Eucablight – pathogen database update
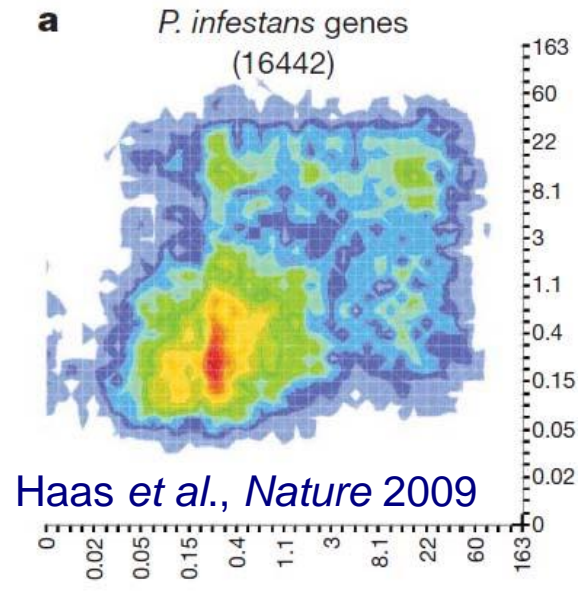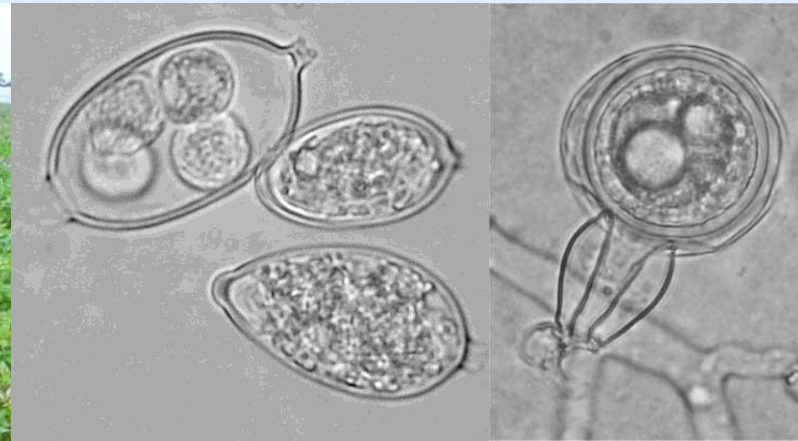
David Cooke

Björn Andersson
Jozsef Bakonyi
Jens Grønbech Hansen
Poul Lassen
Alison Lees
All data submitters

Aims

Haas *et al.*, *Nature* 2009

P. infestans populations
The big questions

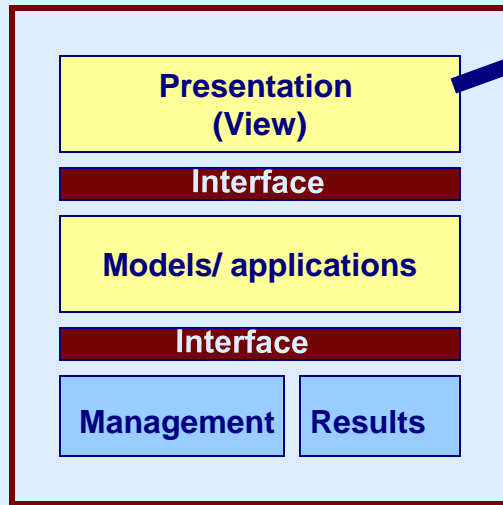Regional variation in mating success and the role of oospores

Mutation rate/recombination/rate of evolution

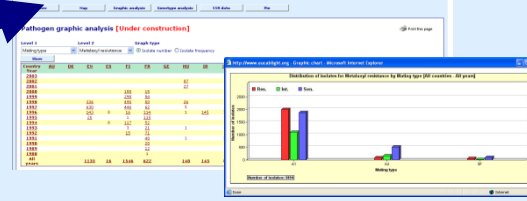Effector diversity, virulence and stability of resistance

