Collating *P. infestans* population data: an update

David Cooke, Poul Lassen, Jens G Hansen









Summary



- Background key findings in past 18 months
- Recent data on European monitoring
- Status and plans for Eucablight database using rust toolbox as an example
- Conclusions and key questions



13_A2 spread in GB published

OPEN ACCESS Freely available online



Genome Analyses of an Aggressive and Invasive Lineage of the Irish Potato Famine Pathogen

David E. L. Cooke¹⁰*, Liliana M. Cano²⁹, Sylvain Raffaele², Ruairidh A. Bain³, Louise R. Cooke⁴, Graham J. Etherington², Kenneth L. Deahl⁵, Rhys A. Farrer², Eleanor M. Gilroy¹, Erica M. Goss^{6,7}, Niklaus J. Grünwald⁶, Ingo Hein¹, Daniel MacLean², James W. McNicol⁸, Eva Randall¹, Ricardo F. Oliva^{2,9}, Mathieu A. Pel¹⁰, David S. Shaw¹¹, Julie N. Squires¹, Moray C. Taylor¹², Vivianne G. A. A. Vleeshouwers¹⁰, Paul R. J. Birch^{1,13}, Alison K. Lees¹, Sophien Kamoun²*

1 The James Hutton Institute, Invergowrie, Dundee, United Kingdom, 2 The Sainsbury Laboratory, Norwich Research Park, Norwich, United Kingdom, 3 SAC, Edinburgh, United Kingdom, 4 Agri-Food and Biosciences Institute, Belfast, United Kingdom, 5 USDA-ARS/PSI-GIFVL, BARC-West, Beltsville, Maryland, United States of America, 6 Horticultural Crops Research Laboratory, USDA ARS, Corvallis, Oregon, United States of America, 7 Emerging Pathogens Institute & Department of Plant Pathology, University of Florida, Gainesville, Florida, United States of America, 8 Biomathematics and Statistics Scotland, The James Hutton Institute, Invergowrie, Dundee, United Kingdom, 9 Escuela Politecnica del Ejercito, Sangolquí, Ecuador, 10 Wageningen UR Plant Breeding, Wageningen, The Netherlands, 11 The Sarvari Research Trust, Henfaes Research Centre, Abergwyngregyn, Llanfairfechan, United Kingdom, 12 Food and Environment Research Agency, Sand Hutton, York, United Kingdom, 13 Division of Plant Sciences, College of Life Sciences, University of Dundee at The James Hutton Institute, Invergowrie, Dundee, United Kingdom



12plex SSR system published



Contents lists available at SciVerse ScienceDirect

Journal of Microbiological Methods





Efficient multiplex simple sequence repeat genotyping of the oomycete plant pathogen *Phytophthora infestans*



Ying Li a,c,d, David E.L. Cooke b,*, Evert Jacobsen c, Theo van der Lee d,*

- Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences, Beijing, 100081, China
- The James Hutton Institute, Invergowrie, Dundee, DD2 5DA, UK
- ^c Plant Breeding, Wageningen UR, P.O. Box 386, 6708 PB Wageningen, The Netherlands
- d Bio-interaction and Plant Health, Plant Research International B.V., Wageningen UR, P.O. Box 16, 6700 AA Wageningen, The Netherlands



 13_A2 in NL and presence of Rpi-blb 1 breaking strains in NL population (G3 journal)

Population Dynamics of *Phytophthora infestans* in the Netherlands Reveals Expansion and Spread of Dominant Clonal Lineages and Virulence in Sexual Offspring

Y. Li,*,† T. A. J. van der Lee,†,1 A. Evenhuis,† G. B. M. van den Bosch,† P. J. van Bekkum,† M. G. Förch,† M. P. E van Gent-Pelzer,† H. M. G. van Raaij,† E. Jacobsen,‡ S. W. Huang,* F. Govers,§,**
V. G. A. A. Vleeshouwers,‡ and G. J. T. Kessel†

*Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences, 100081, Beijing, China, †Bio-interactions and Plant Health, Plant Research International, 6700 AA Wageningen, ‡Laboratory of Plant Breeding, Wageningen University, 6708 PB Wageningen, §Laboratory of Phytopathology, Wageningen University, 6700 EE Wageningen, and **Centre for BioSystems Biology, 6700 AB Wageningen, The Netherlands



13_A2 confirmed in China



Plant Pathology (2012)

