

**Tracking Worldwide Migrations, Evolutionary
Relatedness and Reemergence of *Phytophthora
infestans*: A threat to Global Food Security**

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A constraint to potato production and global food security worldwide



**Has increased in incidence,
geographical and host range**

Spread of *Phytophthora infestans*

Spread by sporangia – spread in
air – 100' kilometers



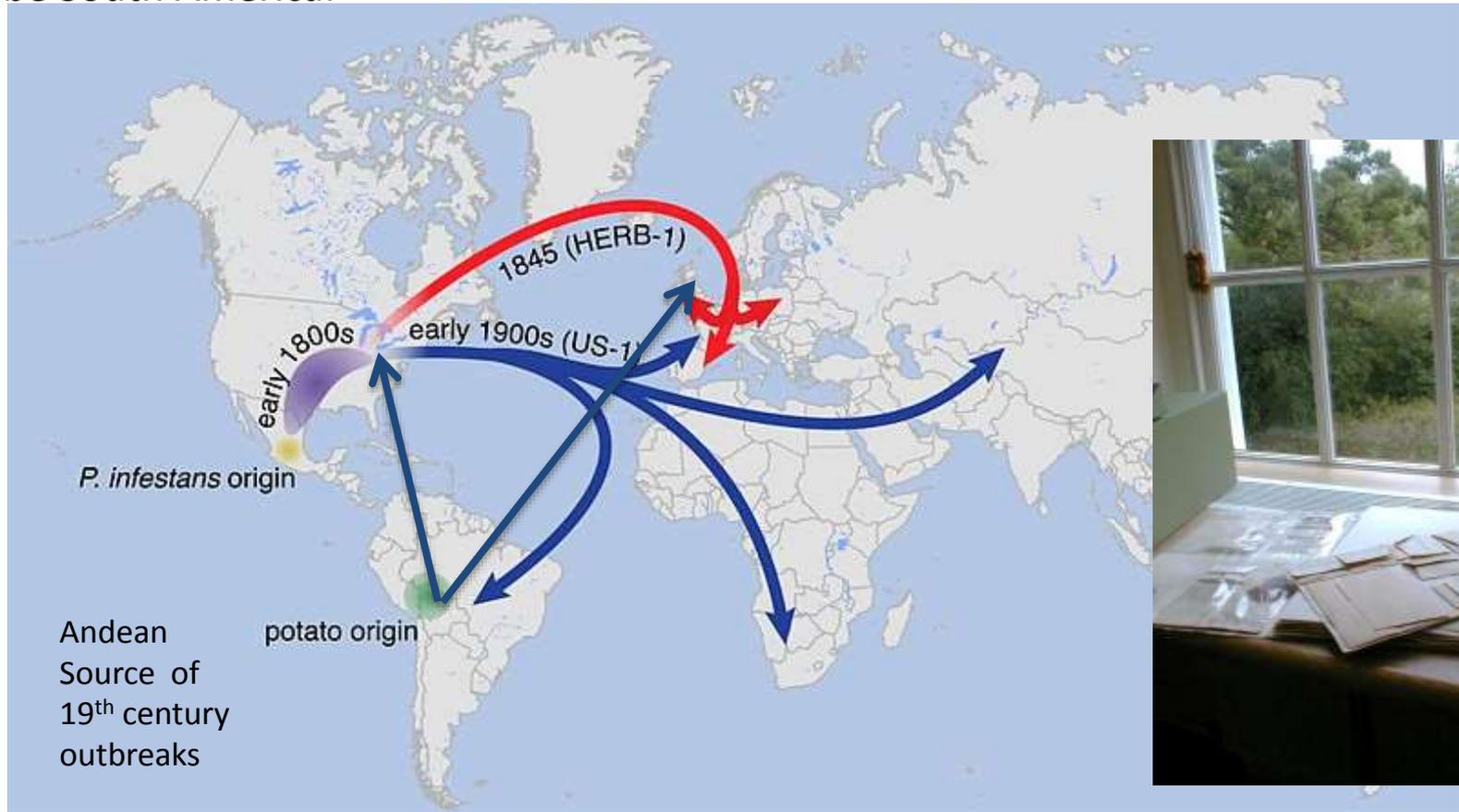
Phytophthora infestans sporangia

Big questions about historical *P. infestans*

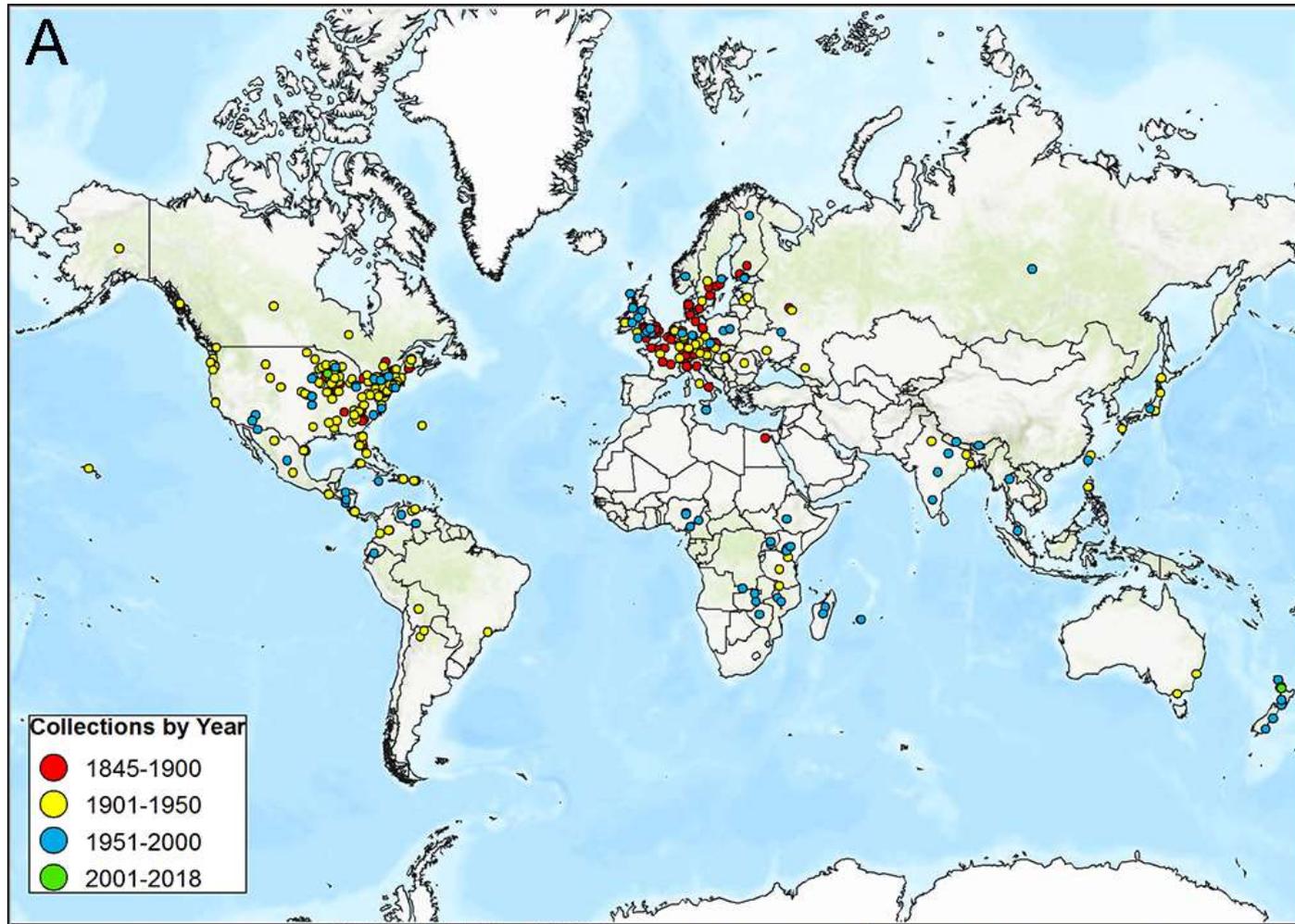
- What lineages are circulating in US today and where are they from?
- What lineage caused the famine?
- Where did the famine lineage come from?
- Has this pathogen always had a large genome?
- Has effector diversity changed with time?
- Are populations clonal or sexual?
- Are historical genotypes still circulating?
- Did same lineage cause disease in the US and Europe?

Source and Center of Origin of *Phytophthora infestans*

- Proposed in the 1990's that the US-1 genotype (Ib haplotype) caused the Irish famine and that this genotype originated in Mexico. Actual famine era samples not investigated
- Others used archival samples and suggested either a Mexican origin of famine lineage (mtDNA lineage Herb 1) - said it went extinct.
- My lab published evidence of a South American origin using multilocus genotyping. Evidence of Andean movement of potatoes to Europe during 19th century so source could be South America.



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



Herbarium specimens used to understand etiology of disease



This is a very rough sketch just to let you
what to look for

Have you not lately written a report on
