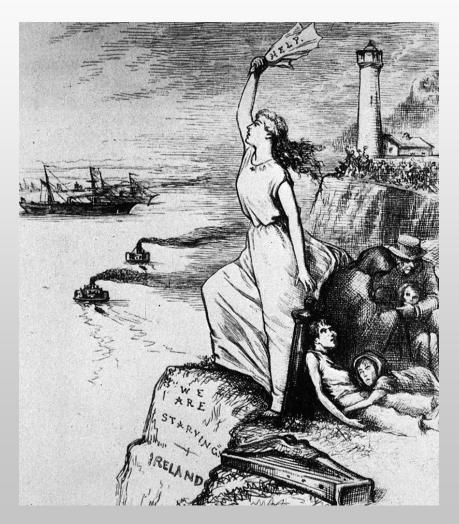
Digital Innovation to Tackle the Global Threat of Late Blight

Jean Beagle Ristaino WNR Distinguished Professor Department of Entomology and Plant Pathology Director Emerging Plant Disease and Global Food Security Cluster





The future of food and agriculture

The global trends and challenges that are shaping our future

Improve income earning opportunities in rural areas and address the root causes of migration

Population growth, globalization, inequalities and climate change will accelerate distress migration

> Make food systems more efficient, inclusive and resilient

End hunger and all forms of malnutrition

Globally, around one-third of all food produced is lost or wasted resulting in losses for farmers and unnecessary pressures on natural resources

~1/2 billion

people in more than 20 countries are affected by protracted crisis

Build resilience to protracted crises, disasters and conflicts Outbreak of transboundary pests and diseases of plants and animals is growing alarmingly

Prevent transboundary and emerging agriculture and food system threats Address the need for coherent and effective national and international governance



Food and Agriculture Organization of the United Nations

fao.org/publications/fofa/en



A constraint to potato production and global food security worldwide

The disease has increased in incidence, geographical and host range

Spread of Phytophthora infestans Spread by sporangia – spread in

air – 100' kilometers



Phytophthora infestans sporangia



Late blight epidemics in the US in 2009 **Emergence of US-22 strain**

- Climate change rainy season
- Movement of infected tomato transplants
- Susceptible varieties

The New Hork Times

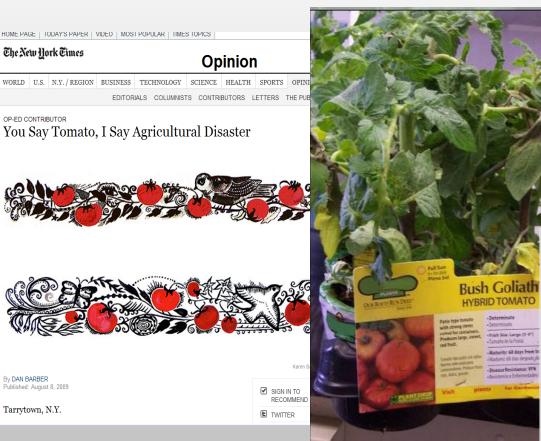
OP-ED CONTRIBUTOR

By DAN BARBER

Published: August 8, 2009

Tarrytown, N.Y.

WORLD U.S. N.Y. / REGION BUSINESS



Science News

& Animals

ssland

orests

🍰 Share 📝 Blog 📮 Cite

Late Blight -- Irish Potato Famine Fungus -- Attacks U.S. Northeast Gardens And Farms Hard

ScienceDaily (July 5, 2009) - Home gardeners beware: This year, late blight -- a destructive infectious disease that caused the Irish potato famine in the 1840s -- is killing tomato and potato in gardens and on commercial farms in the rn United States. In addition, basil downy w is affecting plants in the Northeast.

> "Late blight has never occurred this early and this widespread in the U.S." said Meg McGrath, associate professor of plant pathology and plant Jangered Plants microbe biology

> sts and Parasites One of the most visible early symptoms of the disease is brown Climate spots (lesions) on stems. They begin small and firm, then quickly enlarge, with white fundal growth developing tic Species under moist conditions that leads to a soft rot collapsing the stem

opathology Classic symptoms are large (at least er mould nickel-sized) olive-green to brown loom plant spots on leaves with slightly fuzzy white fungal growth on the underside when conditions have been humid (early

morning or after rain). Sometimes the of the spot is yellow or has a water-soaked appearance. begin tiny, irregularly shaped and brown. Firm, brown spots on tomato fruit.

