

Dynamics and Interactions of Bacterial Species Causing Potato Blackleg and Soft Rot

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Potato blackleg and soft rot

Stand loss, wilting and yellowing leaves, brown, black, and decayed stems, storage rot



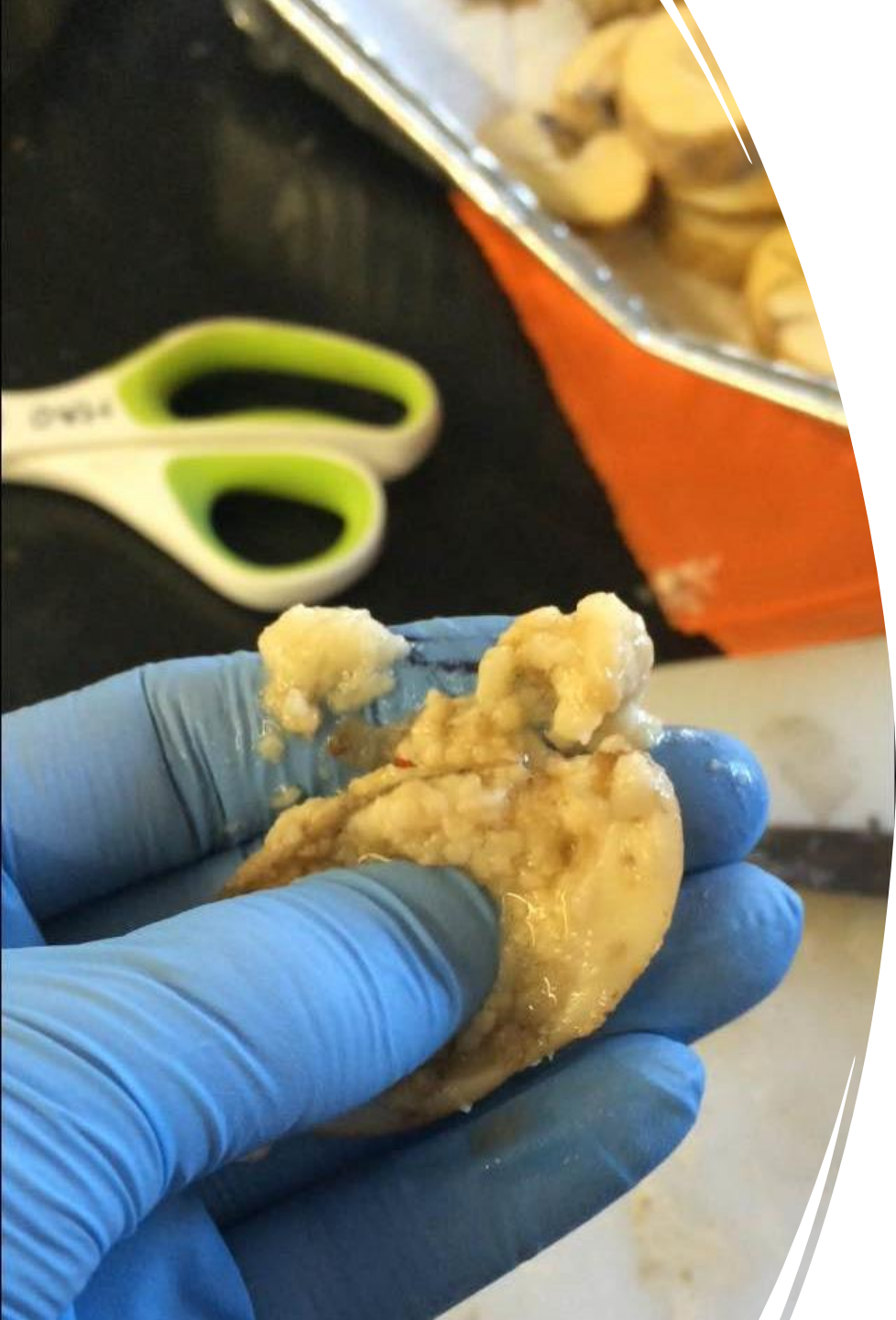
Outbreak of Potato Blackleg and Soft Rot (PBSR) in the Northeast US