the Potato Disease. If so I should be glad
to have it.

Elberfeld
Market Harborough
July 10 1875

Dear Sir

When I wrote a few days since
I forget whether I told you that I
found in the diseased Potato leaves
what I considered as a Protomyces,
Washington Smith has since proved that
these are the resting spores of the
Peronospora, or rather the condition
of the male & female organs before
impregnation. It has been the
perfect Peronospora ^{with sporidia in the fruit} growing from
the same Mycelium which bears the
so called ~~Protomyces~~ ^{Protomyces}. Before you see
this you will probably have seen the
account in the Gardeners Chronicle.
Figures will be given next week. Believe
me always very sincerely yours
M. Westoby.

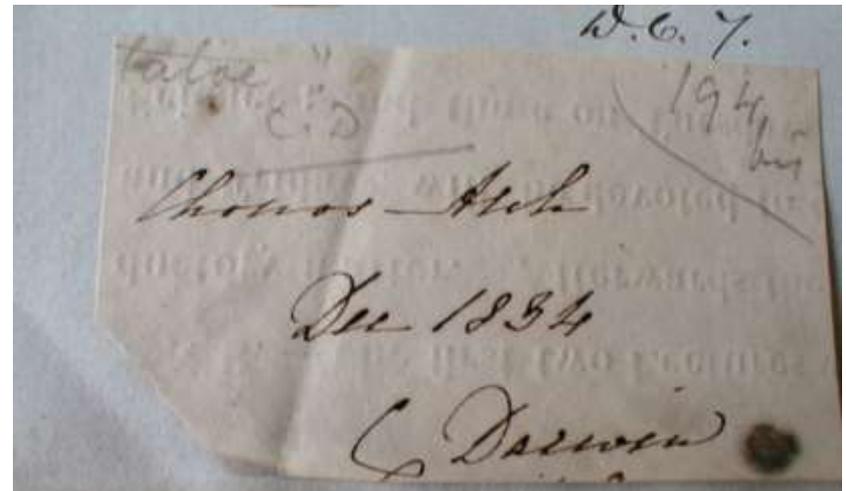


Late blight struck at Darwin's Home- Down House in 1845



“My Dear Henslow, I have to thank you for several printed notices about the potatoes etc etc. What a painfully interesting subject it is: I have just returned home and have looked over my potatoes and find the crop small, a good many having rotted in the ground.”

Darwin's *Solanum maglia*- potato



Darwin's potatoes studied during the Irish famine



“They fared exactly the same as the other kinds, having blotched in the leaf and a few tubers decayed (Fox 1846)”

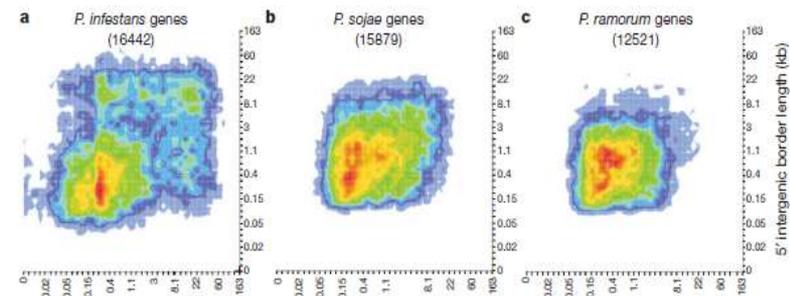
Late blight still occurs at Down House



Ristaino, J. B. and Pfister, D. 2016. “What a painfully interesting subject”: Charles Darwin's studies of potato late blight. *Bioscience* 62: 1035-1045

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 database



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



N.° 1198. *Botrytis fallax* DESMAZ.

