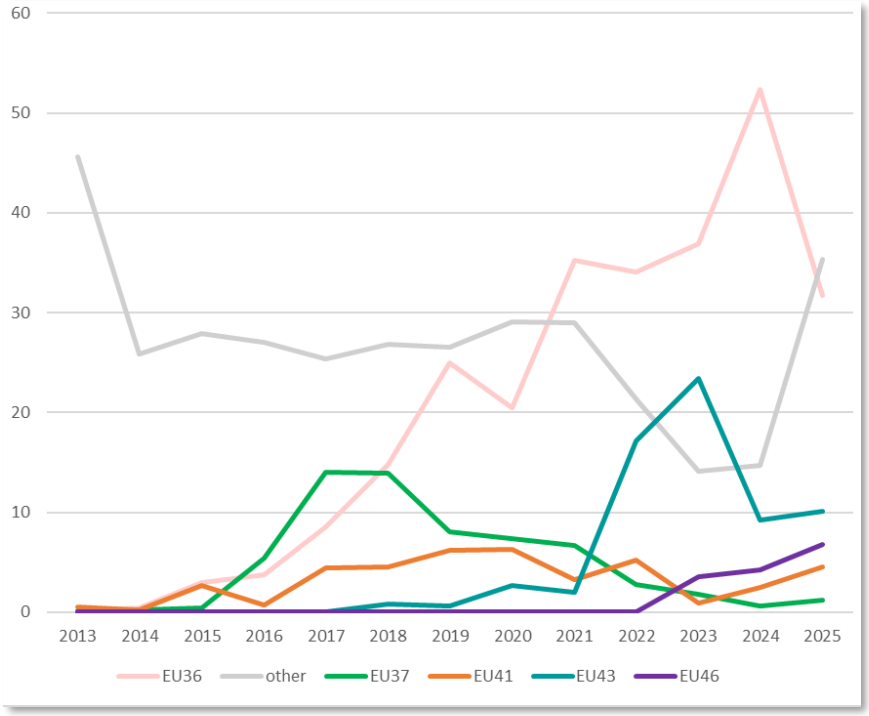
EU23

EU2

EU_1_A1
EU_2_A1
EU_3_A2
EU_5_A1
EU_6_A1
EU_8_A1
EU_10_A2
EU_12_A1
EU_13_A2
EU_22_A2
EU_23_A1
EU_33_A2
EU_34_A1
EU_35_A2
EU_36_A2
EU_37_A2
EU_38_A2
EU_39_A1
EU_40_A2
EU_41_A2
EU_42_A2
EU_43_A1
EU_44_A1
EU_45_A1
EU_46_A1
SIB_1_A1
Other

https://www.euroblight.net/

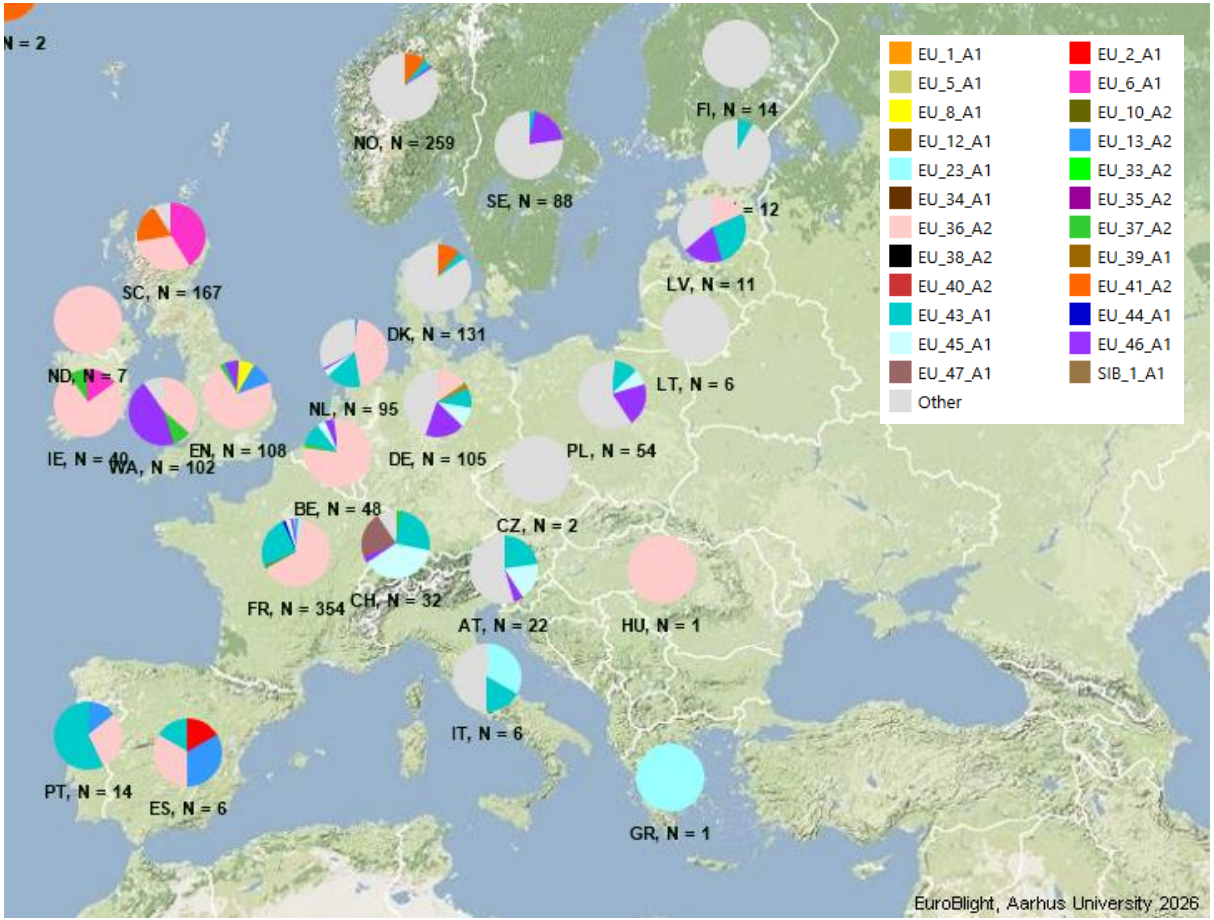
Europe 13 years of data



- Rise of EU36
- Rise and checking of EU43
- Steady rise of EU46
- Rise and fall of EU37
- EU41 stable proportion
- Lower proportion of ‘Other’ types when clonal regions have high incidence and vice versa