- In 2015, PBSR was observed in the Northeastern region
- Associated with seed transmission of a bacteria
- PBSR threatened Maine's potato production, which is a major seed producer



Low emergence of potatoes due to blackleg

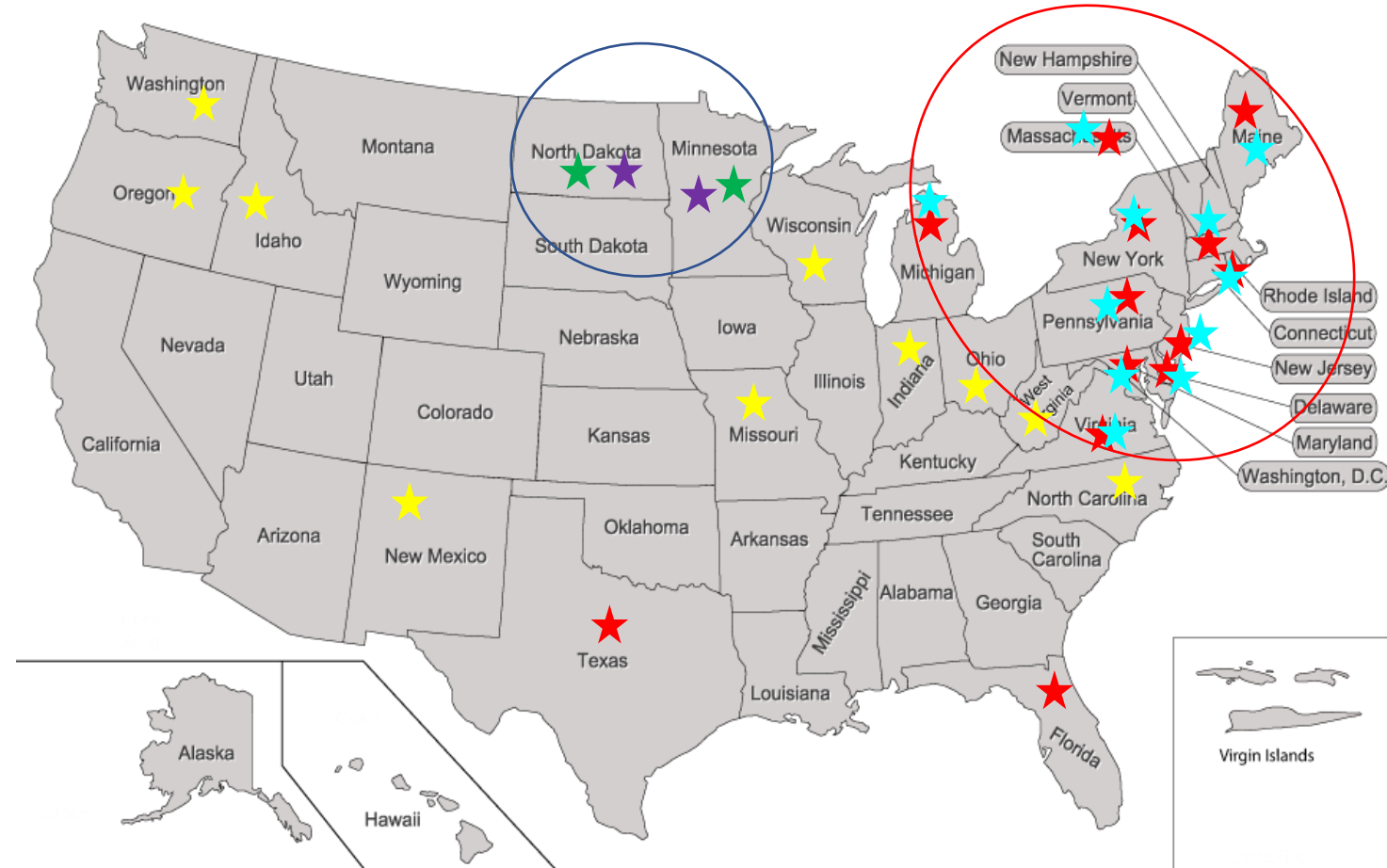




What pathogens are responsible for the outbreak and how did the outbreak occur?

