



EuroBlight

A potato late blight network for Europe



Phytophthora infestans diversity across Europe: 2013-2015

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Monitoring methods

- Scouts issued with sample forms and FTA cards (UK live cultures collected)
- Outbreak data (e.g. location, crop type, cultivar) recorded
- Lesions pressed onto FTA cards to capture pathogen DNA
- DNA fingerprinted using 12-plex SSRs (Li *et al.* 2013)
- Genotypes defined by DNA fingerprint and data stored in Euroblight database
- Data mapped on www.euroblight.net



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Euroblight *Phytophthora infestans* SAMPLING FORM

COMPULSORY: Please write clearly!

Reference number FTA card

Sampler name

e-mail address

Country

Town

Postal Code

OR gps coordinates (decimal)

OR gps coordinates (Deg, min, sec)

Source: [Production field or 'Trial']

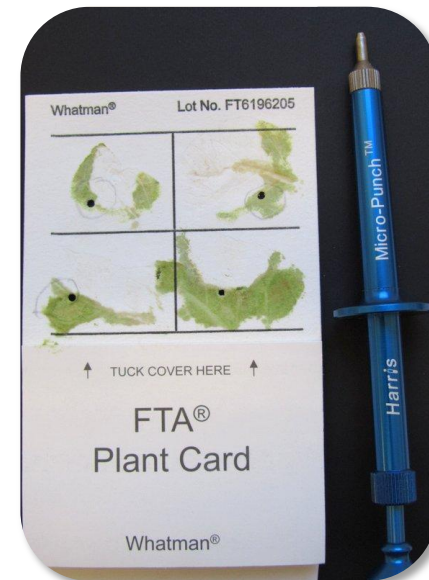
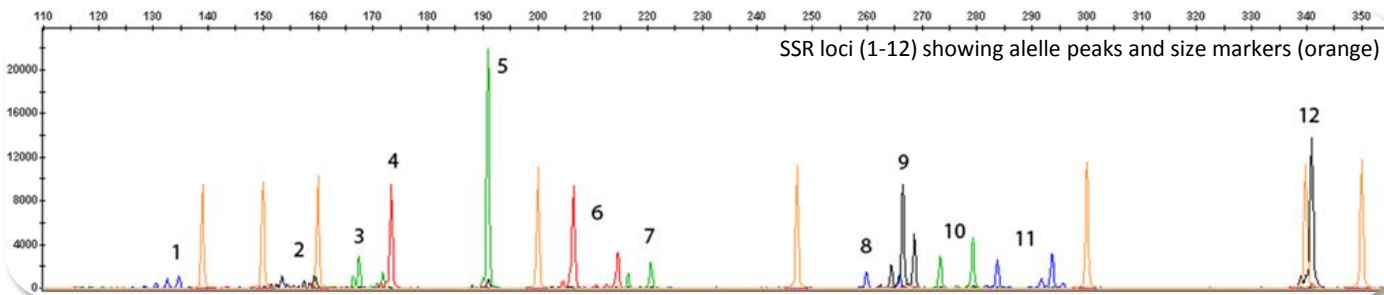
Sampling date

Host (Potato or Tomato)