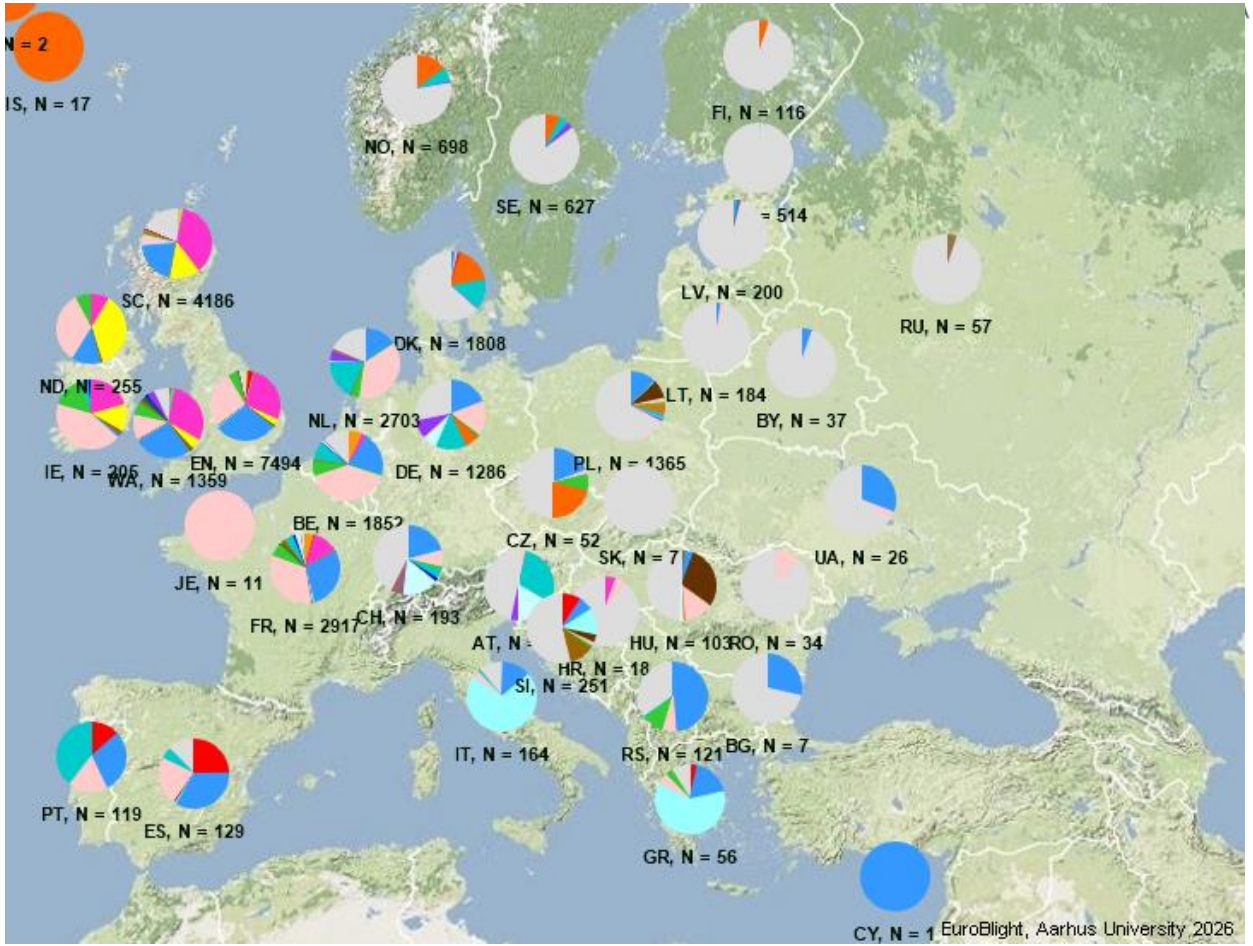
Europe 2025 data by country

EuroBlight
A potato late blight network for Europe



2013-2025 summary

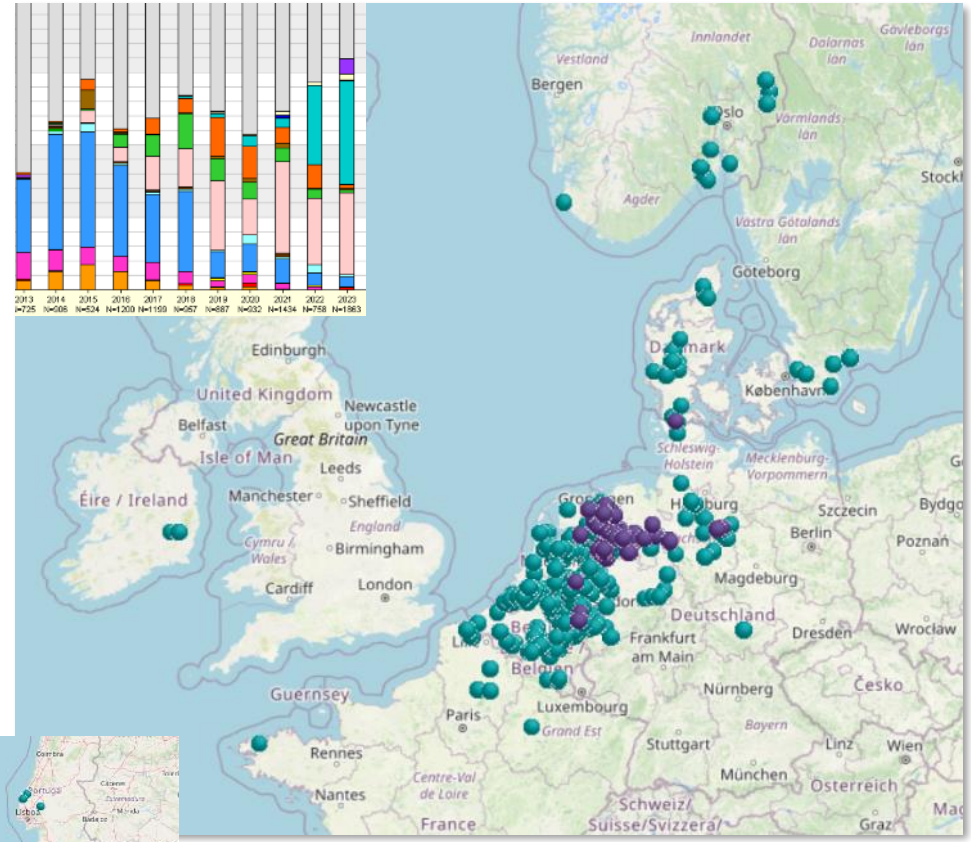
EuroBlight
potato late blight network for Europe