Dickeya dianthicola was associated with the PBRs outbreak

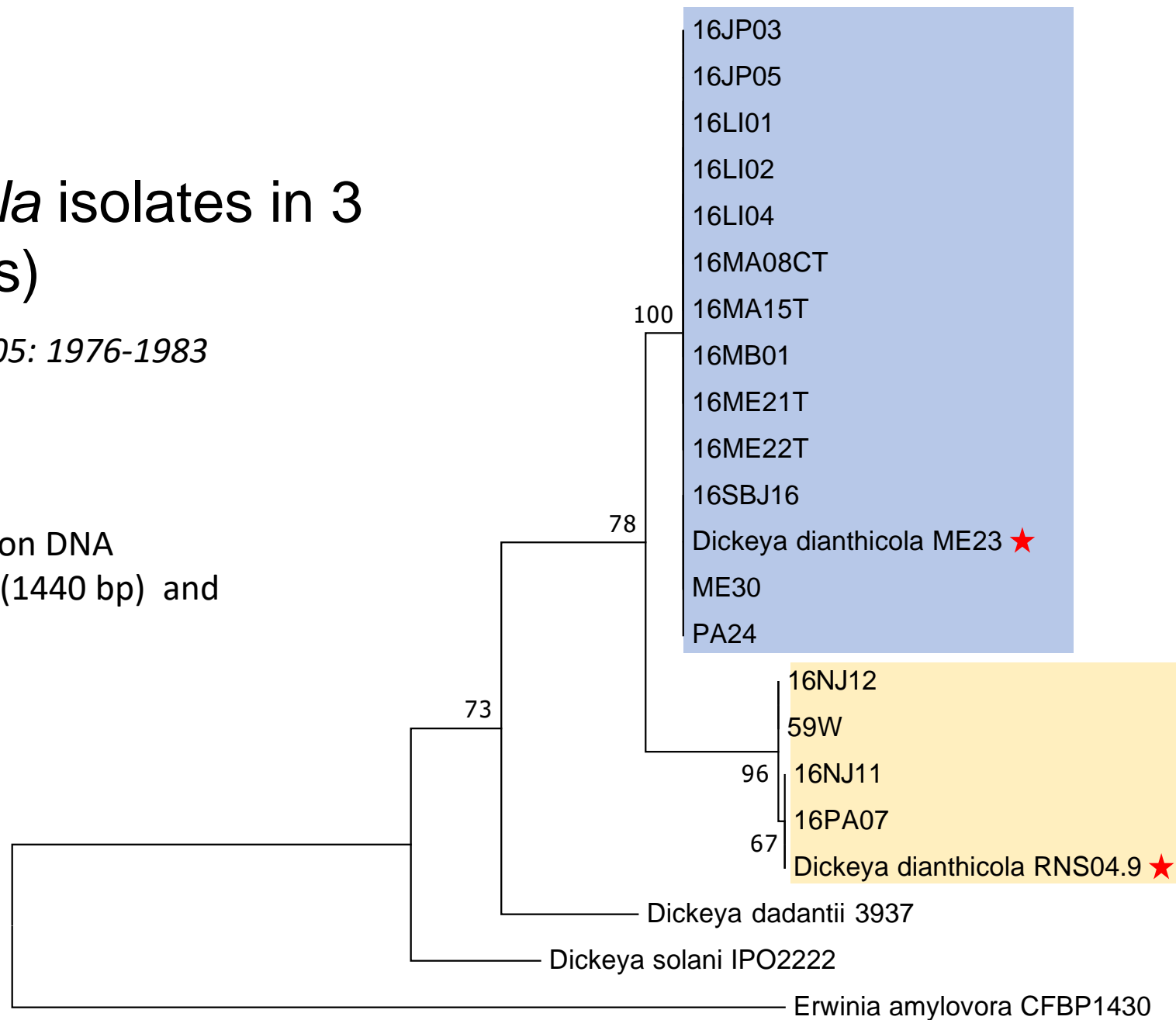
- ★ *D. dianthicola*
- ★ *D. chrysanthemi*
- ★ *P. parmentieri*
- ★ *P. brasiliense*
- ★ Un-identified