Cultivar

Remarks

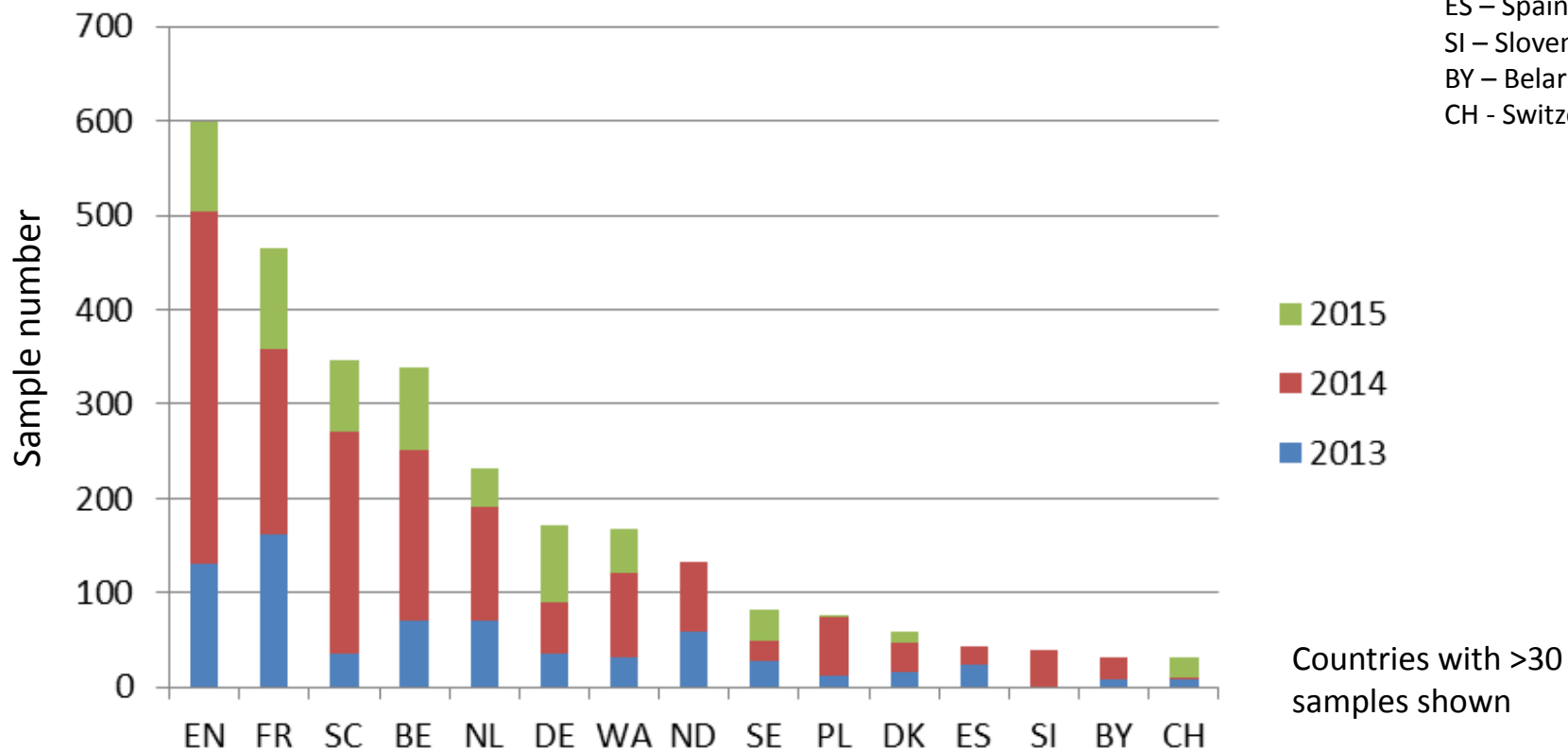
Disease level at sampling High Medium Low