Doi: 10.1111/j.1365-3059.2012.02687.x

Population structure of *Phytophthora infestans* in China – geographic clusters and presence of the EU genotype Blue_13

Y. Li^a, T. van der Lee^{b*}, J. H. Zhu^c, G. H. Jin^d, C. Z. Lan^e, S. X. Zhu^f, R. F. Zhang^g, B. W. Liu^h, Z. J. Zhaoⁱ, G. Kessel^b, S. W. Huang^a and E. Jacobsen^f

^aInstitute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences, 100081, Beijing, China; ^bPlant Research International, 6700 AA, Wageningen, the Netherlands; ^cHebei Agricultural University, 071001,Baoding; ^dHeilongjiang August First Land Reclamation University, 163319, Daqing; ^eFujian Academy of Agricultural Sciences, 350003, Fuzhou, China; ^fWageningen University and Research Centre, 6708 PB, Wageningen, the Netherlands; ^gInner Mongolia University, 010021, Hohhot, Inner Mongolia; ^hSichuan Academy of Agricultural Sciences, 650231, Kunming, China



doi: 10.1111/jph.12031

13_A2 confirmed in India

Journal of Phytopathology

J Phytopathol © 2012 Blackwell Verlag GmbH

Division of Plant Pathology, Indian Institute of Horticultural Research, Bangalore, India

Emergence of 13_A2 Blue Lineage of *Phytophthora infestans* was Responsible for Severe Outbreaks of Late Blight on Tomato in South-West India

Pallem Chowdappa¹, Nirmal B. J. Kumar¹, Shivanna Madhura¹, Mohan S. P. Kumar¹, Kevin L. Myers², William E. Fry², Julie N. Squires³ and David E. L. Cooke³

Authors' addresses: ¹Division of Plant Pathology, Indian Institute of Horticultural Research, Bangalore, 560 089, India; ²Department of Plant Pathology and Plant-Microbe Biology, Cornell University, 334 Plant Science Bldg, Ithaca, NY, 14853, USA; ³The James Hutton Institute, Invergowrie, Dundee, DD2 5DA, UK (correspondence to P. Chowdappa. E-mail: pallem22@gmail.com)

Received May 16, 2012; accepted September 4, 2012



Clonal populations US-1 and KE-1 dominant in Sub-Saharan
 Africa



Plant Pathology (2013) 62, 154-165

Doi: 10.1111/j.1365-3059.2012.02608.x

Phytophthora infestans populations in central, eastern and southern African countries consist of two major clonal lineages

B. B. Pule^{ab}, J. C. Meitz^b, A. H. Thompson^a, C. C. Linde^c, W. E. Fry^d, S. D. Langenhoven^b, K. L. Meyers^d, D. S. Kandolo^a, N. C. van Rij^e and A. McLeod^{b*}

^aAgricultural Research Council – Vegetable and Ornamental Plant Institute, Private Bag X 293, Pretoria 0001; ^bDepartment of Plant Pathology, University of Stellenbosch, Private Bag X1, Matieland 7602, South Africa; ^cDivision of Evolution, Ecology and Genetics, Research School of Biology, Building 116, Daley Rd, Australian National University, Canberra, ACT 0200, Australia; ^dDepartment of Plant Pathology, Cornell University, Ithaca, NY 14853, USA; and ^eKwaZulu-Natal Department of Agriculture and Environmental Affairs, Crop Protection Division, Private Bag X9059, Pietermaritzburg 3200, South Africa



 Evidence for sexual recombination in European P. infestans reviewed



Plant Pathology (2012)

Doi: 10.1111/j.1365-3059.2012.02685.x

REVIEW

What is the evidence for sexual reproduction of *Phytophthora* infestans in Europe?

J. E. Yuen* and B. Andersson

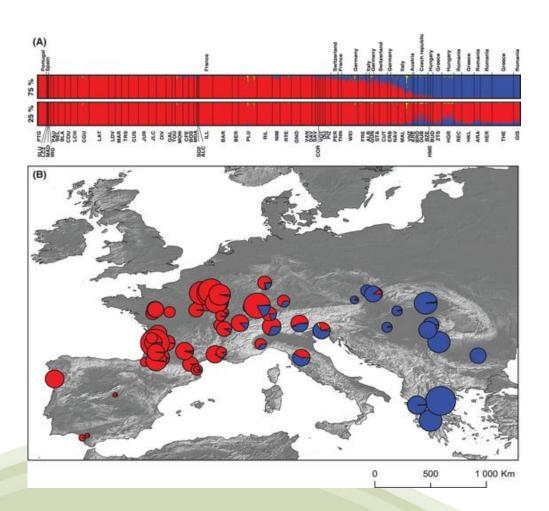
Department of Forest Mycology and Plant Pathology, Swedish University of Agricultural Sciences, SE 750 05, Uppsala, Sweden