Dickeya dianthicola isolates in 3 groups (genotypes)

Ge et al. 2021. *Plant Disease* 105: 1976-1983

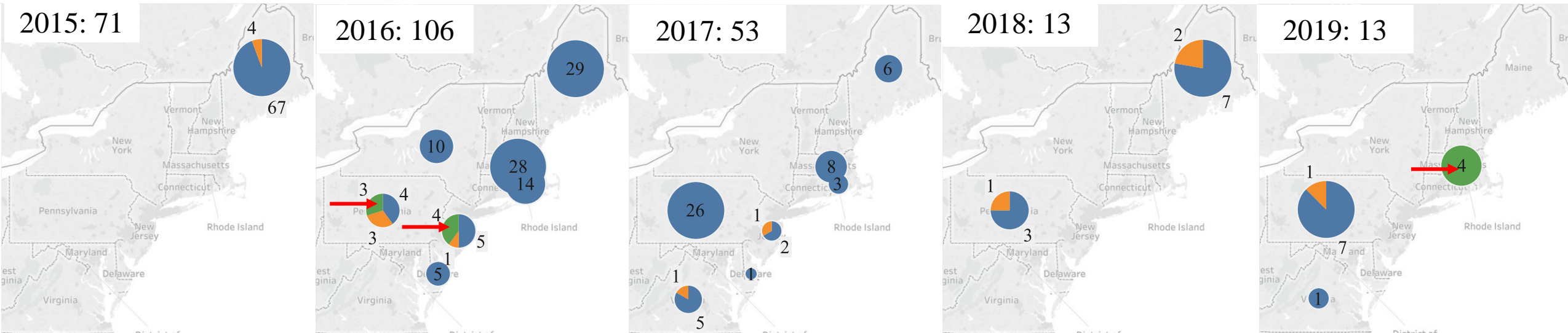
Phylogenetic analysis based on DNA sequencing of the 16S rRNA (1440 bp) and gapA (850 bp) genes.



Genotypic distribution of *Dickeya dianthicola* in the NE US

Samples were collected from 2015 to 2019 (n = 256)

*Ge et al. 2021. Plant Disease*105: 1976-1983



Type I, predominant, comprising 95% in Maine, and 83% from all other states.