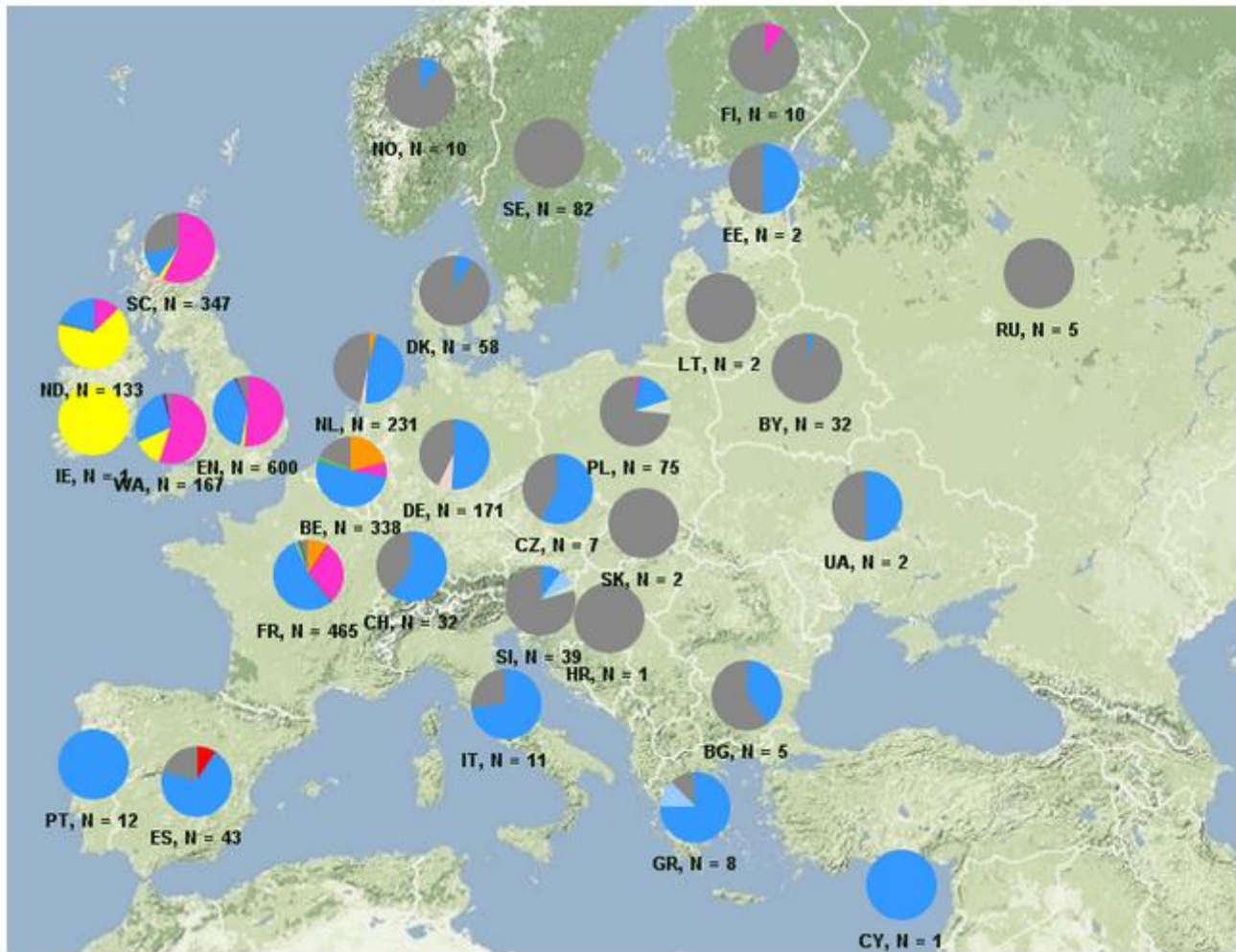
Sample statistics

- 2982 samples from 30 countries genotyped
- Most samples from northwestern Europe
- Long 'tail' of countries with few samples

EN – England
FR – France
SC – Scotland
BE – Belgium
NL – the Netherlands
DE – Germany
WA – Wales
ND – Northern Ireland
SE – Sweden
PL – Poland
DK – Denmark
ES – Spain
SI – Slovenia
BY – Belarus
CH - Switzerland