Aggressiveness variation

Fungicide resistance
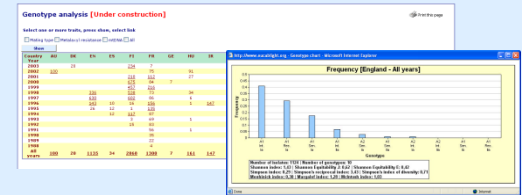
Migration within and beyond Europe

Phytophthora.exe and dataflow

Presentation (View)

Interface

Models/ applications

Interface

Management | Results

Graphic analysis

Genotype analysis

Allelle frequencies

$$H = -\sum_{i=1}^{S} p_i \ln(p_i)$$

For lab records - Export dbase as .csv file to XL

50+ database fields behind each isolate entered into the database = wealth of data to be mined.

Pathogen data

Phytophthora.exe
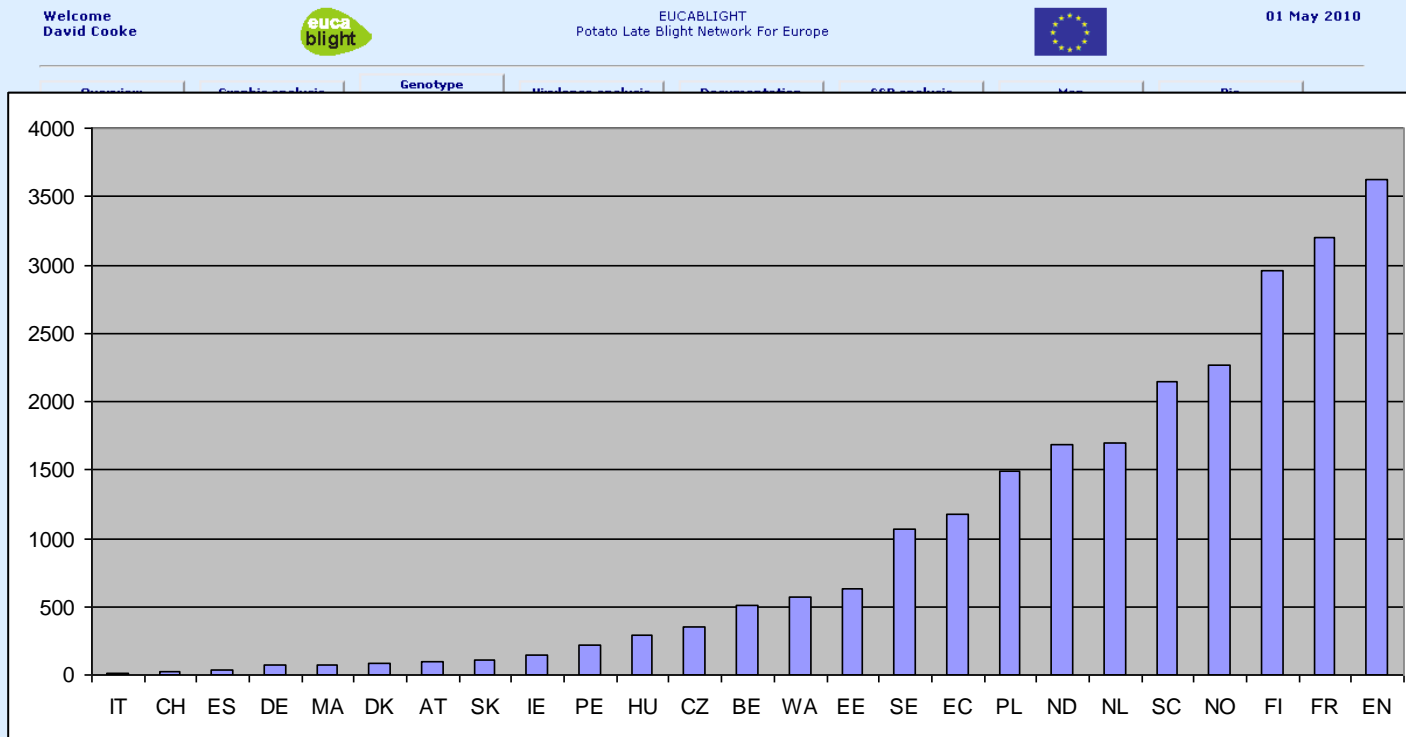Version 2.0

Pathogen data overview
www.eucablight.org

Welcome
David Cooke

euca blight

EUCABLIGHT
Potato Late Blight Network For Europe

01 May 2010

Overview   Graphic analysis   Genotype   Virulence analysis   Documentation   SSR analysis   Map   Bio