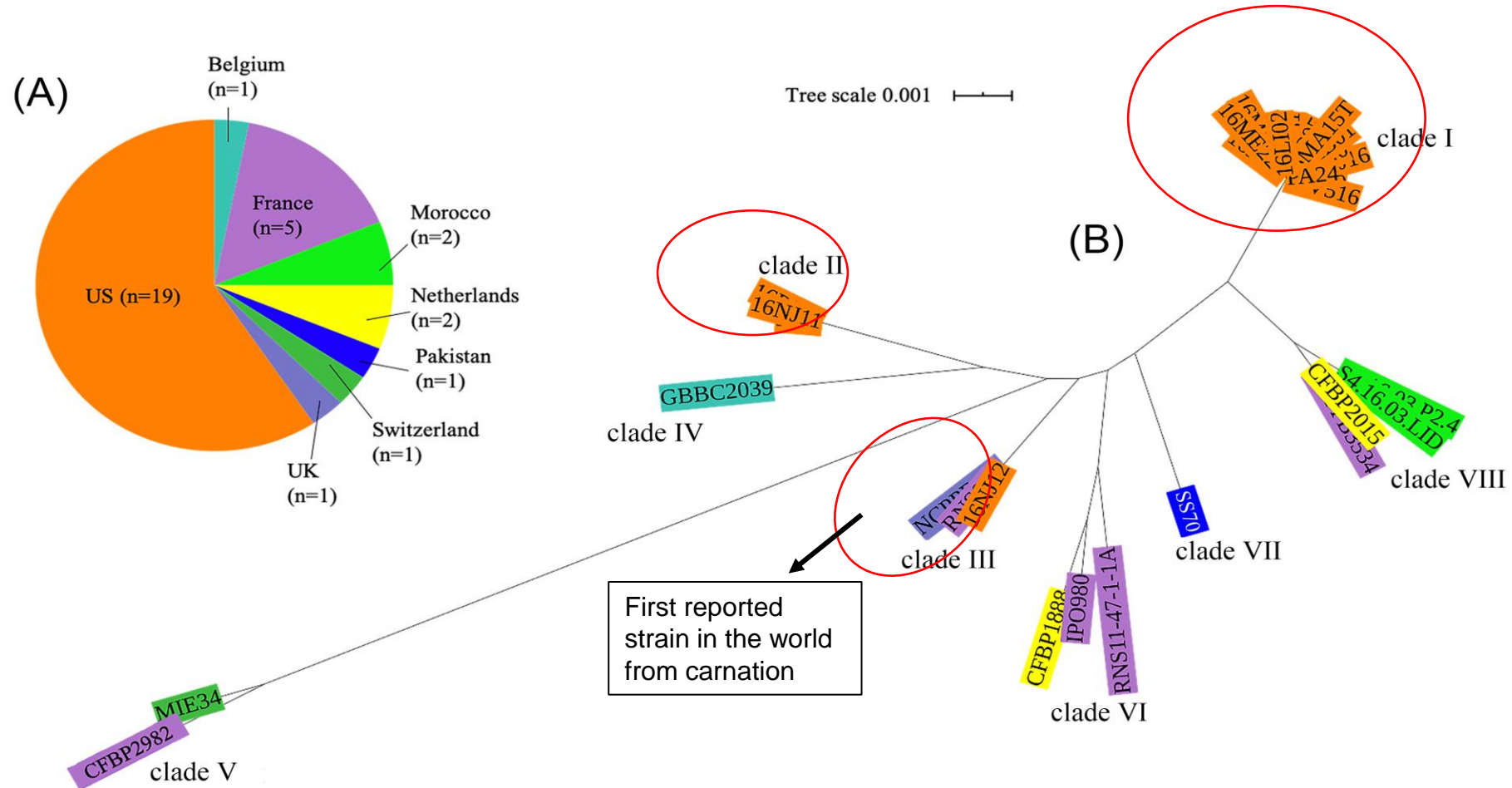
Type II, continuously present in at least one state every year at relatively lower percentages than Type I.



Type III, only present in 2016 in **Pennsylvania** and **New Jersey**, and 2019 in **Massachusetts**, and was not detected in Maine.