DESMAZ. *Pl. crypt. de Franco*, n.° 1192. — Kx. *Rech. Fl. crypt. des Fland.*, 5^o cent., pag. 43, n.° 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



Mike Martin
and Tom Gilbert

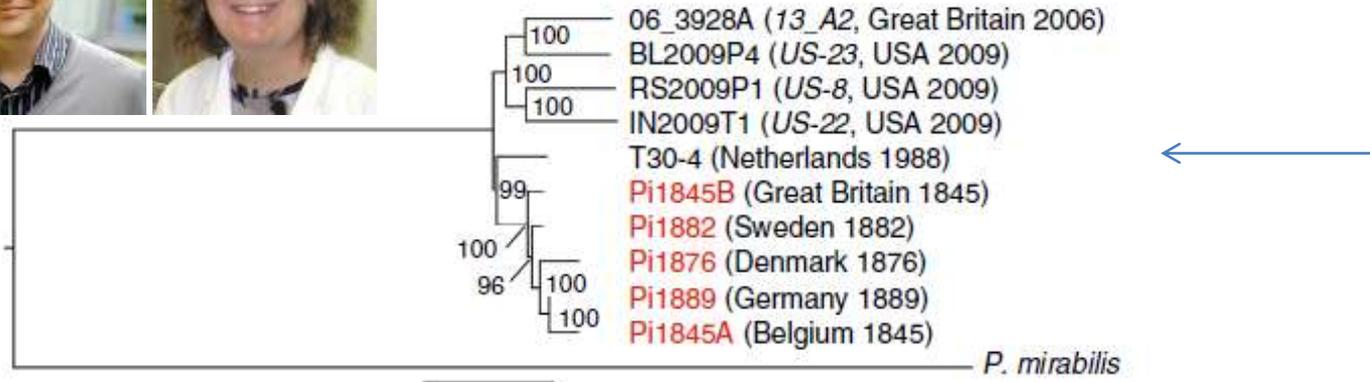


Figure 1 | Maximum-likelihood phylogram of *P. infestans* genomes from the first historic outbreaks of disease and later outbreaks. Nodes are labelled with their support values from 100 bootstrap replicates. The scale bar indicates a branch length of 0.2 nucleotide substitutions per site.

- Highly supported monophyletic clade for historic samples
- Sequenced US-8, US-22 and US-23 lineages
- T30-4 intermediary position and modern genomes in a distinct clade
- Samples from modern and historic time periods differed by > 120,000 SNP's
- Pi1845 and Pi 1889 differed by > 12,000 SNP's
- Differences between the European historical samples from the 1840s and the 1870s and 1880s **suggest that the pathogen was brought to Europe more than once.**

Fewer effectors in historic samples

- 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
- In the areas of the genome that today control virulence, there was little similarity with historical strains, suggesting that the pathogen has evolved in response to human actions like breeding disease-resistant potatoes.

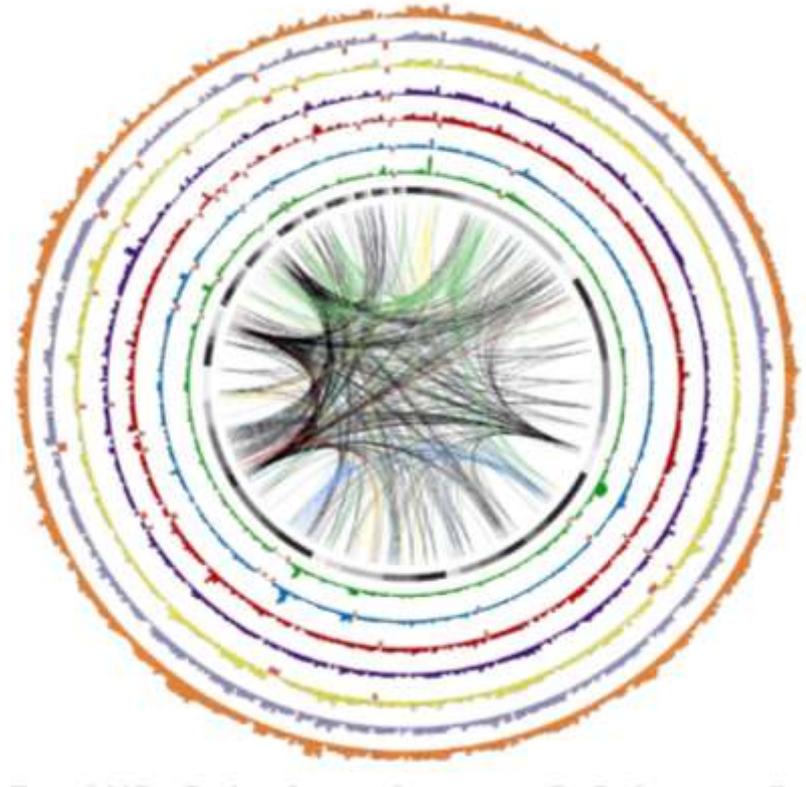
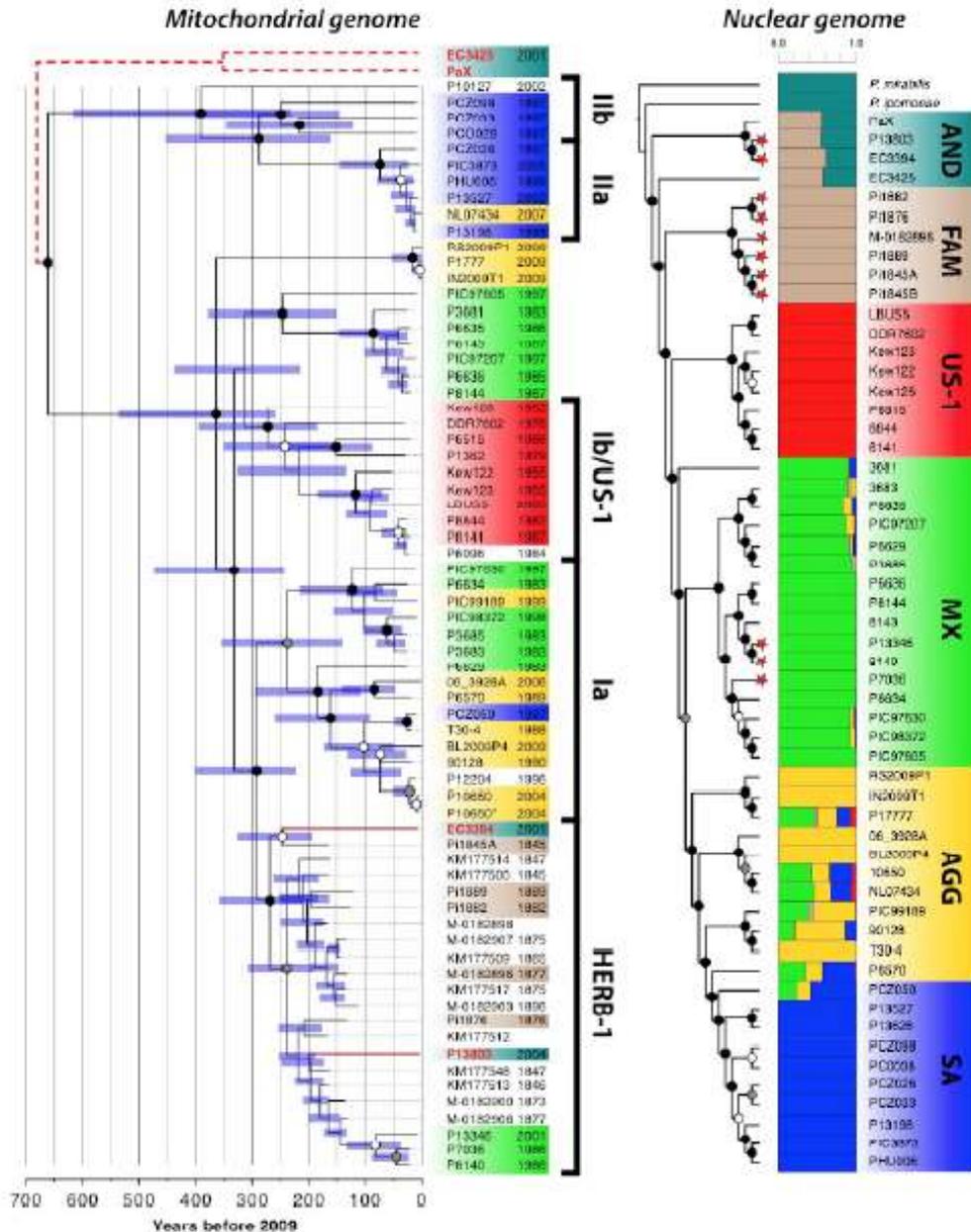