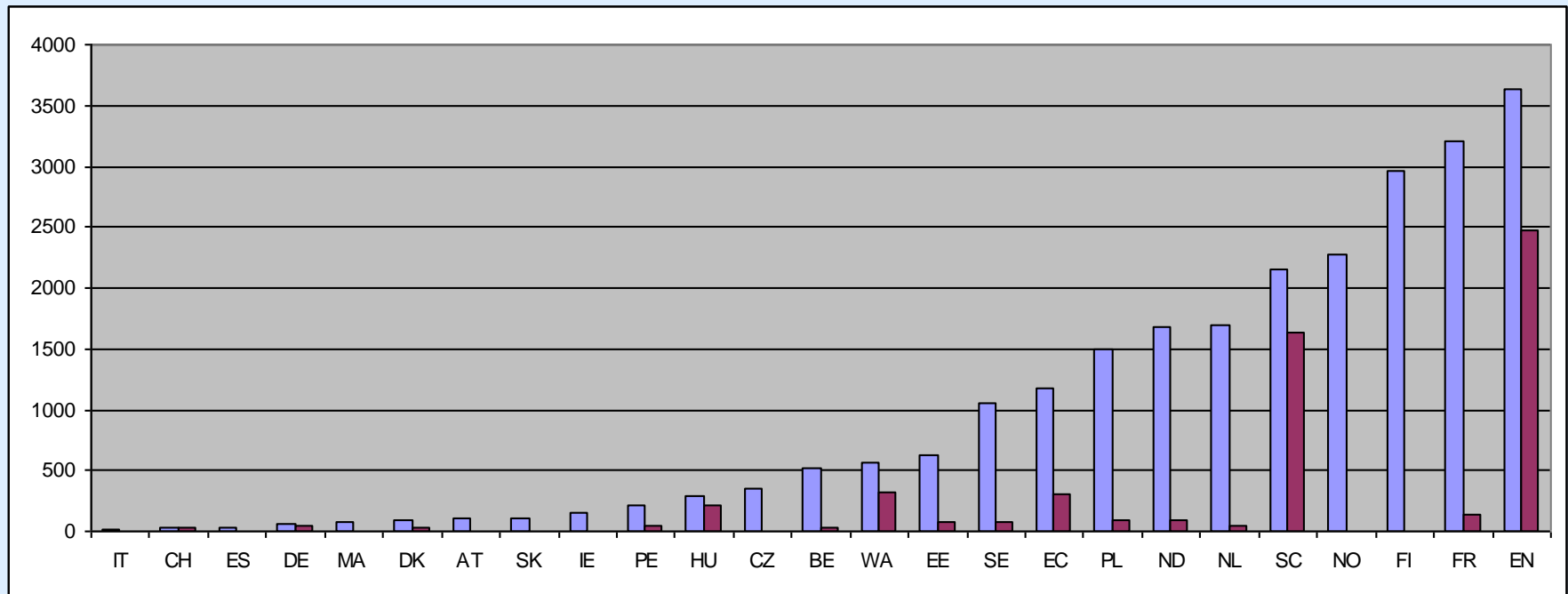| Tallinn Oct 2005 | 12,300 |
Rennes Jan 2006	13,600
Bologna May 2007	15,500
Hamar Oct 2008	19,200
Arras May 2010	24,600