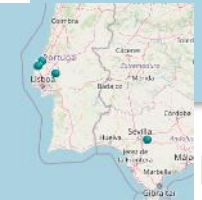


- Long-term trend of dominant clones observed in the west and south of Europe and 'Other' genetically diverse populations towards the north and east

EU_1_A1
EU_2_A1
EU_3_A2
EU_5_A1
EU_6_A1
EU_8_A1
EU_10_A2
EU_12_A1
EU_13_A2
EU_22_A2
EU_23_A1
EU_33_A2
EU_34_A1
EU_35_A2
EU_36_A2
EU_37_A2
EU_38_A2
EU_39_A1
EU_40_A2
EU_41_A2
EU_42_A2
EU_43_A1
EU_44_A1
EU_45_A1
EU_46_A1
SIB_1_A1
Other

2023 expansion of EU43





ES and PT

- **EU_43_A1** increase to 37%
- Range extended IE, FR & ES
- Related **EU_46_A1** sampled id-July
- Resistance to CAA continues to 2023
- Resistance to OXTP emerges in 2023

2024 distribution of EU43

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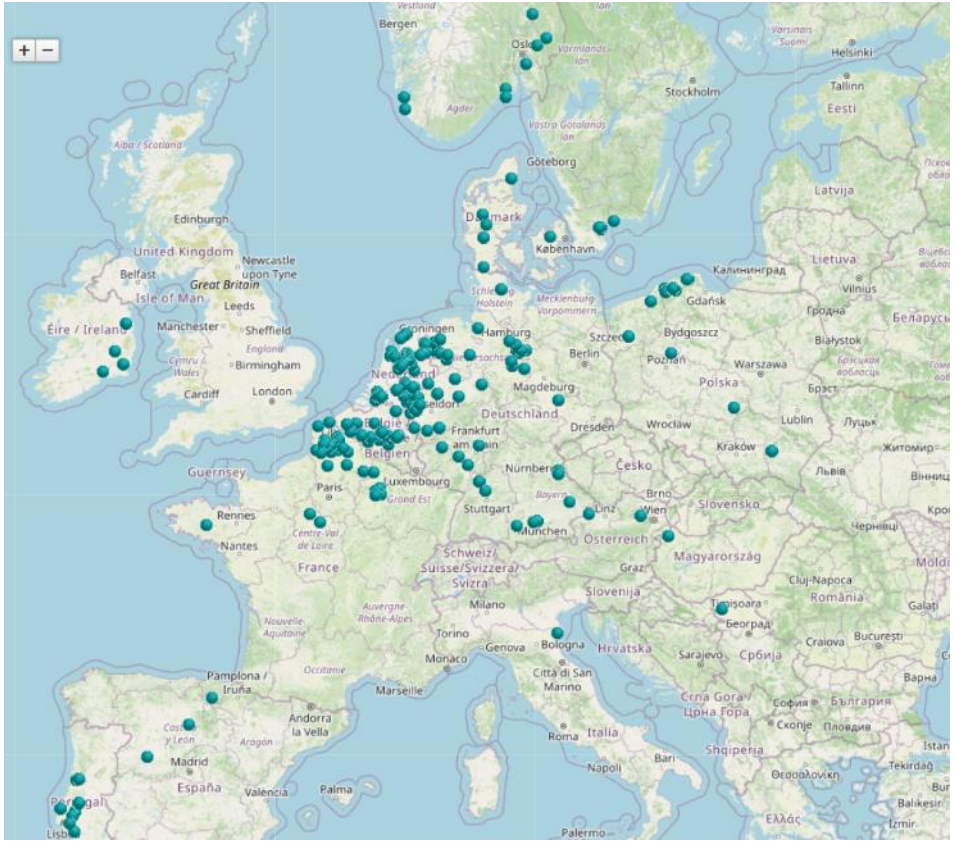
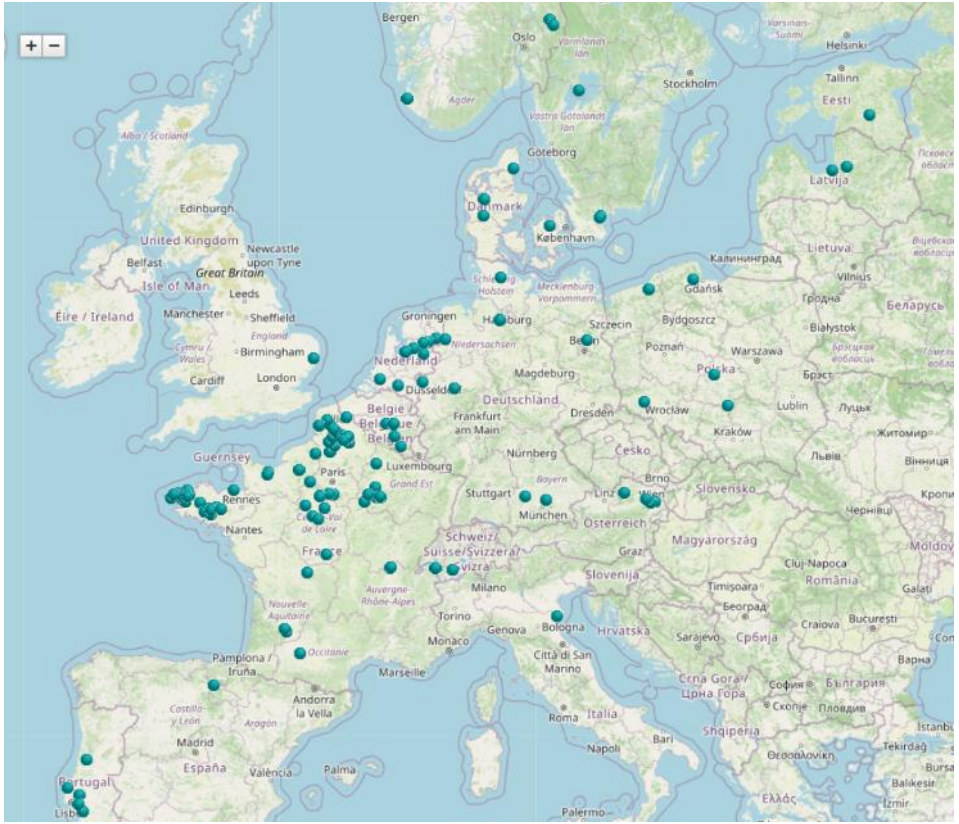
A potato late blight network for Europe