enlarge

Leaf lesions due to late blight. (Credit: Copyright College of Agriculture and Life Sciences, Cornell University)

Ads by Google

Plant Problems? Try BASF Control downy mildew diseases with BASF Stature SC fungicide www.BetterPlants.BASF.us

2009 Mazda Clearance

Inventory blowout pricina! Dealers are liquidating inventory Mazda.Reply.com

```
Adam
```

The New York Times

uly 18, 200

Outbreak of Fungus Threatens Tomato Crop

By JULIA MOSKIN

A highly contagious fungus that destroys tomato plants has quickly spread to nearly every state in the Northeast and the mid-Atlantic, and the weather over the next week n determine whether the outbreak abates or whether tomato crops are ruined, according to federal and state agriculture officials.

The spores of the fungus, called late blight, are often present in the soil, and small outbreaks are not uncommon in August and September. But the cool, wet weather in June and th ggressively infectious nature of the pathogen have combined to produce what Martin A. Draper, a senior plant pathologist at the United States Department of Agriculture, described in "explosive" rate of infection

William Fry, a professor of plant pathology at Cornell, said. "I've never seen this on such a wide scale

A strain of the fungus was responsible for the Irish potato famine of the mid-10th century. The current outbreak is believed to have spread from plants in garden stores to backyar ardens and commercial fields. If it continues, there could be widespread destruction of tomato crops, especially organic ones, and higher prices at the market

Locally grown tomatoes normally get \$15 to \$20 a box" at wholesale, said John Mishanec, a pest management specialist at Cornell who has been visiting farms and organizin mergency growers' meetings across upstate New York. "Some growers are talking about \$40 boxes already." Tomatoes on almost every farm in New York's fertile "Black Dirt" r in the lower Hudson Valley, he said, have been affected

sor Fry. who is genetically tracking the blight, said the outbreak spread in part from the hundreds of thousands of tomato plants bought by home gardeners at Wal-Mart, Lowe' Home Depot and Kmart stores starting in April. The wholesale gardening company Bonnie Plants, based in Alabama, had supplied most of the seedlings and recalled all remaining plant starting on June 26. Dennis Thomas. Bonnie Plants' general manager, said five of the recalled plants showed signs of late bligh

"This pathogen did not come from our plants." Mr. Thomas said on Wednesday. "This is something that has been around foreve

Mr. Draper said the diseased seedlings, found in stores as far west as Ohio, were at least one source of the illness, but, he added, "It's possible that we are looking at multiple

USABlight.org – Disease alerts

Sample Submission

Alerts and Mapping



INCETATE USABlight | A National Project on Tomato & Potato Late Blight
Home About Late Blight Outbreak Map Report Late Blight Identify Genotype Managing Late Blight Decision Support Tool Publications About U