Camille Bedard, Wallonia, BE
Ludovic Dubois & Serge Duvauchelle
Bayer CropScience
Syngenta
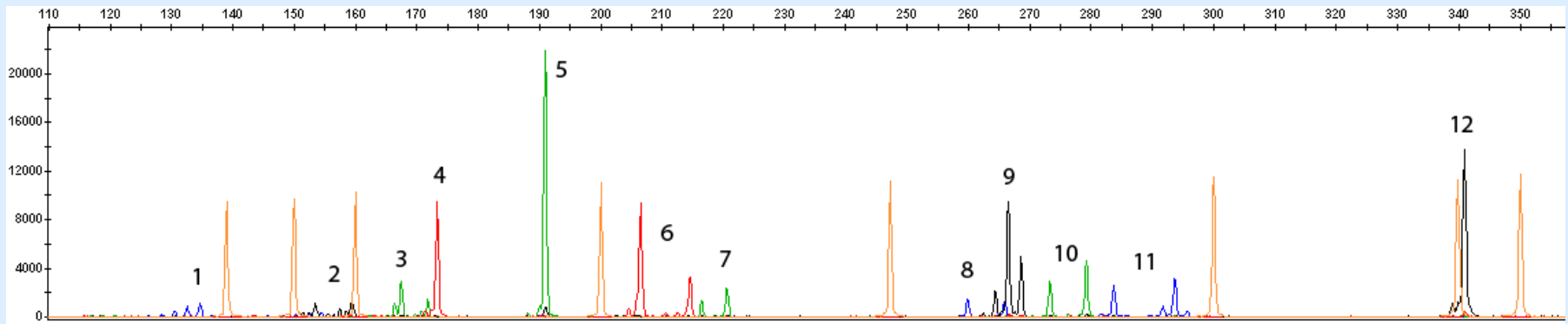**SCRI**

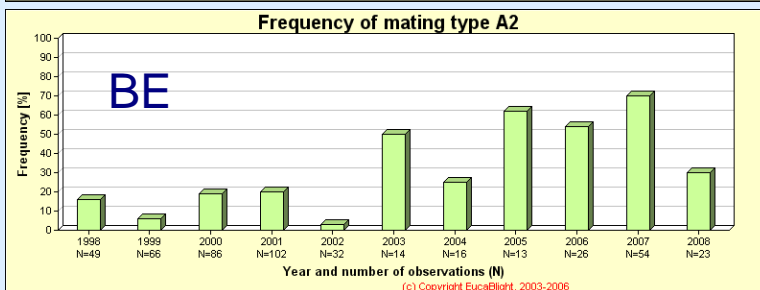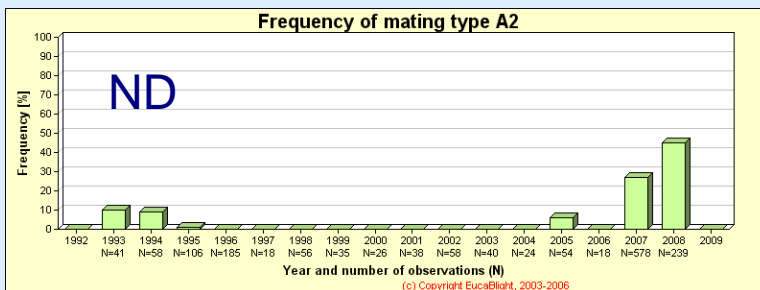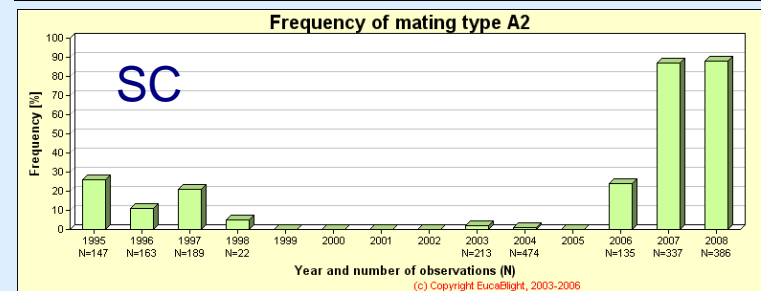# SSR data critical and more needed to fill in details