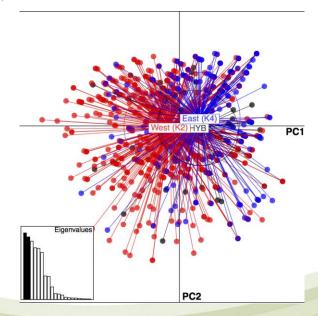
- Hamed & Gisi 2012 Generation of pathogenic F1 progeny from crosses of *Phytophthora infestans* isolates differing in ploidy. *Plant Pathology*
 - Ploidy of some EU isolates and increased viability of diploid x diploid crosses compared to crosses involving triploid isolates confirmed
- Lees, et al 2012. The Effect of a dominant Phytophthora infestans genotype (13_A2) in Great Britain on host resistance to foliar late blight in commercial potato cultivars. Potato Research 55, 125-134
 - Confirmed decrease in resistance ratings

Genetic signature of a range expansion and leap-frog event after the recent invasion of Europe by the grapevine downy mildew pathogen *Plasmopara viticola*





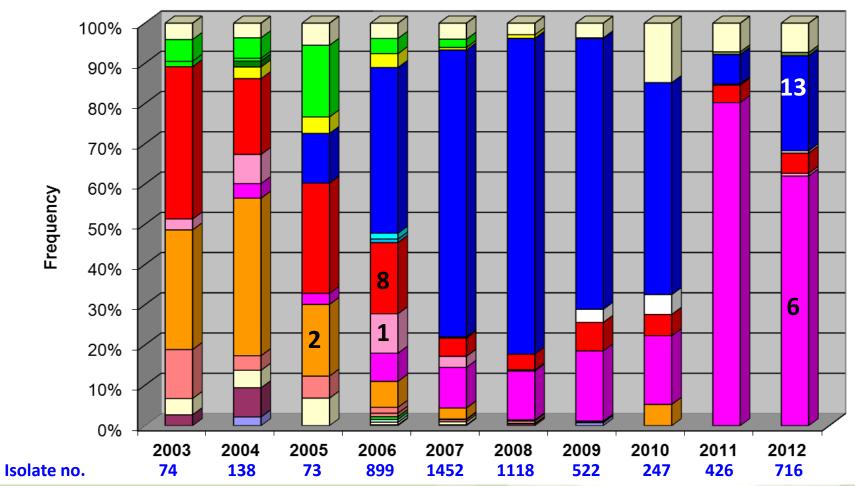
- 1146 samples from 68 vineyards
- 8 SSR loci
- 515 genotypes
- Generally low diversity interbreeding population suggests single introduction in 1870s
- Weak discrimination of East and West populations



GB P. infestans population update



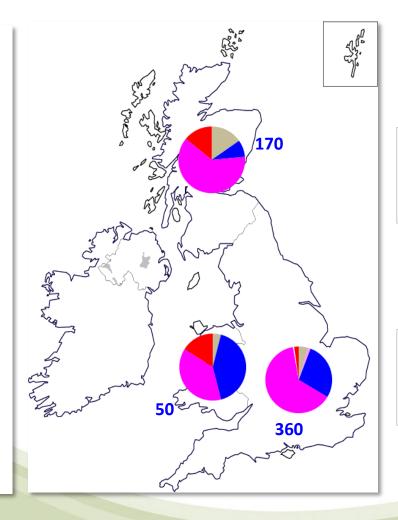
GB genotypes

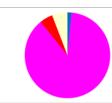


2012 GB P. infestans genotype by country

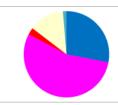


- Scotland higher proportion of 6_A1 relates to last years dominance of this genotype. Greater number of novel genotypes than in England and Wales
- England 6_A1 dominated despite a cooler wetter season that was expected to have been more conducive to 13_A2
- Wales greatest frequency of 13_A2
- Summary
 - GB still dominated by two agressive clonal lineages
 - primary inoculum from last season is important