Welcome to USABlight





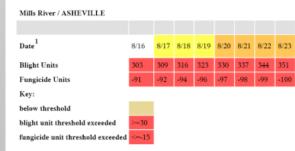
New Diagnostics





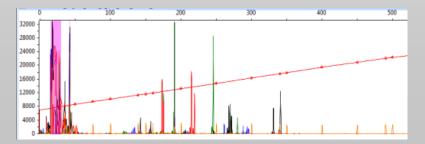
Decision Support Tool

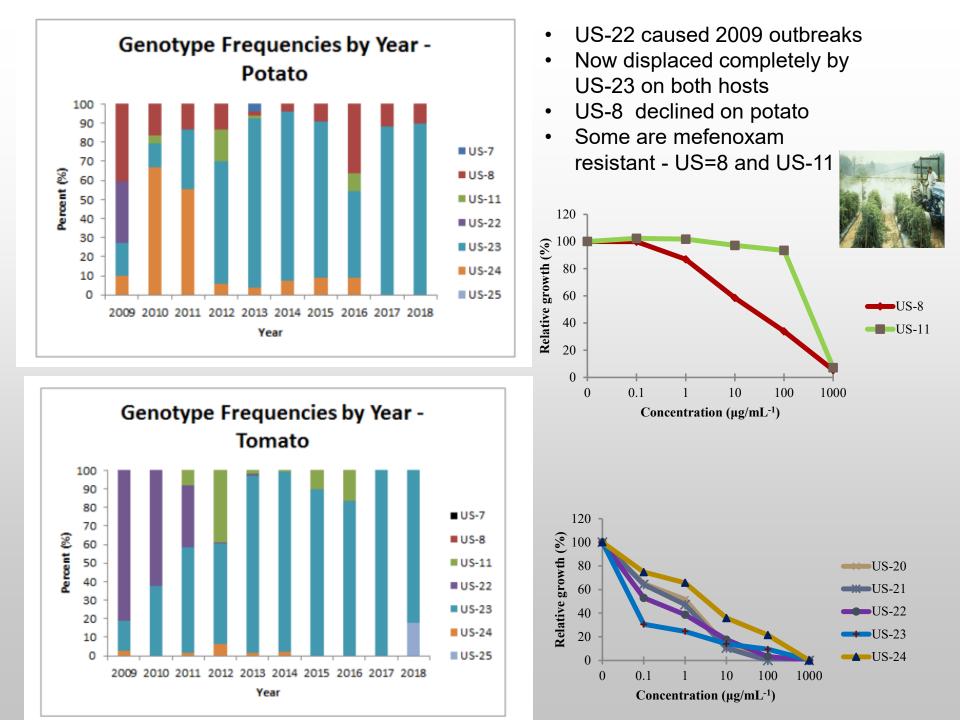
DSS Daily Email Report



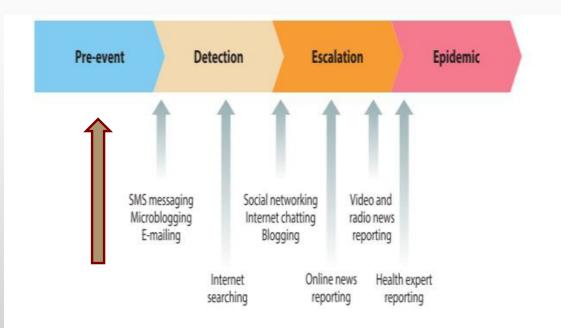


Genotyping





Digital Disease Surveillance



Introduce sensors here

New diagnostics to identify *P. infestans* LAMP Assays and Sensors

- LAMP primers can be designed to be specific to a particular pathogen
- Rapid protocol for field identifications
- Amplification product visualized in the field with visual nucleic acid stains (e.g. SYBR green or HNB)
- Can be adapted to lateral flow devices(LFDs)



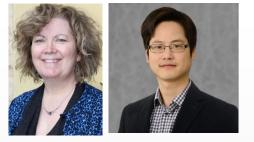
Samples with SYBR green. The three samples on the left are positive