- 24,600 isolates
- 5660 isolates with SSRs
- 2300 more isolates than at Hamar

SSR system update

- Theo van der Lee, Ying Li and David Cooke designed and validated 12-plex assay of best SSR markers
- QIAGEN Type-it SSR Kit proved effective
- Quality equivalent or better
- Throughput increased
- 26 markers available – best 12 used
- (SSR1, SSR2, SSR3, SSR4, SSR5, SSR6, SSR7, SSR8, SSR11, Pi4B, PiG11, Pi4G, Pi1D, Pi2D, Pi2H, Pi02, Pi04, Pi16, Pi26, Pi33, Pi56, Pi63, Pi66, Pi70, Pi89, D13)

New 12 marker set combined SCRI and PRI

Increases in A2

EU-scale distribution of genotype 13_A2
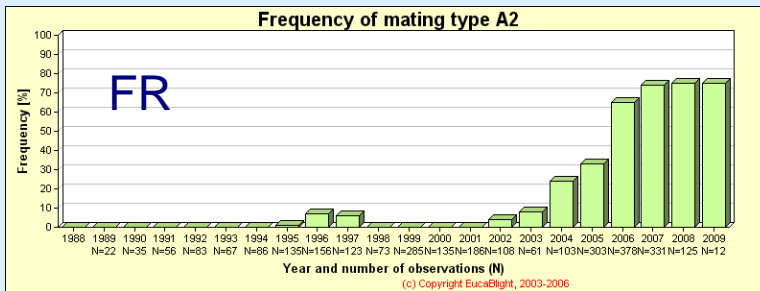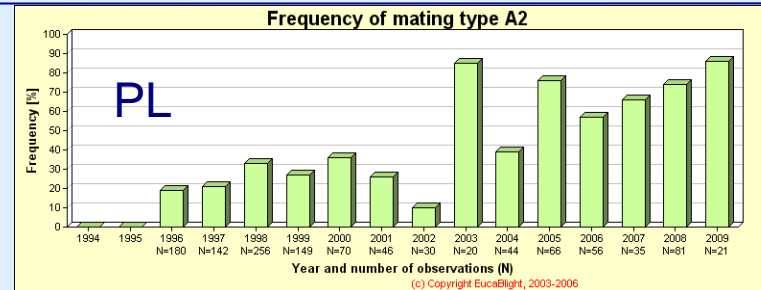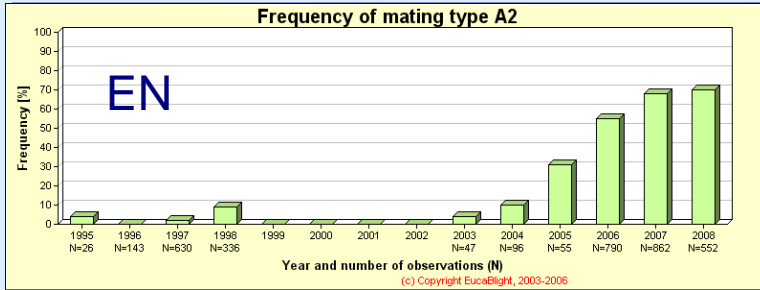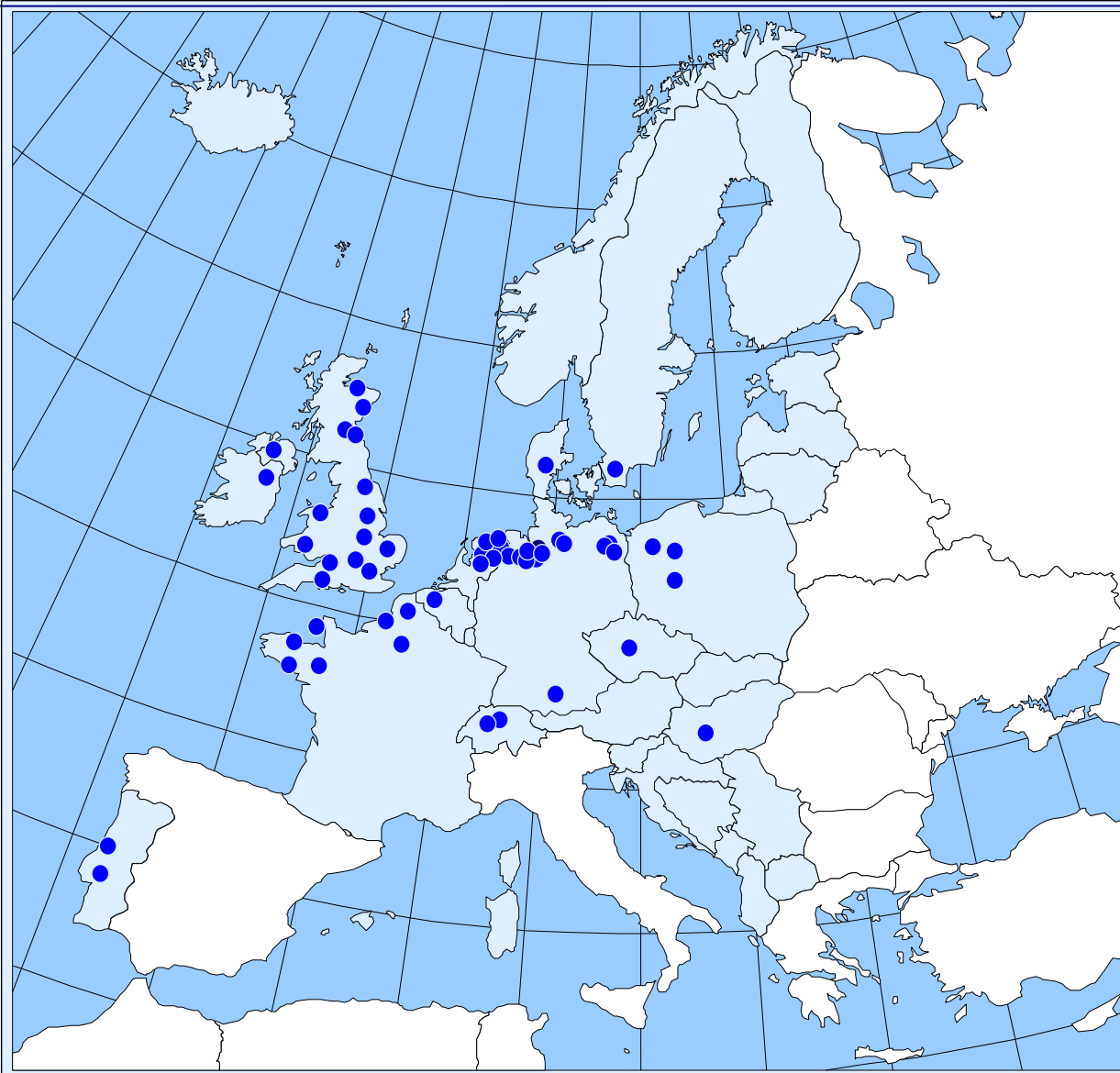
- **New records PL, CZ, HU, PO, J, SE, IE, ND, DK**