Figure 2 | Visualization of sequencing coverage distribution across all reference RXLR effectors. Bar heights represent the mean-normalized coverage of 583 reference RXLR effector genes in the resequenced genome of a particular sample).



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

Mitogenomes

- **Herb-1 lineage persists in *P andina* (Ia)** from *S. betaceum* (red)
- Two distinct Herb-1 mt lineages –diverged
- 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 (EC-1, PE-3, BR-1) from domesticated potato most derived
- Probably ancestral lineages of the pathogen exist on wild *Solanum* hosts in SA

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

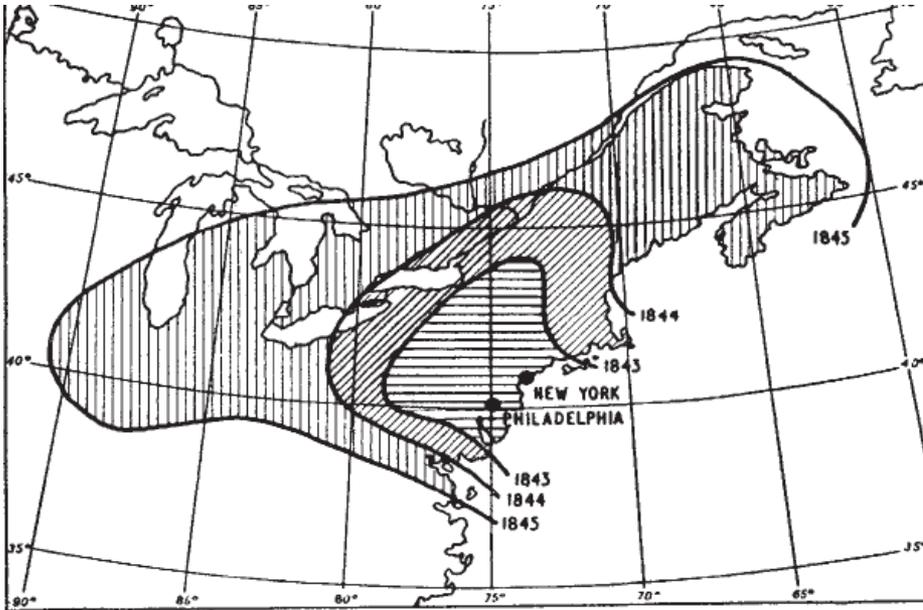


Fig. 1. Approximate extent of potato blight attacks in the United States and Canada during 1843-45 (after Stevens)