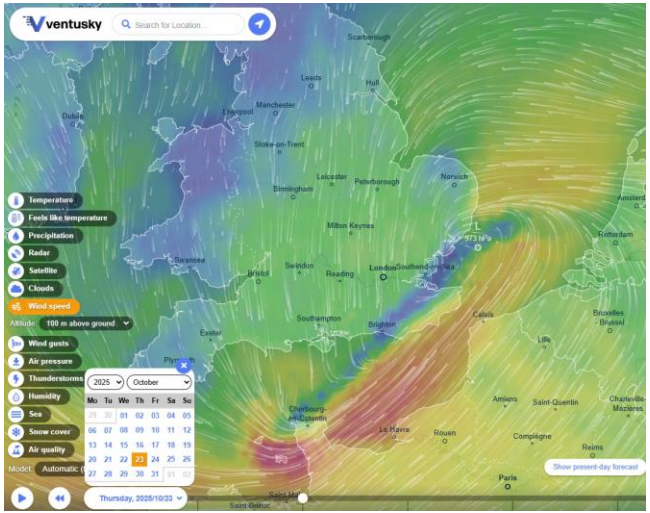
- **EU43** dropped from 23 to 9%
- Range extended AT, RS, PL, IT

2025 distribution of EU43

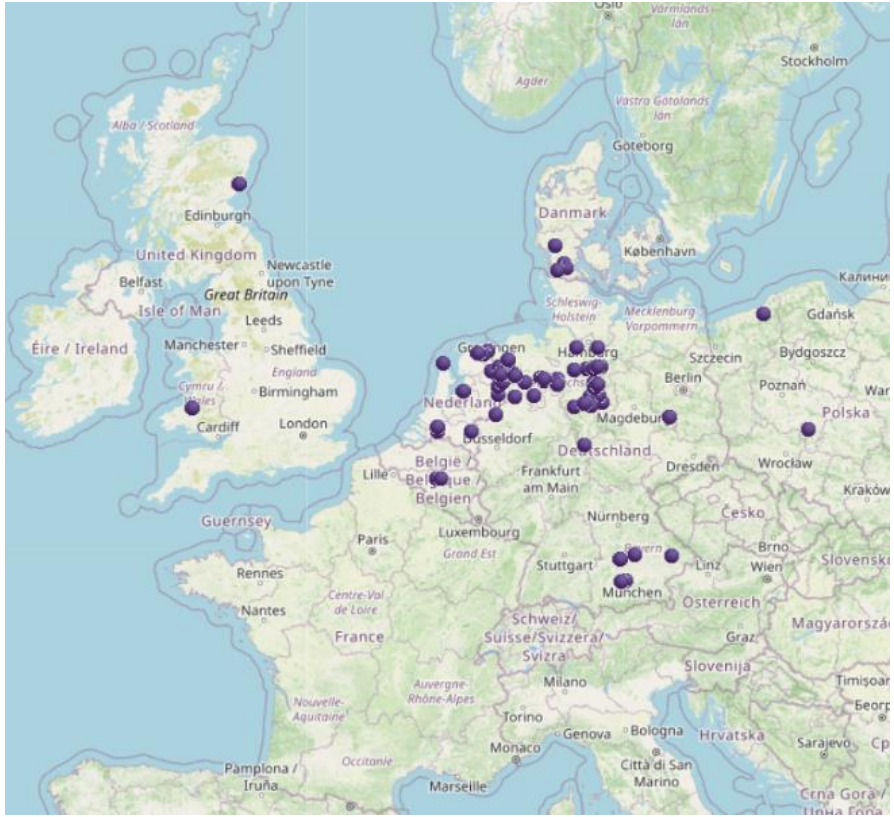
EuroBlight
A potato late blight network for Europe



- **EU43** stable at 10%
- Range extended EN, CH, EE, LV
- Spread to EN in Nov by storm?