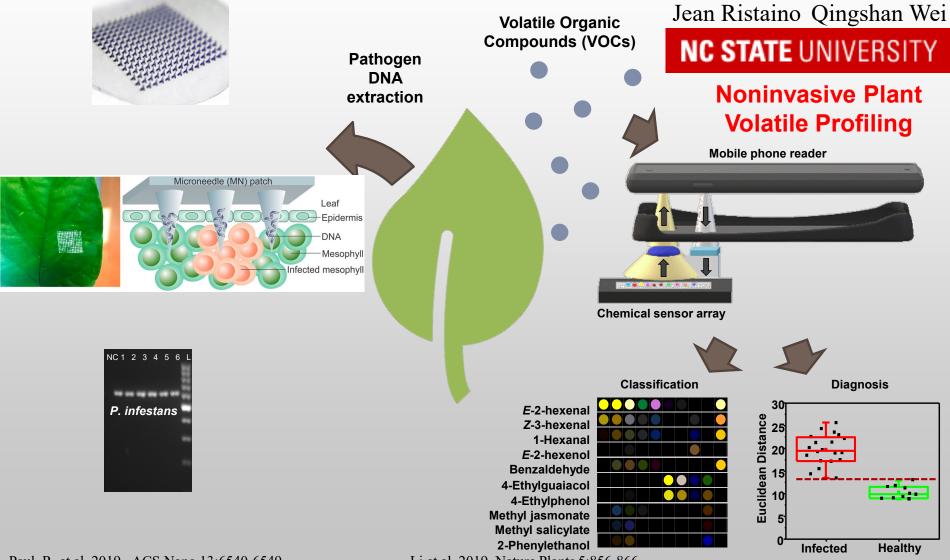




Ristaino et al., 2019. Plant Disease First Look

Sensors for plant disease detection in the field



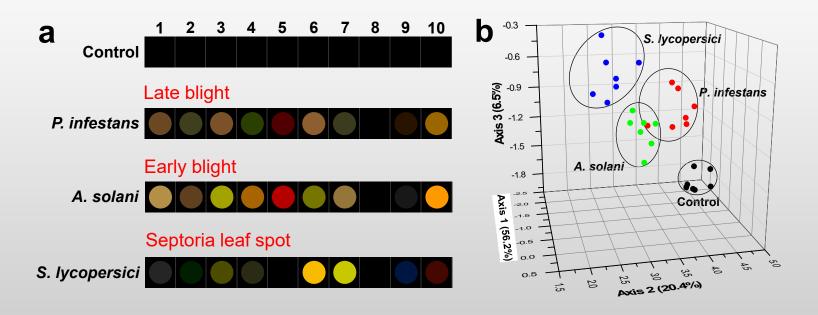


Paul, R. et al. 2019. ACS Nano 13:6540-6549

Li et al, 2019. Nature Plants 5:856-866.



We can differentiate three tomato pathogens by VOC's before symptoms



Classification accuracy: ~93% (2 errors out of 28 samples tested in total)

Li, Z. et al., 2019. Noninvasive Plant Disease Diagnostics Enabled by Smartphone-Based Fingerprinting of Leaf Volatiles. Nature Plants 5:856-866

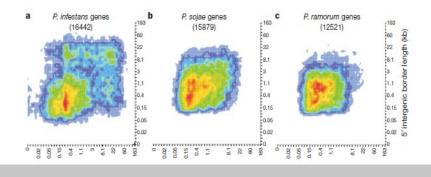
Pathogen Genome Sequenced

- Genome is highly expanded –repetitive -75%
- Effector diversity Avirulence proteins needed to overcome host resistance





- What is driving expansion? Breeding?
- Pathogen/population genomics and databases

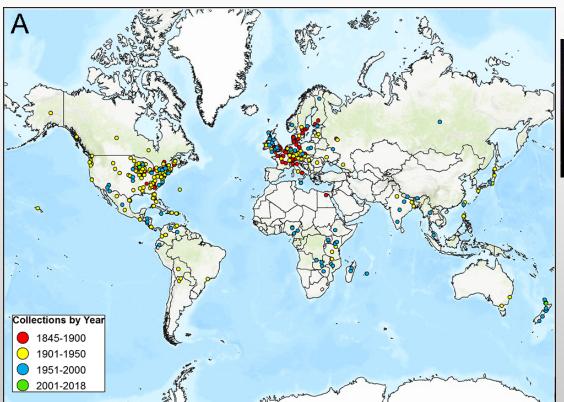


Haas, B. J., et al. 2009. Nature 461:393-398

Big questions about historical *P. infestans*

- P infestans origin
- What lineage caused the famine?
- Where did it come from? SA or Mexico
- Has this pathogen always had a large genome?
- How different is effector diversity?
- Clonal or sexual?
- Are historical genotypes still circulating?
- Did same lineage cause disease in the US and Europe?

Over 1200 samples of *P. infestans* in mycological herbaria





Jean in Royal Botanic Gardens Herbarum Kew 2001 (above), Farlow Herbarium, Harvard, 2003 (below)



How different is modern *P. infestans* genome from the genomes of historic *P. infestans*



N.º 1198. Botrytis fallax DESMAZ.

DESMAZ. Pl. crypt. de France, n.º 1492. — Kx. Rech. Fl. crypt. des Fland., 5° cent., pag. 45, n.º 85. — Botrytis infestans Mont. — Botrytis vastatrix Lib. — Pritchardia solani Muhlenb. — Choléra de la Pomme de terre.

Sur les feuilles languissantes du Solanum tuberosum, aux environs d'Audenarde. (M.r TOSQUINET.)