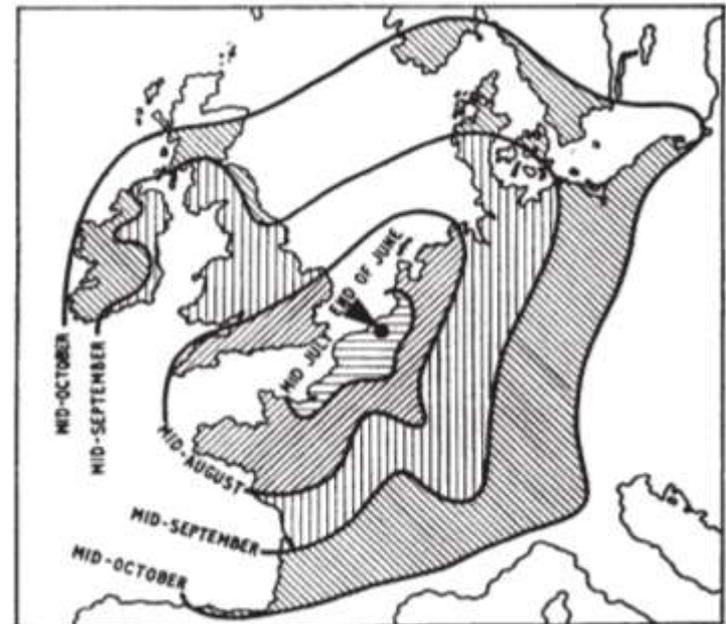


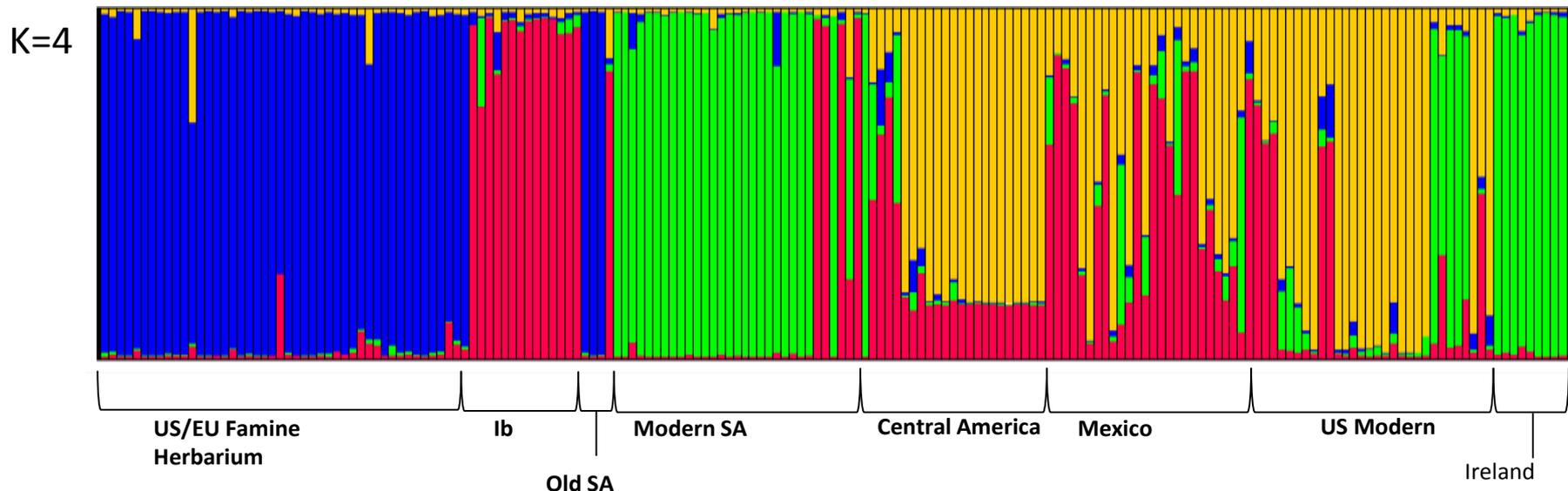
Fig. 2. Approximate dates of first report of potato blight in Europe in 1845

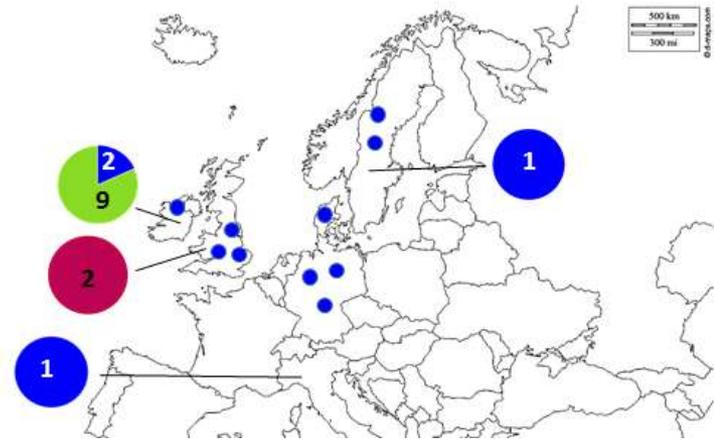
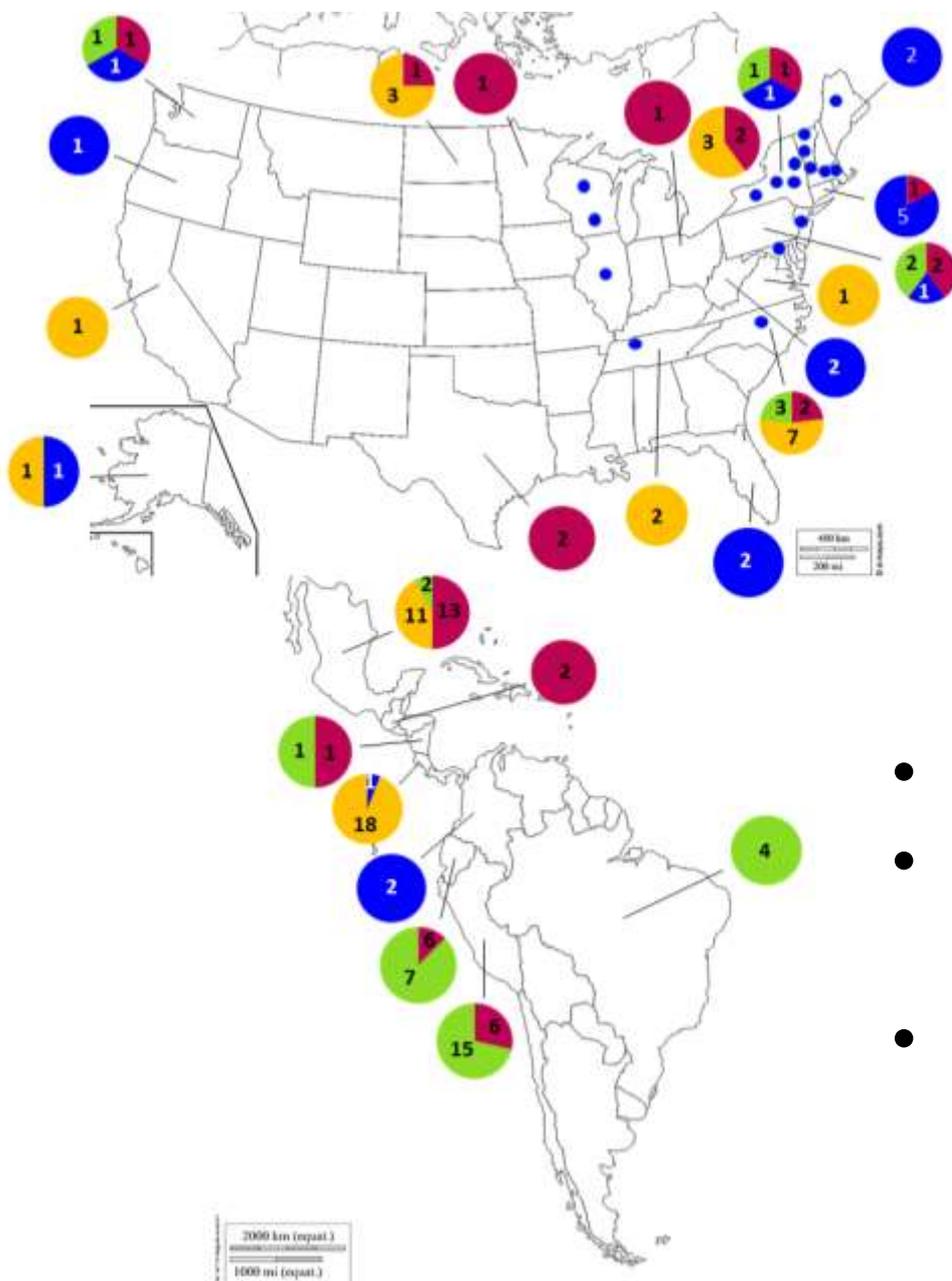
12 Plex SSR data -modern and historic samples