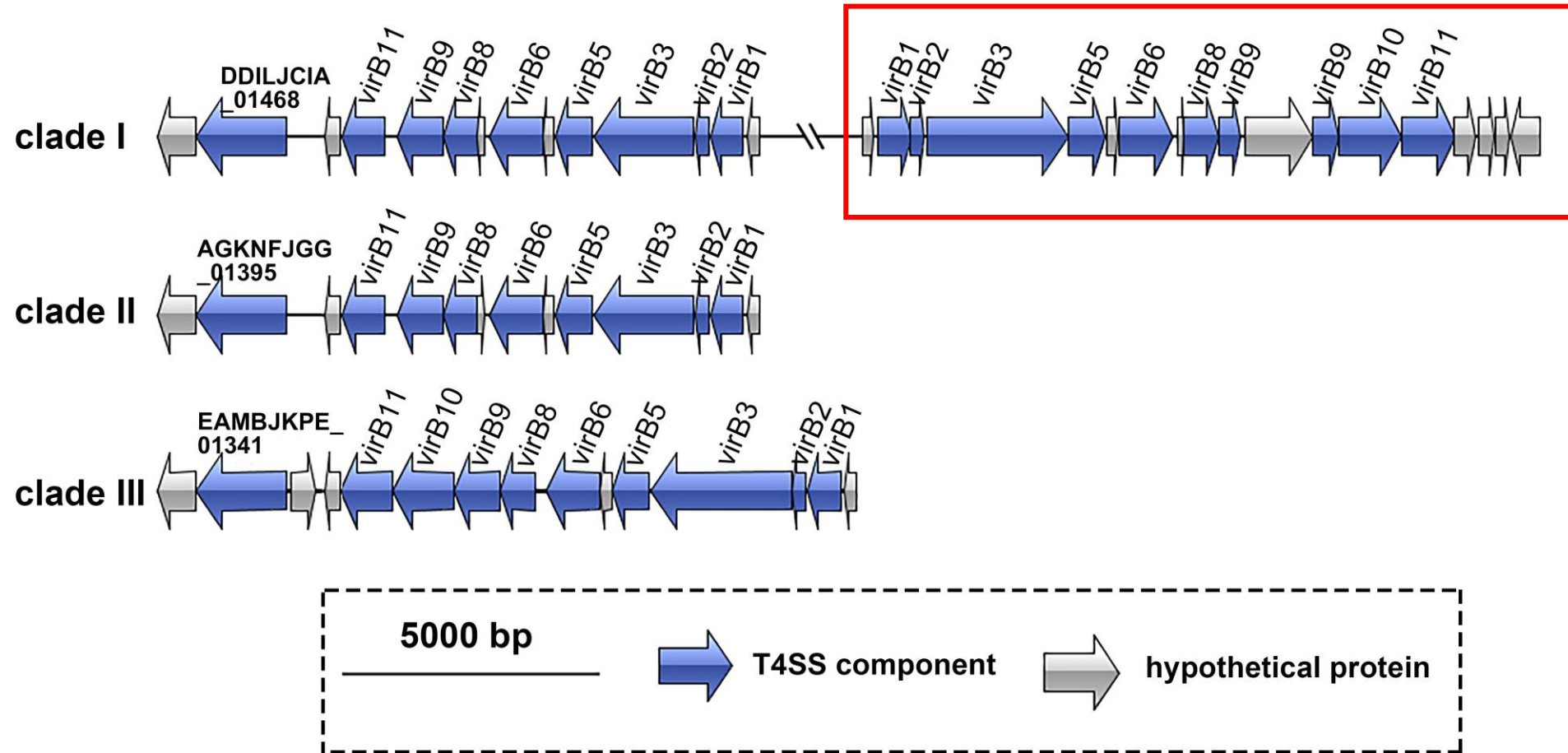
Phylogenetic tree based on SNPs in the core genome, N = 32

Ge et al. 2021. *Plant Disease* 105: 3946-3955

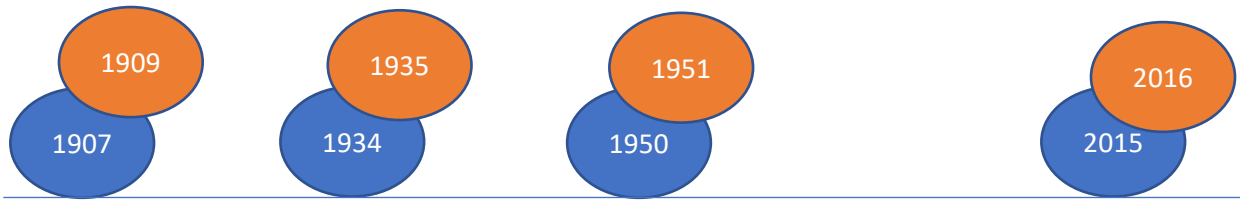


Type IV secretion system (T4SS) involved in genetic exchange or effector translocation