Genome evolution of *P. infestans* Collaboration with Univ. Copenhagen

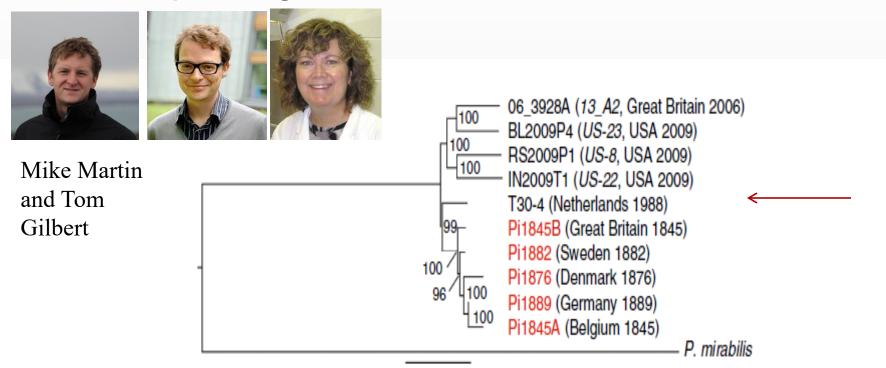


Figure 1 | Maximum-likelihood phylogram of *P. infestans* genomes from the first historic outbreaks of disease and later outbreaks. Nodes are labelled with their support values from 100 bootstrap replicates. The scale bar indicates a branch length of 0.2 nucleotide substitutions per site.

•Highly supported monophyletic clade for historic samples (shown in red)

Martin, M. D. et al. 2013. Nat. Commun. 4:2172 doi: 10.1038/

Fewer effectors in historic P. infestans

Historical

1845 (green) and Pi1889 (blue) Modern

T30-4 (orange) - outer ring; US-22 (red); US-23 (purple); US-8 (yellow); 13_A2 (light purple)

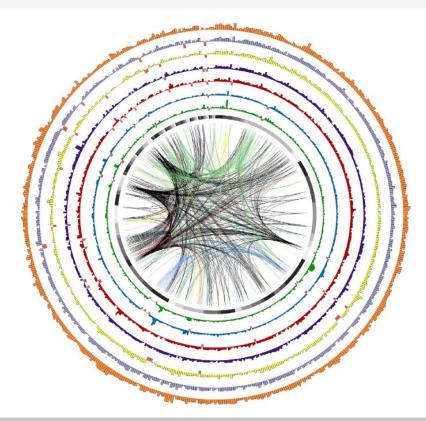
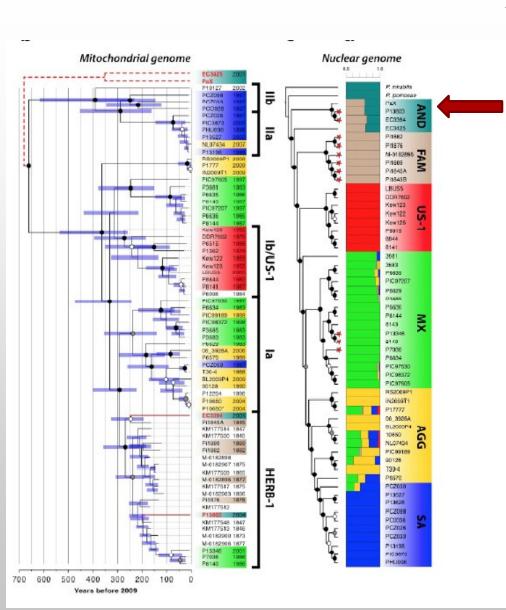


Figure 2 | Visualization of sequencing coverage distribution across all reference RXLR effectors. Bar heights represent the mean-normalized coverage of 583 reference RXLR effector genes in the resequenced genome of a particular sample).

- Effectors deleted in gene sparse regions
- Avirulence genes considered important for pathogenesis were absent in historic genomes.
- Expansion of effectors over time
- Virulent form of *Avr2* and *Avr3a* were absent in historic samples
- Suggests that the pathogen has evolved in response to human actions like breeding disease-resistant potatoes.



Genomic characterization of South American *Phytophthora* hybrid mandates reassessment of geographic origin of *Phytophtora infestans.* Martin et al, 2015. Mol. Biol. Evol. 33:478-491

Mitogenomes

- Herb-1 lineage persists in *P* andina (la) from *S. betaceum* (red)
- Divergence of Herb-1 mt lineage
- Herb-1 mtDNA lineage not strictly associated with FAM lineages of *P. infestans*

Nuclear genomes - 6 lineages

- *P. andina* shows mixed ancestry with famine lineages and outgroup species indicating hybrid, basal in tree
- Famine era lineages form highly supported sister clade at base of tree
- US-1 and Mexican lineages diverged later
- Modern Mexican lineages and US aggressive lineages – admixture- MX likely source of some AGG lineages
- Modern SA lineages most derived
- Ancestral lineages of the pathogen may be on wild Solanum hosts in SA