2013-2015 summary

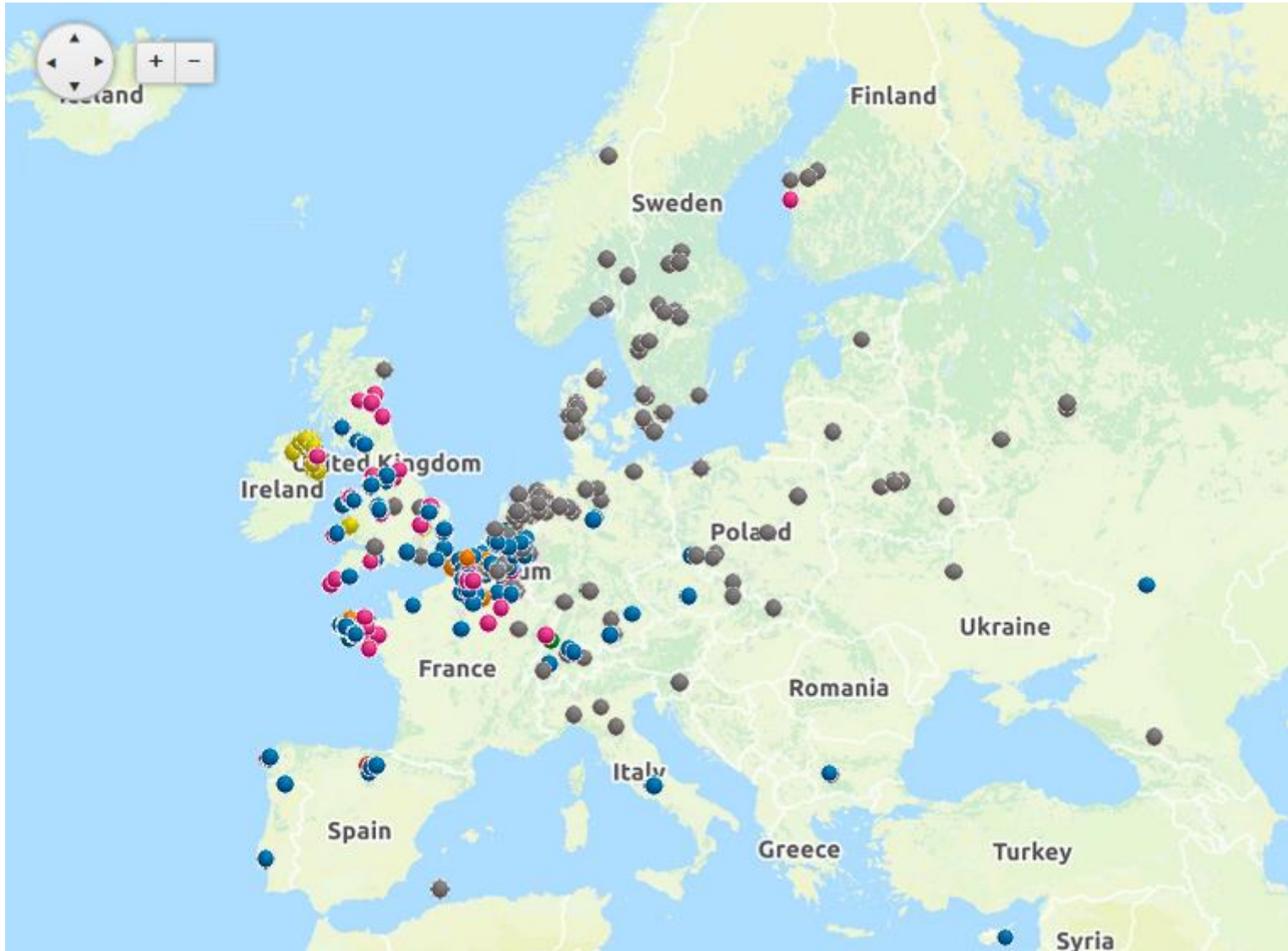


- EU_13_A2 clone most widespread
- Other clones clustered, e.g.
 - EU_6_A1 in UK and France
 - EU_8_A1 in Northern Ireland
 - EU_1_A1 in France and Belgium
- Higher proportion of 'Other' types in northern and eastern Europe