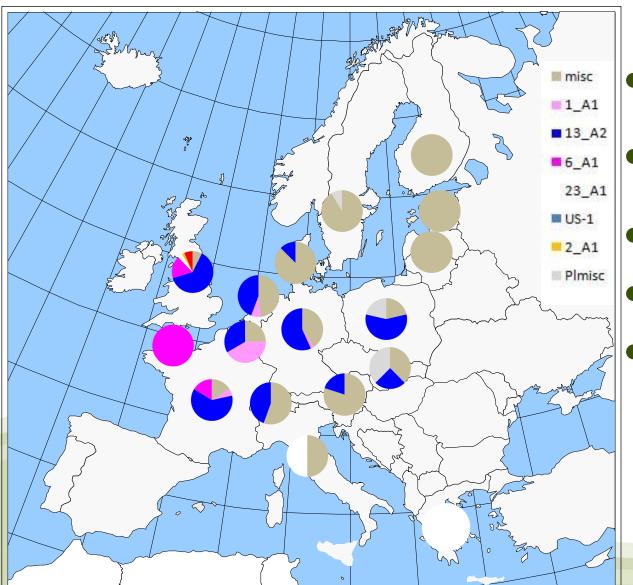


2011



Sample of EU *P. infestans* genotypes (2008-10) (n=350)

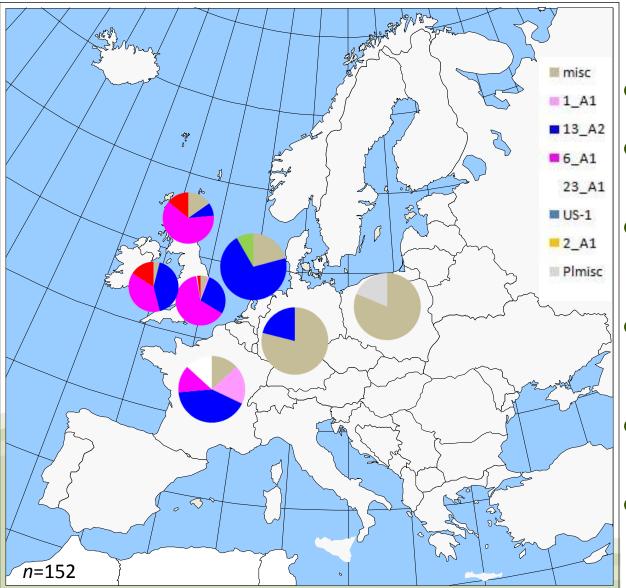




- 13_A2 still present in many areas (less due to reduced Metalaxyl use?)
- A high proportion of novel 'misc' types particularly in NE
- New genotype in PL, SK & SE
- 23_A1 on tomato in Italy & GK
- Thanks to Bayer and Syngenta, Howard Hinds, Vangelis Vellios

Genotypic diversity in 2012 (mainland Europe)





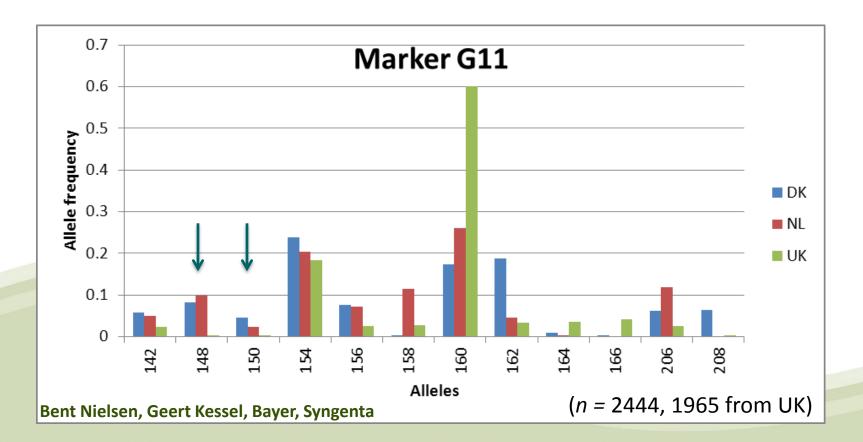
- Christophe Andreas-Braun (fungicide session)
- France (n = 53) the population remains mainly clonal
- Germany (n= 57) fewer
 13_A2 isolates and more novel misc genotypes
- Netherlands (n=24)
 13_A2 dominant with
 misc and genotype 33
 also present
- Poland (n=16) One Polish clone and many diverse isolates
- UK (PCL) (n=578)