2024 distribution of EU46



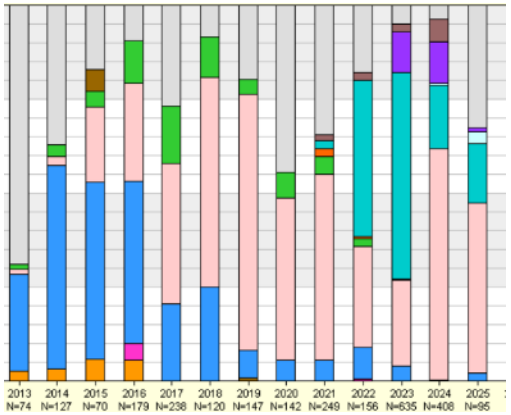
- **EU46** up from 3.5 to 4.2%
- Range extended SC, WA, BE, PL

2025 distribution of EU46

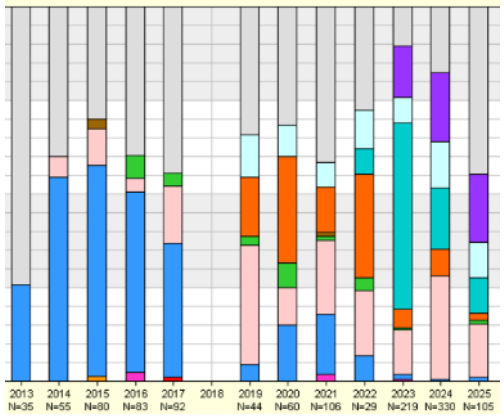
- **EU46** up from 4.2 to 6.8%
- Range extended to EN, FR, NO, SE, CH, AT & LV
- How spread?
- Even in a dry year it spread what would consequence be in a wetter season?

2024-5 national changes

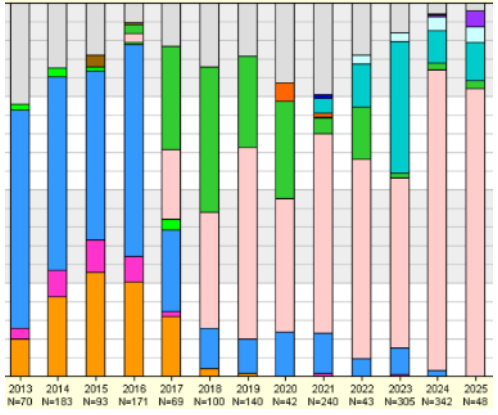
NL



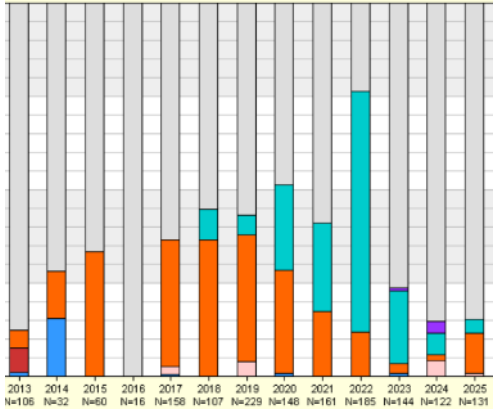
DE



BE



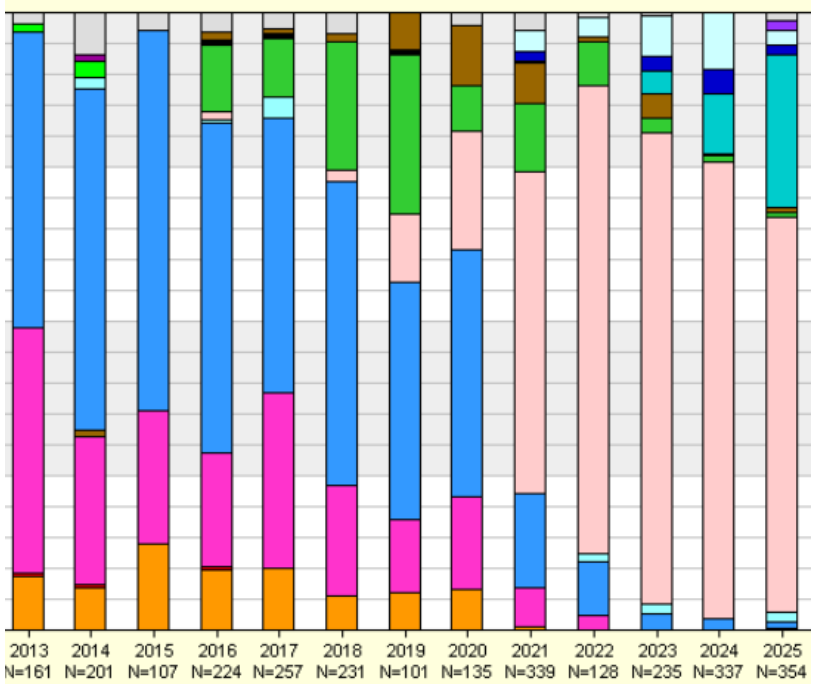
DK



- **EU43** striking decrease then stability in all four countries
- **EU46** also managed but little change in DE, rise seen in PL and BE and marked drop in NL
- **EU37** still 2% in BE compared to other countries

Changes in EU43 in France

FR



- Peak levels of **EU43** in FR in 2025 from 10 to 25%
- EU36 remains dominant at 64%
- Severe pressure in west
- Different fungicide use?

New clone EU47 defeats specific Resistance genes

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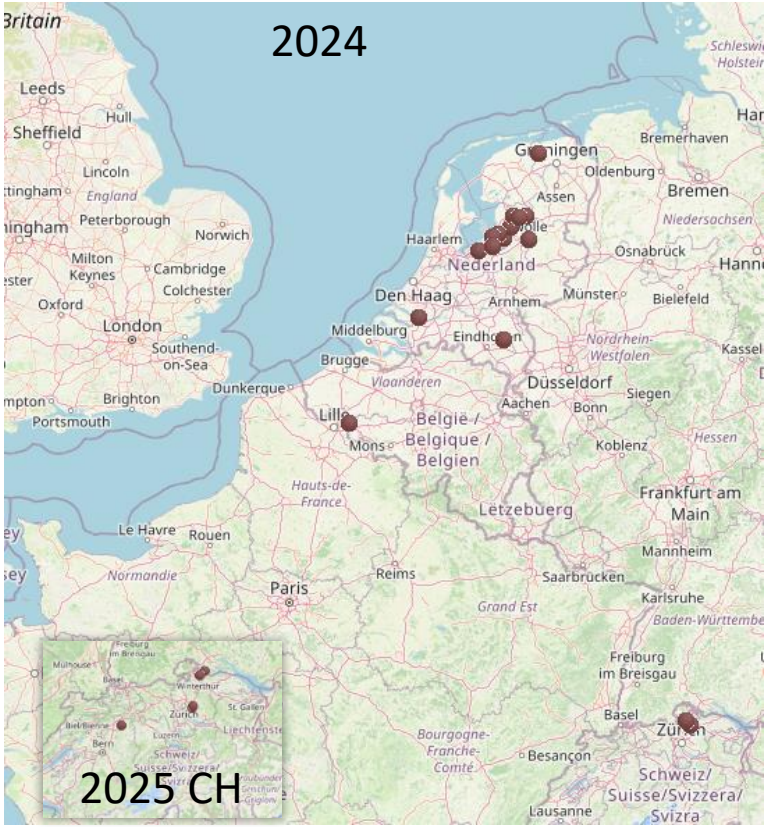
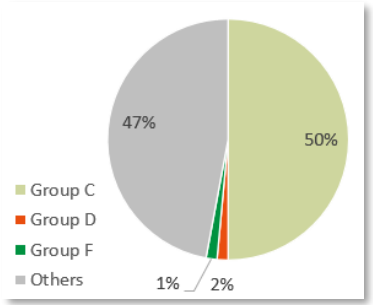