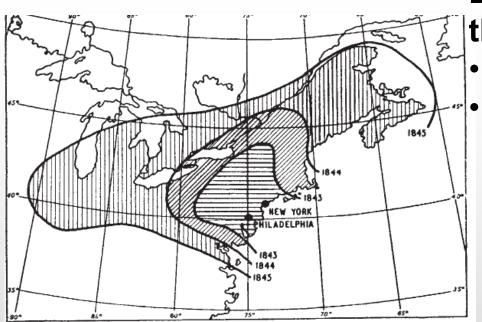
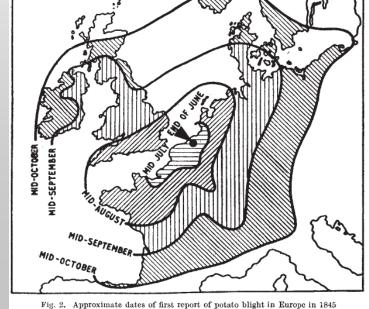


Fig. 1. Approximate extent of potato blight attacks in the United States and Canada during 1843-45 (after Stevens)

Did 19th century *P. infestans* in the US migrate to Europe?

Late blight first to US in 1843 Reports in Europe and Ireland by the fall 1845



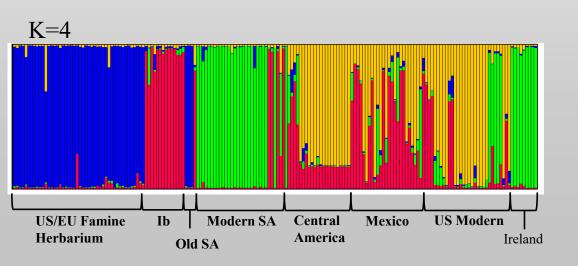


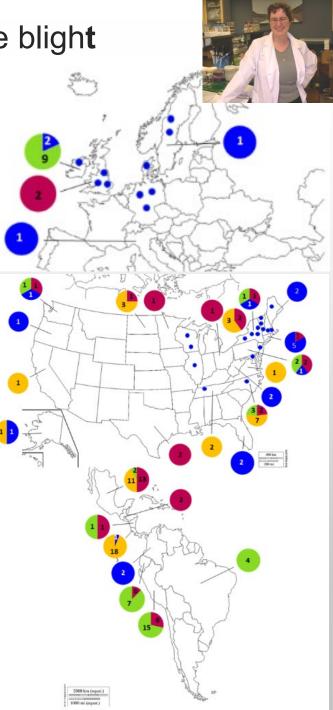


Fam-1 SSR lineages caused historic late blight

K=4 based on examination of Ln P(D).

- US/EU historic lineages cluster into one group
- The oldest South American samples from Colombia similar to historic US and EU populations.
- US-1 (Ib) lineage forms a second group
- South American (SA) and Irish lineages form a third group.
- The US-23 lineage clusters with SA lineages
- Central American, Mexican and Modern US aggressive lineages (US-6, 7, 8, 11, 22, 24) similar to Mexican lineages suggesting a Mexican origin of these recent lineages into the US

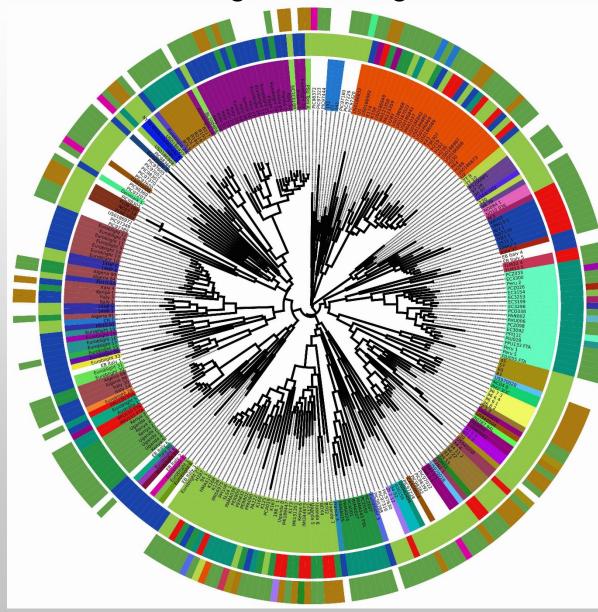




Conclusions

- Largest populations genomics study to date on a *Phytophthora* species
- At least two historic mitochondrial lineages were introduced to historical Europe
- Hybridization between parents of *P. andina* (one is *P. infestans* and other unknown parent) must have occurred in Andes where they share a host range.
- The most basal *P. infestans* like haplotypes survive within *P andina,* found in the highlands of Peru and Ecuador
- Clonal lineages of *P. andina* and *P. infestans* diverged earlier than Mexican lineages
- Most modern aggressive lineages (except US-23) derived from MX
- *P. infestans* jumped from wild host to *S. tuberosum* in MX