SSR Allele frequency differences



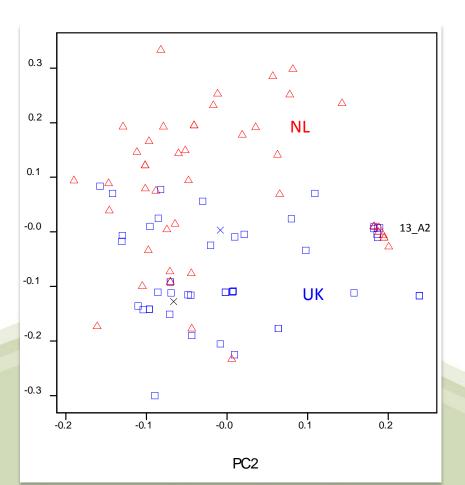
- Many alleles in common across Europe
- Country-specific differences in allele frequencies noted
- Comparisons on standard data in database easier & faster



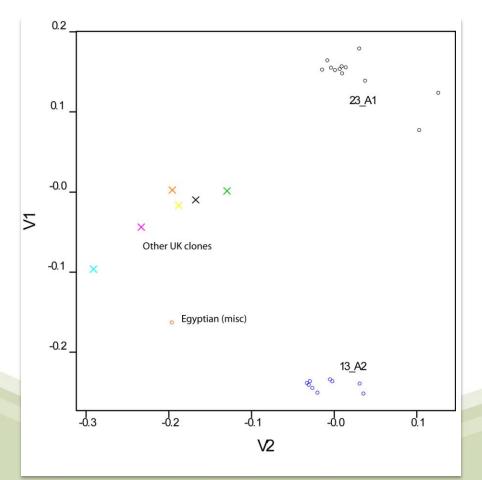
Population comparisons – ssrs & Polysat

The James
Hutton
Institute

- Li et al 2012 J. Microb. Methods 12 plex script
- Clones versus novel isolates
- NL vs UK populations



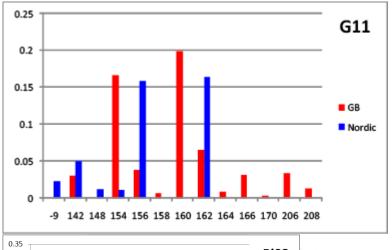
- Sherif El Ganainy, Giza, Egypt
- Clonal population
- Sub clonal comparisons may identify source population

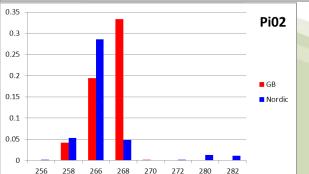


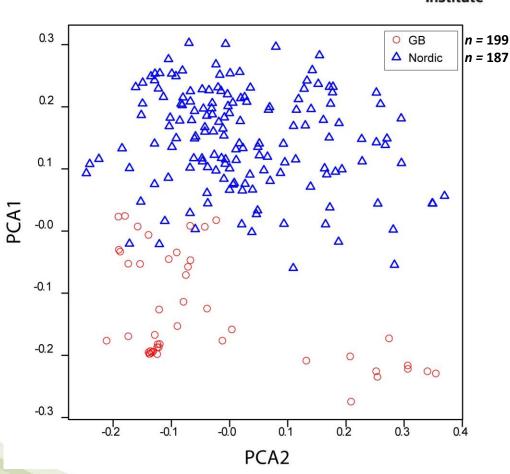
UK versus Nordic regions

The James
Hutton
Institute

- Nordic population (2003)
 more diverse than GB (2006)
- Populations distinct due to specific alleles