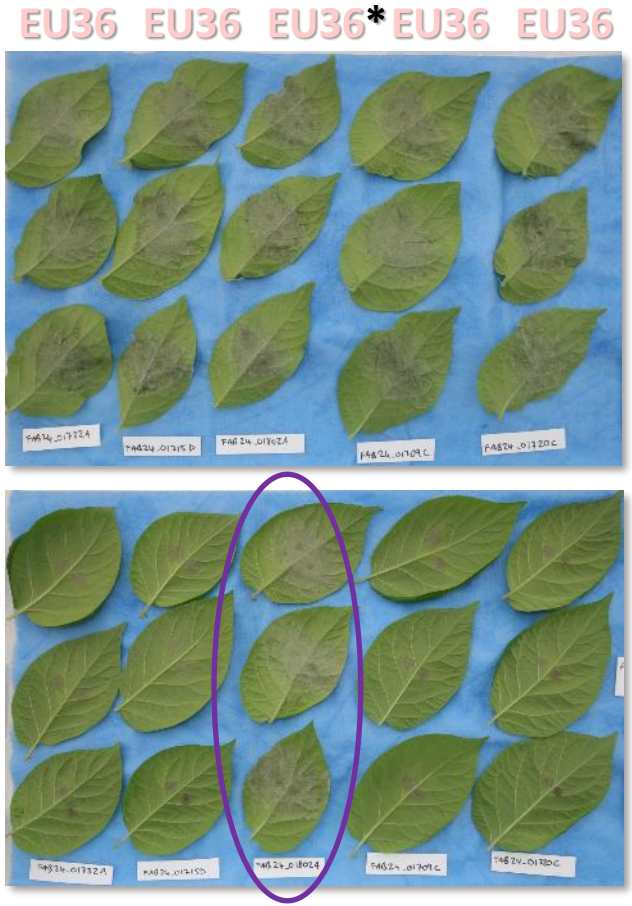
- First sampled 2021 NL
- By 2025 - 70 samples in NL, CH & BE
- More than 50% sampled from Group C cultivars – mostly Vitabella
- No known fungicide resistance (Hutton tests)



Groep	Veredelaar/Handelshuis	Rasnaam *
A	Agrico	Carolus, Twinner, Twister
	Averis	Antora
	HZPC	Cayman
	Meijer Potato	Sound, Lady Jane
B	Agrico	Alouette, Ardeche, Nofy
C	Agrico	Levante
	Geersing Potato Specialist	Camillo, Cammeo, Esperanto
	Plantera	Vitabella
D	Agrico	Beyonce, Sevilla
	Geersing Potato Specialist	Peter Pan
	Meijer Potato	Acoustic
E	Agrico	Jacky
	Solana Holland	Nola
F	Averis	Aveline, Avenger, Avito
G	HZPC	Invictus
H	Solana Holland	Connect

Wageningen Task Force Plantum host resistance groups

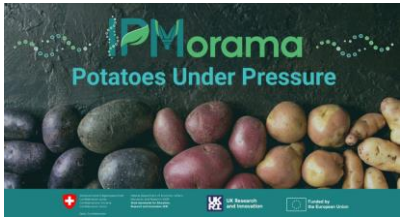
UK EU36 variant defeats *vnt-1*



- Breakdown observed in *vnt-1* UK blight resistant organic crop late in 2024 season
- Isolate genotyped as EU36
- Detached leaf testing of 5 2024 EU36 isolates on Maris Piper showed all aggressive
- *vnt-1* breaking stable in culture – need to explore cause in detail and inform industry

Stefańczyk E, Brylińska M, Brurberg MB, Naerstad R, Elameen A, Sobkowiak S, Śliwka J, 2018. Diversity of Avr-vnt1 and AvrSmira1 effector genes in Polish and Norwegian populations of *Phytophthora infestans*. *Plant Pathology* **67**, 1792-802.