- 2892 samples from 30 countries

2013 samples



- 733 samples from 27 countries

2014 samples



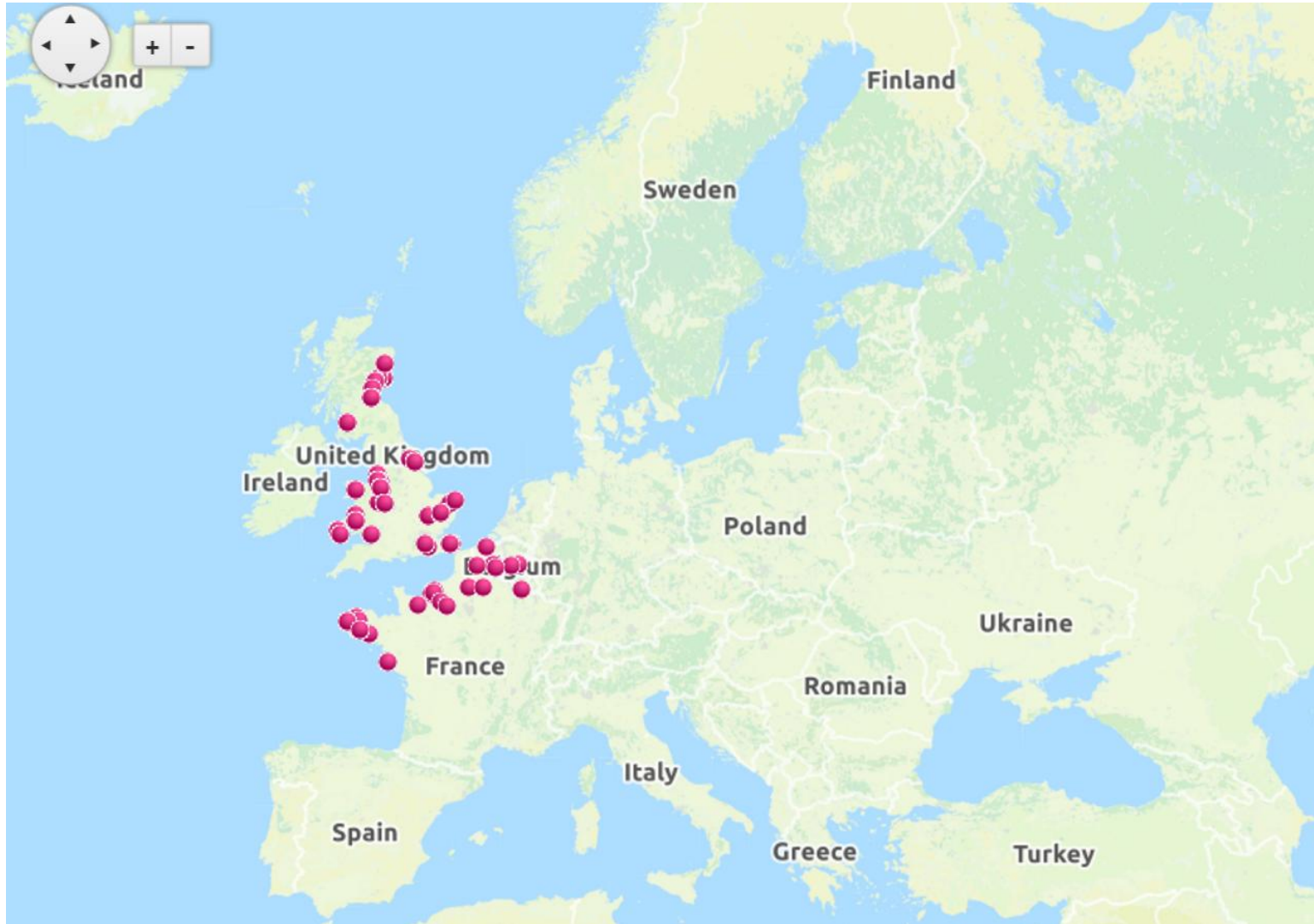
- 1545 samples from 24 countries

2015 samples



- 614 samples from 16 countries

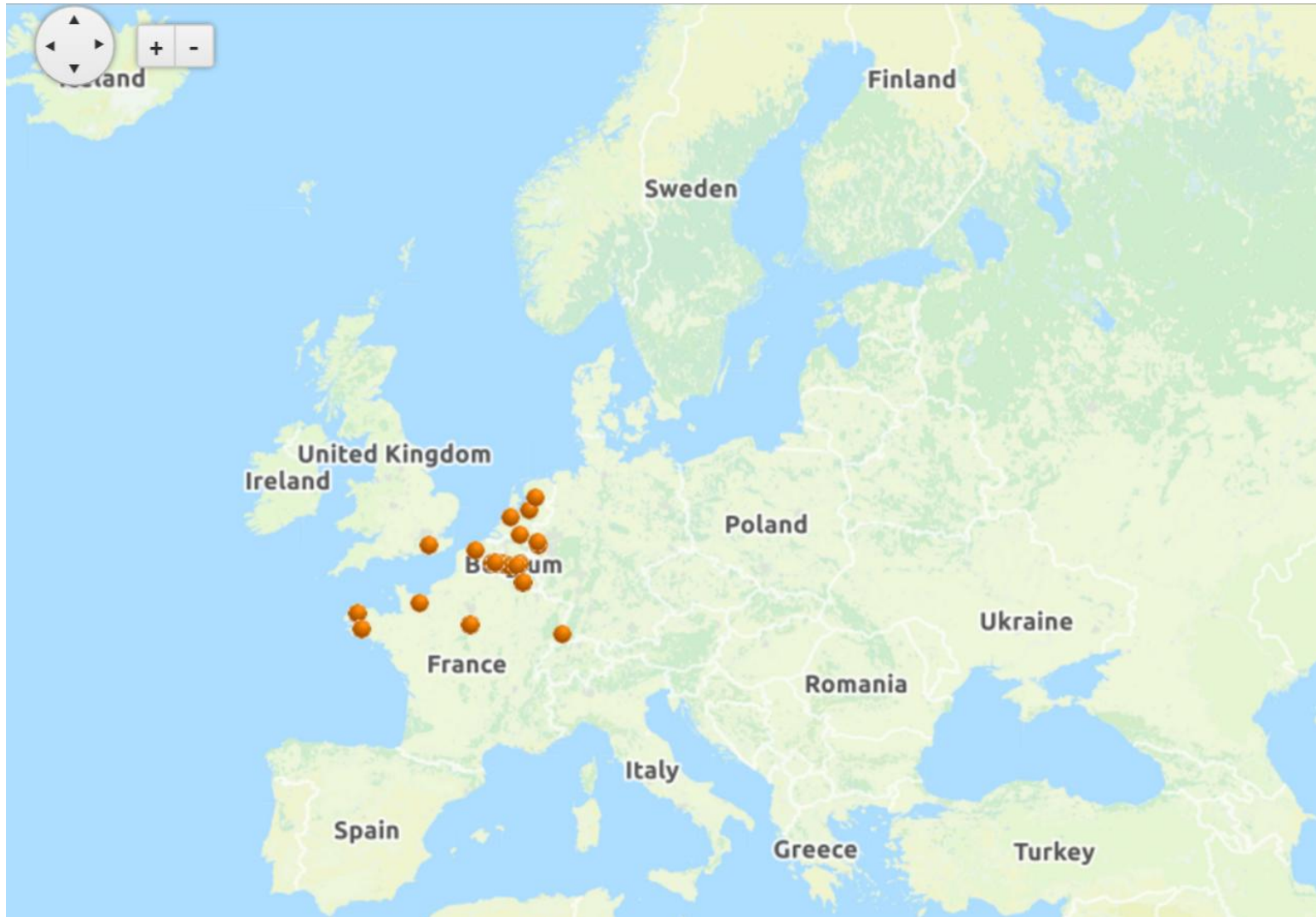
2015 samples – EU_6_A1



2015 samples – EU_13_A2



2015 samples – EU_1_A1



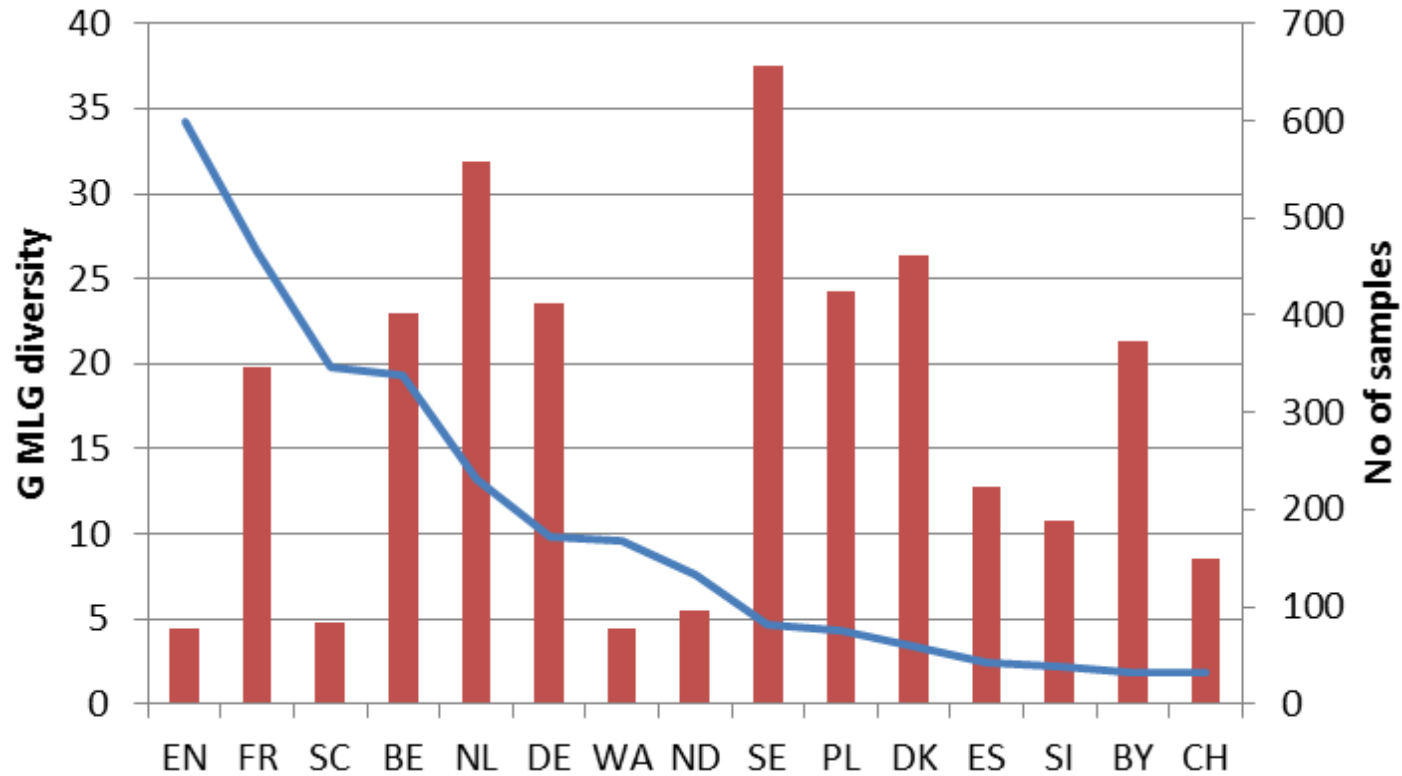
2014 samples – EU_36_A2



2015 samples – EU_36_A2



Genetic diversity of *P. infestans* by country (2013-2015)



- Multi-locus genotype (MLG) diversity measure (Stoddart and Taylor's G) shows variation by country (red bars)
- High sample numbers in UK (EN, WA, SC, ND) but mostly clonal thus overall diversity is low
- Higher proportion of 'Other' genotypes in some countries results in greater diversity



Conclusions

- Survey providing new insights on pathogen diversity
- Dominance of a few clones across large areas of European crops indicates that EU growers/industry share management challenges
- New clone (EU_36_A2) identified and decline of EU_33_A2 continues (1 isolate only in 2015)
- Much primary inoculum is locally generated and spread. Better management of inoculum sources would aid management
- Other populations highly diverse, ephemeral and most likely the result of sexual oospore formation
- High genetic diversity increases the risk of blight management problems due to a greater probability of pathogen types evolving virulence against novel host resistance genes and reduced sensitivity to specific fungicide active ingredients
- **Phenotypic traits of existing and novel genotypes will be examined in a new ERA-NET project (IPMBlight2.0)**
- Live data mapped on www.euroblight.net