Nordic data (Brurberg, Elameen, From Brurberg et al., 2011) GB data - JHI

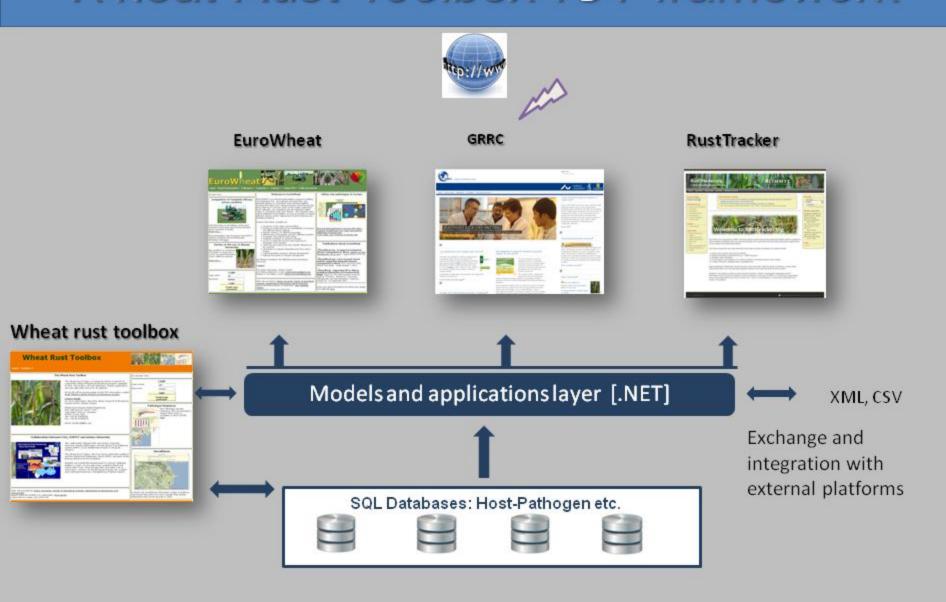


The Wheat Rust Toolbox for global wheat rust surveillance and monitoring

Jens G. Hansen¹, Poul Lassen¹, Mogens Hovmøller¹ & David Hodson²



Wheat Rust Toolbox ICT framework



Data Management: Wheat Rust Toolbox

NB: Generic - Applicable to all rusts & other diseases Wheat Rust Toolbox On-line Data Entry

Quality



Outputs:

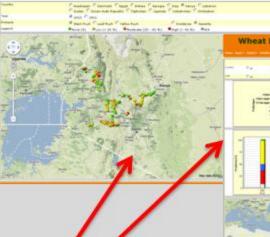
- Survey Mapping
- · Pathotypes, +...





Smartphone / tablet survey tool

control/publish User





Data Export / Exchange

Management

Wheat Rust Toolbox

Host Pathogen Dbase (survey, pathotypes,)

Trap nursery, Barberry, Molecular



External Applications e.g., RustMapper



Rust Tracker.org / Toolbox – Platform for all rusts

Importance of Rusts

underlying database will automatically be displayed on the graphs.

Yew C 2012 © 2011 C 2018 C 2008 C 2008

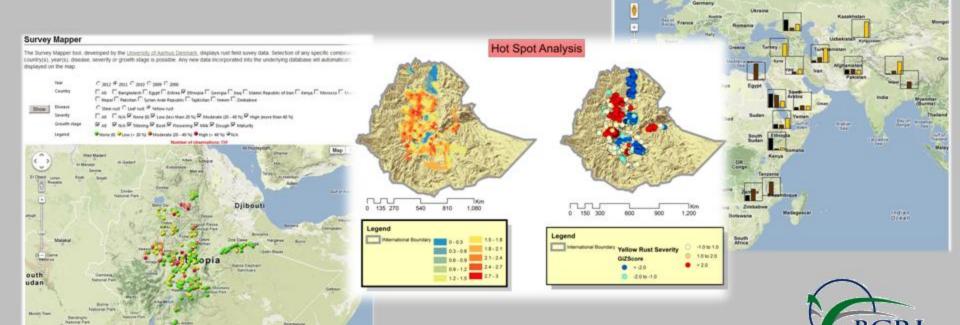
The importance of Rusts tool, developed by the <u>University of Aarhus Denmark</u>, displays the relative importance (freque

observed on field survey) of the three wheat rusts – stem, leaf, and yellow rust, per country and year. Selection of any si Black bars represent stem rust, brown bars represent leaf rust and yellow bars represent yellow rust. Any new data inco