- Protect our resistance



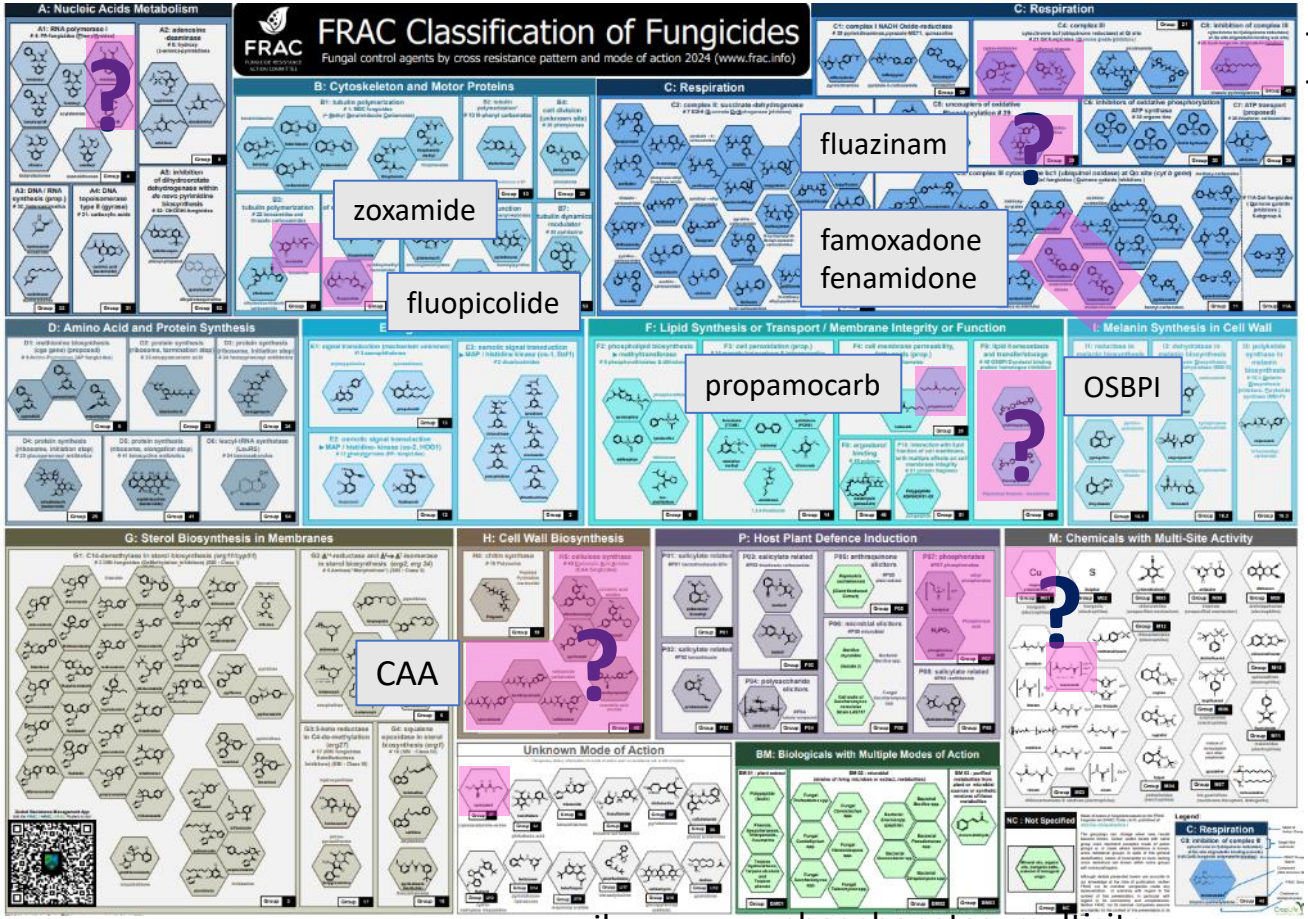
James Lynott

Navigating fungicide choices just got harder

metalaxyl

cyazofamid & amisulbrom

ametoctradin



cymoxanil

phosphonates

multisite

- Thanks to FRAC we have good information on FRAC groups active against *P. infestans*
- Resistance reports & withdrawal – more care needed (*Plasmopora*)
- Pressure on remaining actives increased

The James Hutton Institute

FRAC FUNGICIDE RESISTANCE ACTION COMMITTEE

Detached leaf fungicide test summary – 7 years

- UK isolates unless indicated
- Full resistance reported in four actives only
- Some variation within clones e.g. EU43, EU46, EU36
- Numbers in cells show number of isolates tested N.B. solid red does not infer that all isolates of that genotype are resistant

X

Genotype	Oxathiapiprolin	Mandipropamid	Metalaxyl	Fluazinam	Propamocarb	Ametoctradin	Zoxamide	Amisulbrom	Cyazofamid	Fluopicolide	Mancozeb
36_A2	41*	43	15	12	46	5	5	29	36	36	19
37_A2	20	32	5	**15**	30			15	30	30	15
6_A1	33	28	10	6	33	5	5	22	28	23	17
13_A2		6	**3**	1	6				6	1	
41_A2 (DK)	5	6	**6**	5	6	5	5	5	1		
41_A2 (UK)	10	10	**6**		10			5	**5**	5	
43_A1 (DK)	5	**28**	15	10	5	5	5	5			
43_A1 (NL)	**5**	**5**	5		5			5	5	5	
46_A1 (NL)	**5**	**5***	5								
46_A1 (UK)	**5**	**5**	5		5			5		5	
Other (NL)	**4**	4									

* R reported on continent

* one NL R

Sensitive

Difference at low doses

Intermediate

Resistant

DNA DNA (– active ingredients with DNA testing available)

Alison Lees & James Lynott

Digital droplet PCR - improving timeliness of fungicide advice

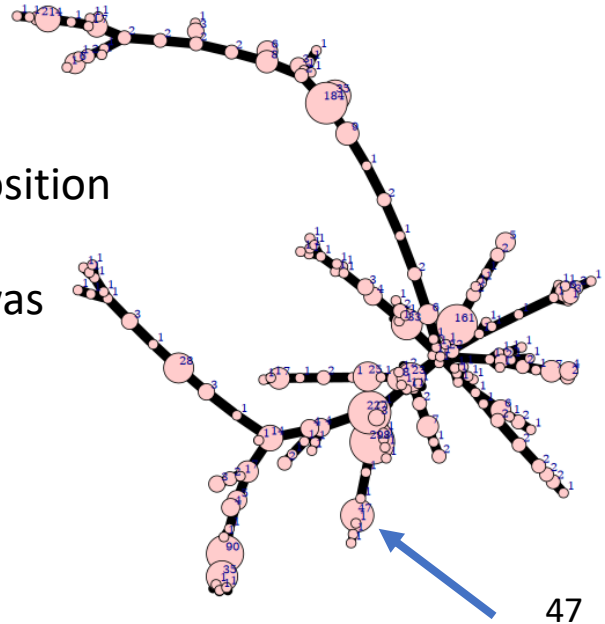
- Assays for CesA gene and OSBPI SNPs developed at Hutton – James Lynott will cover in more detail on Weds
- First applied in 2025 against FAB FTA card disks from 90 samples (every outbreak)
- Effective - detected expected resistances in EU43 and EU46