-Tree Based Alignment Selector Tools– *P. infestans* global lineages





- Allison Coomber-AgBioFews PhD student
- Montana Knight-Bioinformatics
- Amanda Saville
- Thanks to Ignazio
 Carbone- T-Bas and
 DiCIFR tools

Tree Based - *Phytophthora* Phylogeny- evolutionary placement of unknown species multilocus genealogy Over 140 species described



IMA FUNGUS · 8(2): 355-384 (2017)

An expanded phylogeny for the genus Phytophthora

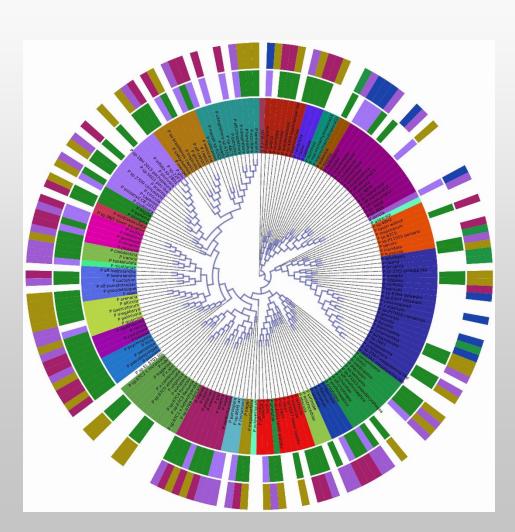
Xiao Yang¹, Brett M. Tyler², and Chuanxue Hong¹

¹Hampton Roads Agricultural Research and Extension Center, Virginia Tech, Virginia Beach, VA 23455, USA; corresponding author e-mail: yxiao9@vt.edu

²Center for Genome Research and Biocomputing, and Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331, USA

Abstract: A comprehensive phylogeny representing 142 described and 43 provisionally named *Phylophthora* species is reported here for this rapidly expanding genus. This phylogeny features signature sequences of 114 ex-types and numerous authentic isolates that were designated as representative isolates by the originators of the respective species. Multiple new subclades were assigned in clades 2, 6, 7, and 9. A single species *P. Illii* was placed basal to clades 1 to 5, and 7. *Phylophthora stricta* was placed basal to other clade 8 species, *P. asparagi* to clade 6 and *P. intercalaris* to clade 10. On the basis of this phylogeny and ancestral state reconstructions, new hypotheses were proposed for the evolutionary history of sporangial papillation of *Phylophthora* species. Non-papillate ancestral *Phylophthora* species were inferred to evolve through separate evolutionary paths to either papillate or semi-papillate species. Key words: oomycetes systematics taxonomy evolution plant pathology

Article info: Submitted: 8 June 2017; Accepted: 31 October 2017; Published: 21 November 2017.



Solving global late blight

Population genomics

- Role of hybridization, host jumps and migration in spread of this and other Phytophthora diseases
- Use next generation sequence data sets and populations genomic tools to study global population biology
- Collaborative sharing of datasets open data and queryable database

Surveillance Technologies

- Use text and data mining and natural language processing to map outbreaks
- Deployment of a Global Blight disease alert and genotyping system still segmented
- Use sensor and ICT technology to deliver disease outbreak information into surveillance systems smart phones – crowd sourcing – with geospatial analytics

Host resistance

- Deploy resistant varieties on a landscape level many countries still growing susceptible varieties
- Deploy transgenic or gene edited potatoes/tomatoes with stacked R genes in areas where fungicide use is limited or impacted negatively by high rainfall

Strengthen phytosanitary standards

- Improve seed certification programs and clean seed distribution
- Improve diagnostic capabilities of partner institutions in the developing world
- Build human capacity through training next generation of plant science students broadly



J. Ristaino's laboratory website http://ristainolab.cals.ncsu.edu//





KECK FUTURES INITIATIVE