- **EUCABLIGHT data suggests this shift to A2 not universal: 2006 % A2 data (CZ 10, EE 12, HU <10, FI 40)**

- **Updates in SSR data needed**

- **Thanks to Bayer and Syngenta**

Tracking genotypes

Frequency of genotypes [England - 2007]

Number of isolates: 715 | Number of genotypes: 43
Shannon index: 2,14 | Shannon Equitability J: 0,57 | Shannon Equitability E: 0,20
Simpson's index of diversity: 0,74

(c) Copyright EucaBlight, 2003-2006
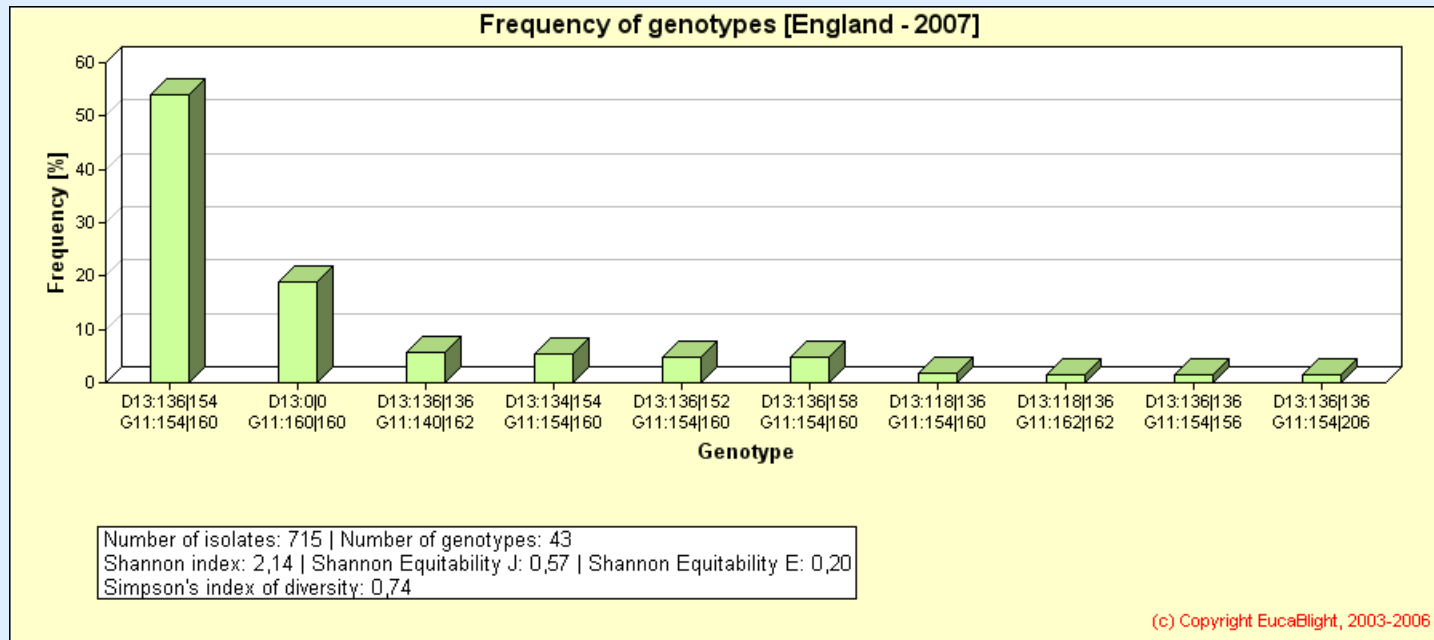
Genotype 13 at SSR D13 locus = 136/154

SSR Analysis methods

- Challenges due to ploidy (Bruvo distances)
- Challenges due to clonality
- Minimum spanning trees
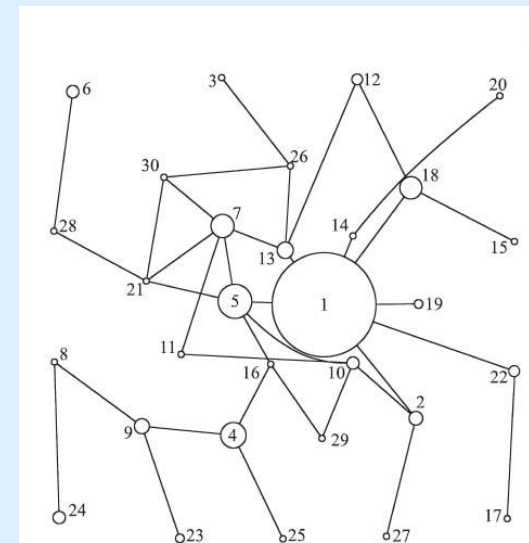- Collaboration with Nik Grunwald

Fig. 1 Minimum spanning network of all Belgian multilocus genotypes (30 MGs). Branch sizes are proportional to genetic distance and surface areas of the circles are proportional to the numbers of isolates detected. The numbers refer to the multilocus genotypes (Table S1, Supporting information).