- **No resistance in other lineages in UK**

Within-lineage fungicide resistance variation

- Resistance to OSBPI fungicides already reported in EU36 lineage

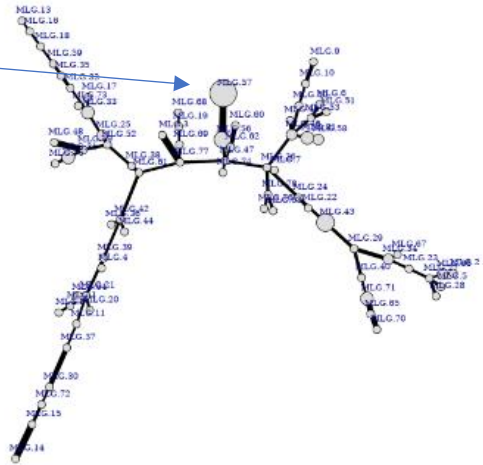
- Vincent Cesar CRAW detected 40% of EU36s with OXTP resistance in 2024
- Sequenced OSBP gene for 14 BE samples - R = N837 AA position
- 8 - WWC* mutation as per EU43s
- 6 - MWC* novel SNP also specific to novel SSR MLG that was present 47 times in 2024 population in BE, NL, DE and FR
- A factor in dominance of EU36?



* IUPAC nucleotide ambiguity codes W = A/T M = A/C

Below radar ‘mini-clone’ spread

- 1 NL2023 trial sample then DK2024 1 sample
- 24 DK 2025 samples across the country



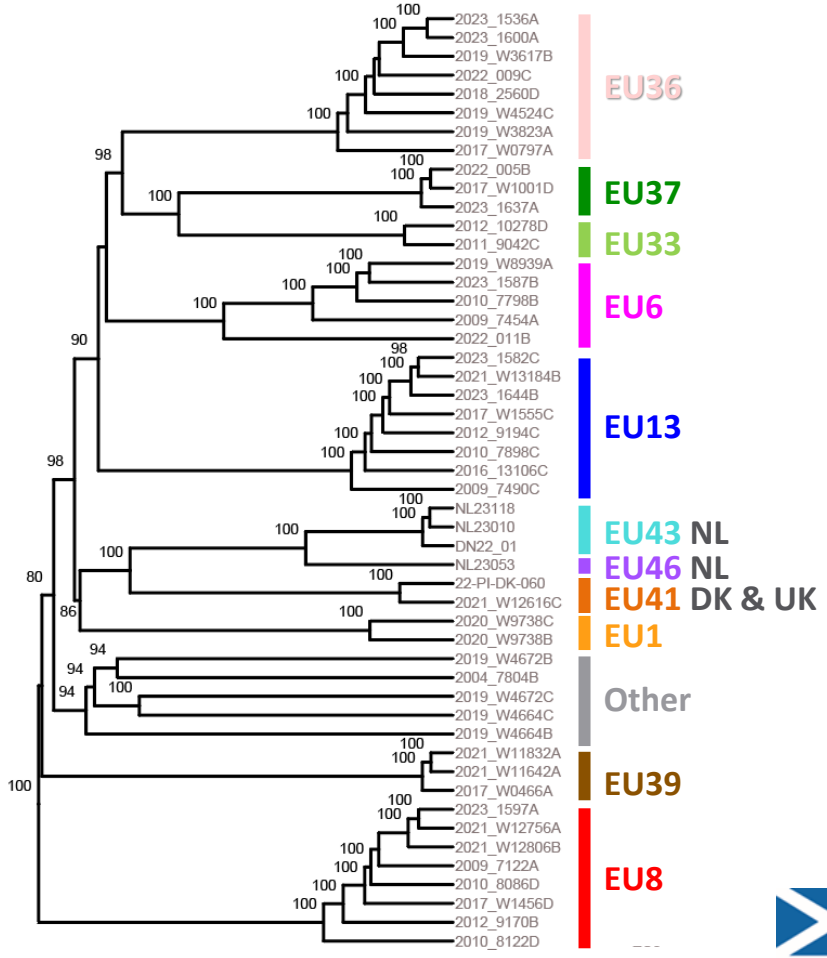
- DK & NO 11 samples 2024 & 2025
- DK & DE 18 samples 2023 to 2025
- DK, DE, NO 23 samples 2023 to 2025
- DK, BE, NL 18 samples 2021 to 2025

- NL 2021 & 2022 (26) & BE 2021 (1)

- RS2014 to 2025 clone 27 samples in RS, GR, IT, SL & DE
- HR2016 to 2025 tomato clone 41 samples DE, HR, HU, ES, PL

Could be early hints of trouble?

Effector and fungicide target site diversity



- 50 UK isolates across 16 years
- 580 effector and fungicide MoA genes sequenced with Penseq
- Diversity within lineages lower than between
- ‘other’ isolates distinct
- More detailed analysis needed
  - Amanpreet Kaur – Weds

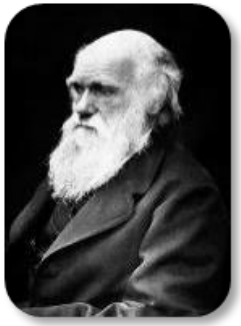
The James Hutton Institute

Scottish Government
Riaghaltas na h-Alba
gov.scot

Steve Whisson, Ingo Hein, Amanpreet Kaur

Reflections on improving IPM/ICM

EuroBlight
A potato late blight network for Europe



- Thinking like *Phytophthora* - Darwinian selection allows pathogen to exploit ‘chinks in our armour’
- Maximise complexity of route to crop infection - more layers of armour - fungicide actives & resistance genes
- Using sources wisely
  - Deploying intelligently in combination over time and space
  - Good reconnaissance - early warnings (examples given here)
- Reduce infection pressure
  - Inoculum sources - oospores, seed and volunteer tubers
  - Better awareness of weather conditions and spore load
- Improvements?
  - Population genomics - better understanding of MoA & virulence?
  - Revisions to naming within pathogen lineages and ‘Other’ types?