- **US/EU historic lineages** cluster into one group –named FAM-1 lineage
- The oldest South American samples from **Colombia** share allelic similarity with historic US and EU populations.
- **US-1 (Ib)** lineages forms a second group
- **Modern 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) share allelic diversity with Mexican lineages suggesting a Mexican origin of these recent lineages into the US



Plos One December 28, 2016





- FAM-1 lineage – not extinct.
- Remained in US for 100 years.
- Same lineage caused disease in US and Europe during famine and into early 20th century

Was FAM-1 in Africa and Asia?

- FAM-1 in East Africa (Uganda, Tanzania, Kenya, Zimbabwe, Cameroon, and Ethiopia)
- FAM-1 lineage in India, Philippines, Malaysia and Nepal- colonization brought lineage to both continents
- US-1 not found on either continent until the 1950's
- Will report full data set and analysis APS 2019

Mediterranean *P. infestans*



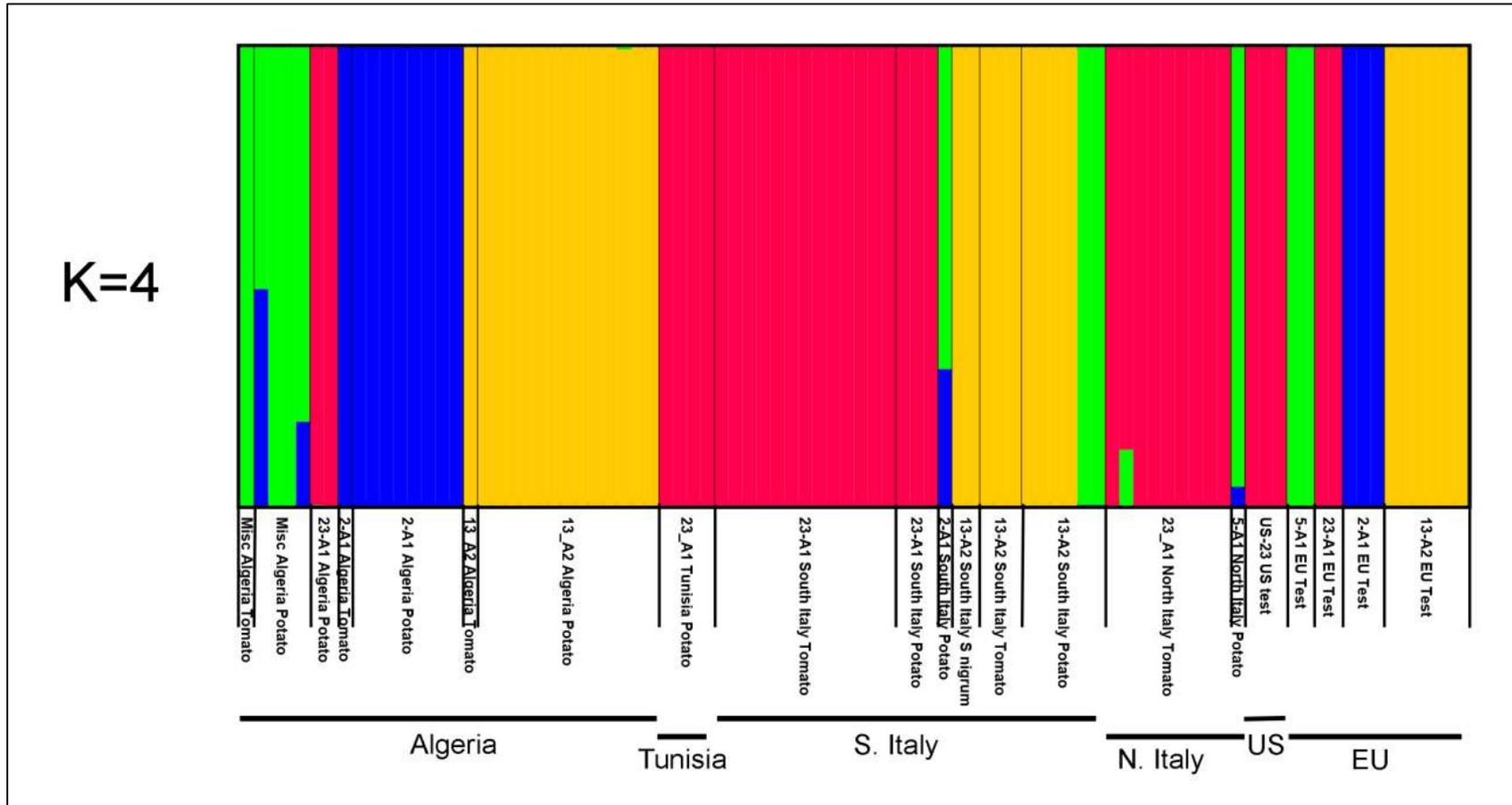
- Only 14 Italian samples in EuroBlight- 2013 (12),2014 (1),2016(1)
- 83 samples from fields in Italy and Tunisia
- Four lineages identified in Italy; one in Tunisia