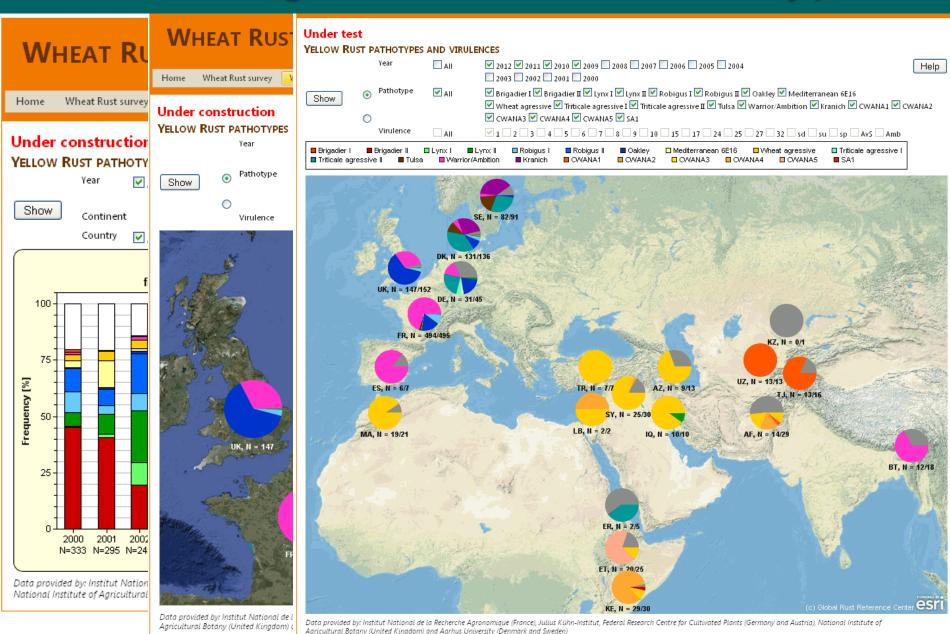
Map Satelite

Borlaua Global Rust Initiative

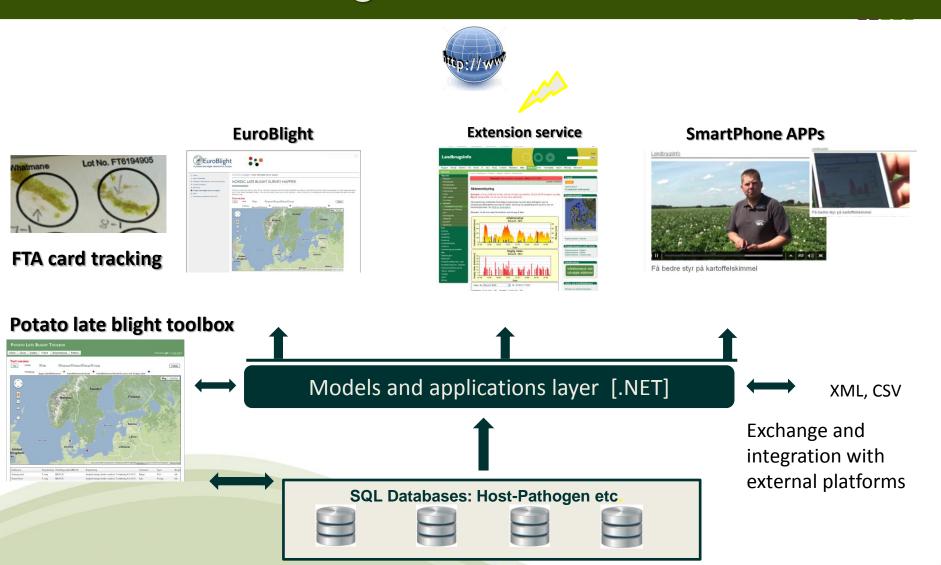
- All examples show Yellow Rust
- Increased focus on other rusts
- (Platform for other diseases)



Monitoring: Virulences / Pathotypes



Potato Late Blight Toolbox ICT framework



Potato Late Blight Toolbox: Status

- A Potato Late Blight Toolbox constructed
- Existing *P. infestans* data to be transferred to new Host Pathogen DB that stores the global wheat rust data.
- Data entry tools, data management tools and display tools can be re-used for *P. infestans* with minor adaptations.
- Include R-statistical server based components. This is under development
- Import of data and data visualization on Web / smartphone / Web services
- Obvious synergy between experiences from organisation, integration and collaboration on a global scale from the Wheat rust databases

Conclusions, questions & thanks



- P. infestans population diverse but structured in EU
- Database upgrade will provide more powerful analysis and visualisation tools to inform management
- We need to better understand phenotype genotype link
- Why do clones dominate in some regions and not in others?
- Does sexual recombination drive adaptation to fungicides & host resistance? Does theory match fact?

Thanks to all current and future data submitters