P. ramorum Vercauteren *et al.,* 2009

Future directions

Sequences (P. exe ready)

- ## Effectors
  - RxLR, CRNs – related to virulence

- ## Fungicide resistance genes
  - (e.g. Blum *et al*., 2010, *MPP*. Mandipropamid moa determined and *P. infestans* gene now known

- ## Whole genome sequences
  - 454, Solexa, etc
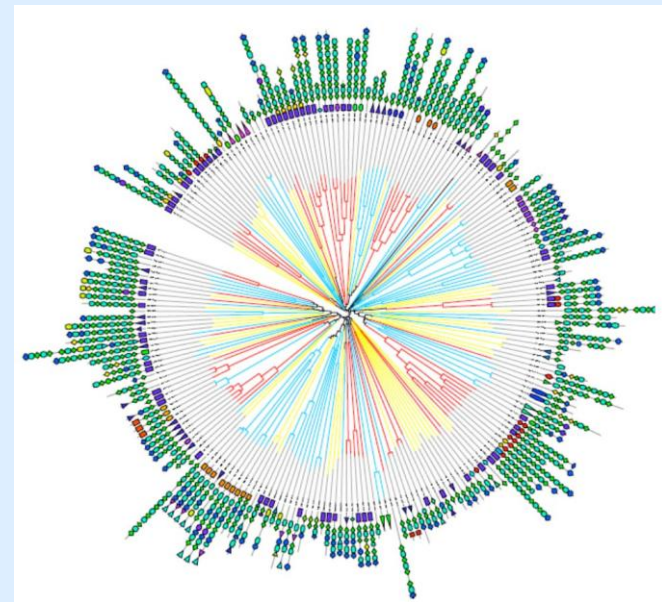
Web-tools needed

Refined tools needed to:

Track changing allele frequencies over time and space
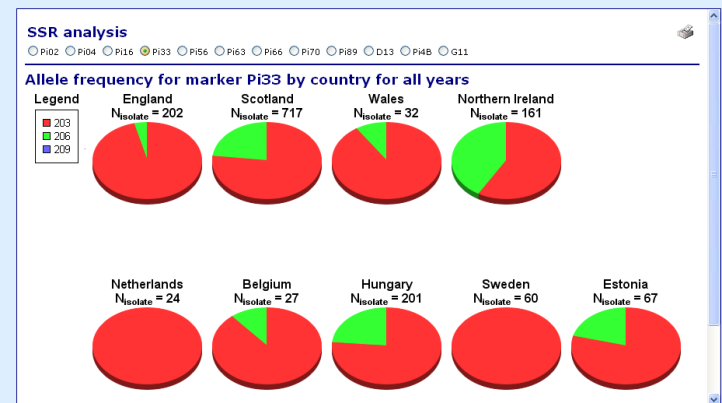
Genotype identification and naming

Plot relationships between genotypes

Search for specific genotypes

Relate phenotype to genotype

Map diversity – GIS systems

Sequence diversity

Funding bids

- EU Framework 7 bid – Jan 08 – not funded
- USDA Biosecurity bid - June 08 – not funded
- NSF EID bid - Nov 08 –not funded
- 2 USDA Bids – Pending

- Synergy from Eurowheat platform in Endure project - Jens Hansen University of Arhus
- Support of GILB/CIP

- Need to build Eucablight database development into other funding bids
- Sponsorship?

Conclusions & Future plans

- Unique resource to help understand pathogen population change on a range of scales
  (thanks to all data submitters and UoA)
- *P. infestans* population diverse and structured
- Association between factors observed (e.g. fungicide resistance and mating type)
- Dramatic shift in popn. noted in many EU regions

- Database updates and more interpretation at local and EU scale required.
- Link data on population change with the drivers of change.
  (e.g. increased aggressiveness and fitness – need better links to fundamental research on effectors and R-genes)
- Better exploitation of host resistance (GM-based?) – will only work if we understanding pathogen population
- Continue expansion beyond Europe - setting context of EU populations