Algerian data from Rekad et al. 2017

Mediterranean -Late blight collecting in Sicily

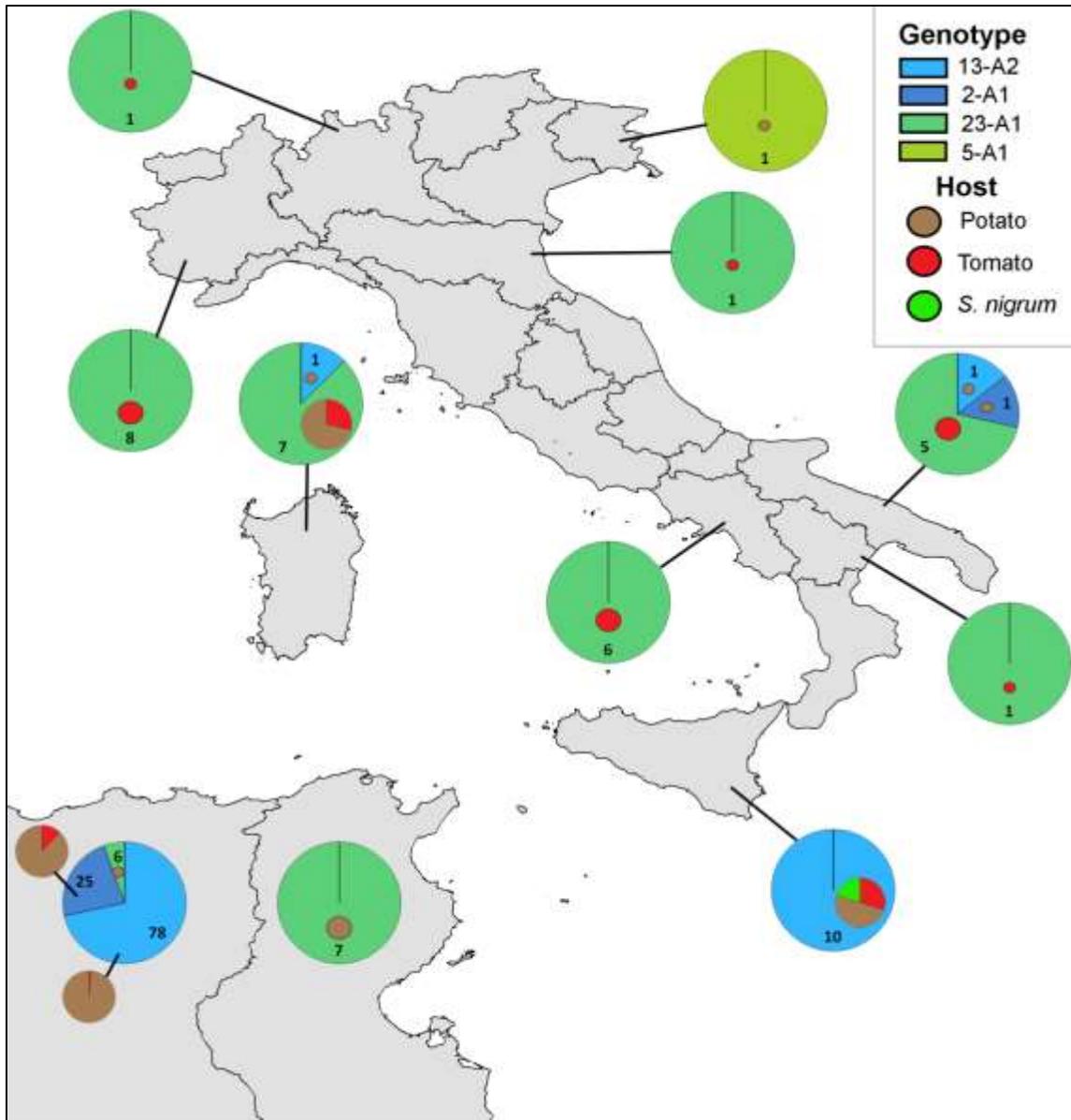


Mediterranean *P. infestans*



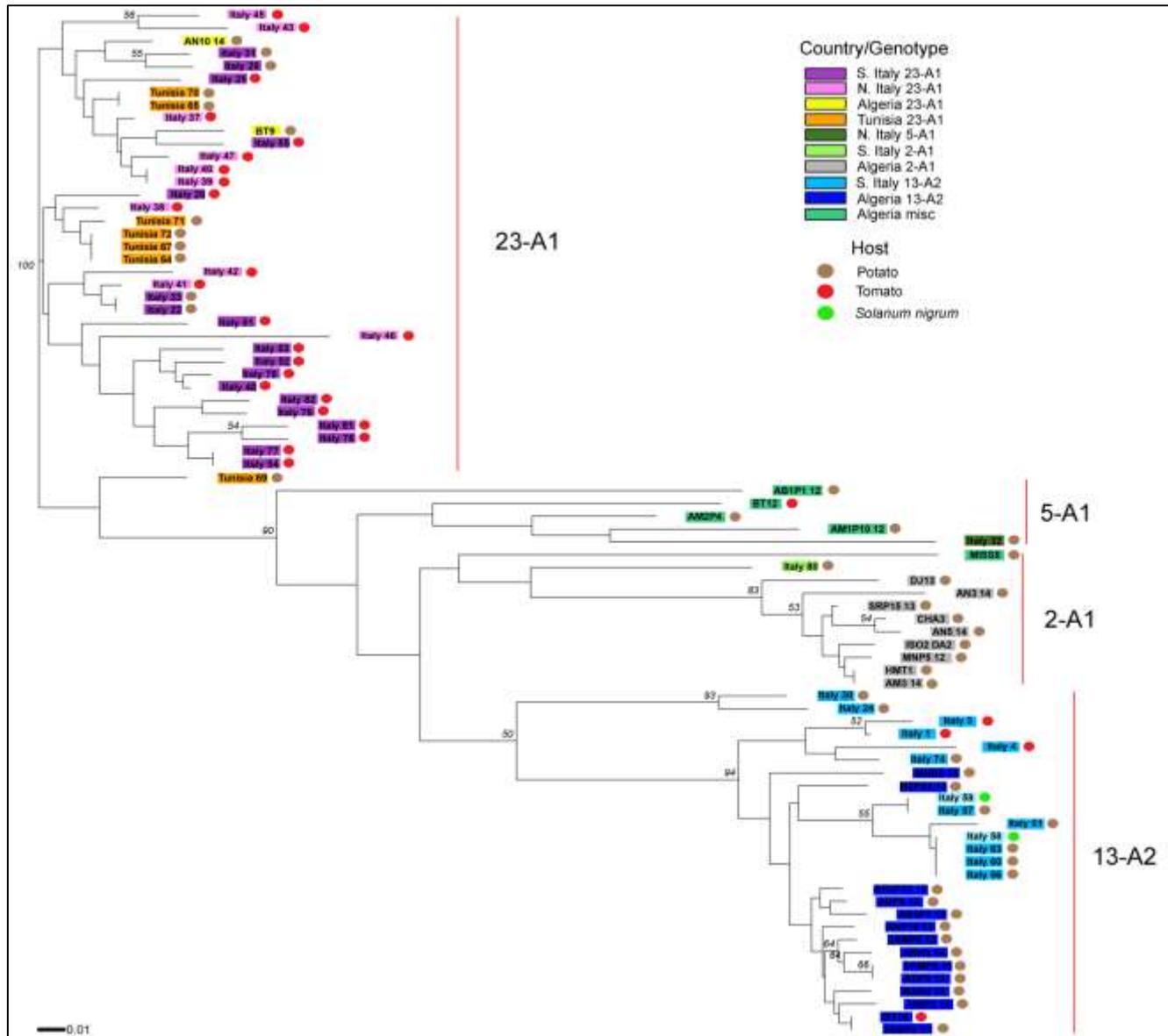
4 lineages identified 23_A1, 13_A2, 2_A1, 5_A1

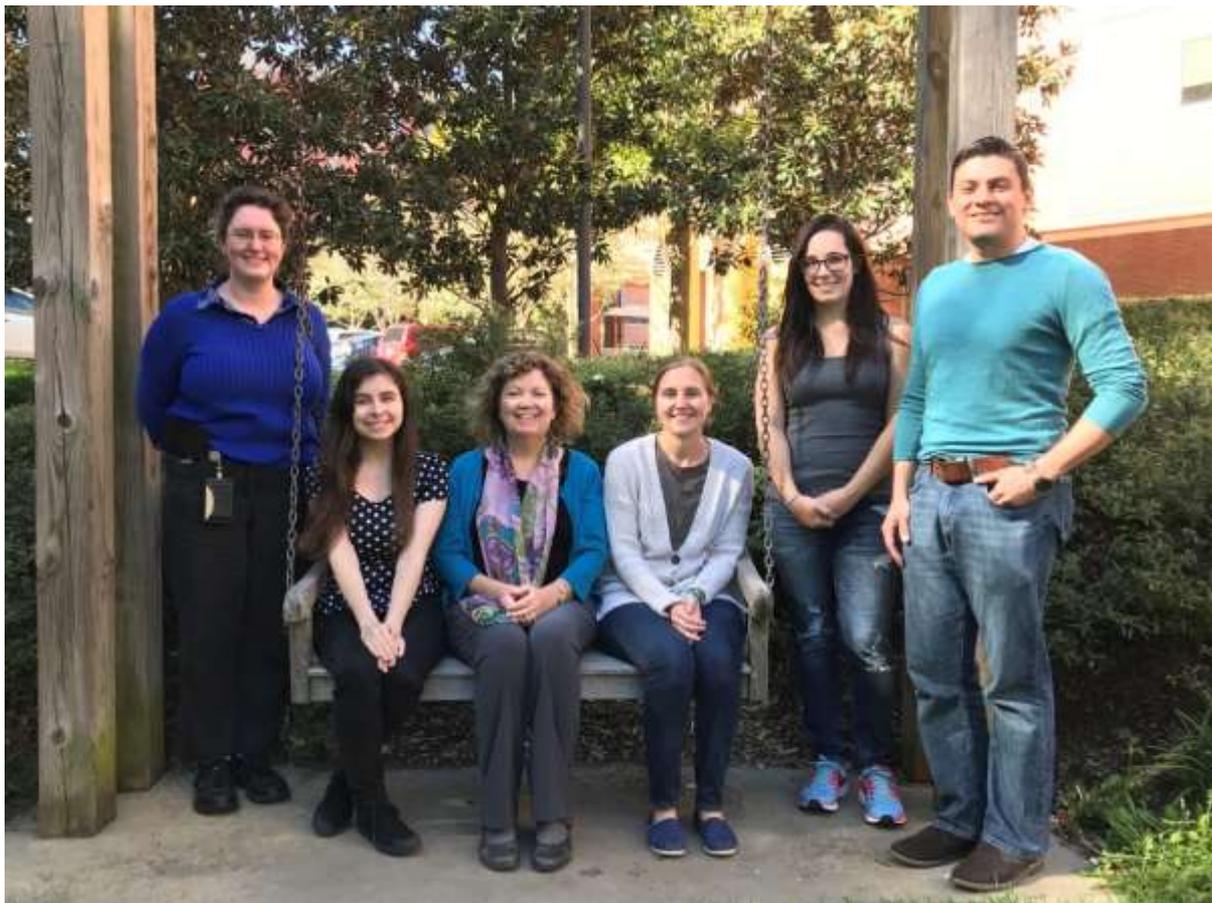
Mediterranean *P. infestans*



- 4 lineage found in Italy
- Geographic substructuring
- 23-A1 dominant lineage in Italy
- 13-A2 only lineage in Sicily
- 5-A1 Northern
- 2-A1 Puglia

Mediterranean *P. infestans*





United States Department of Agriculture
National Institute of Food and Agriculture



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J. Ristaino's laboratory website

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www.globalfoodsecurity.ncsu.edu/