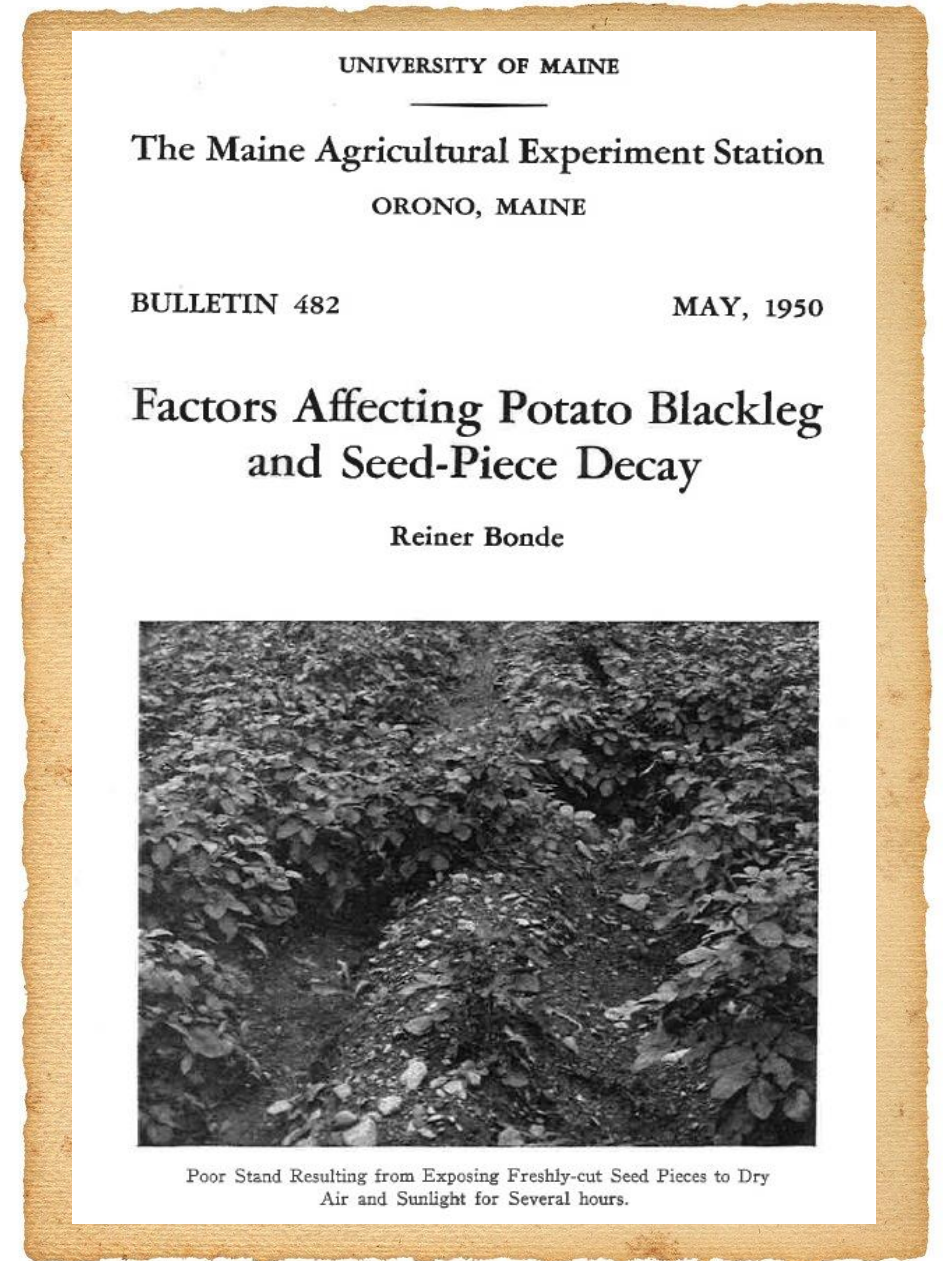
Ge et al. 2021. Plant Disease 105: 3946-3955



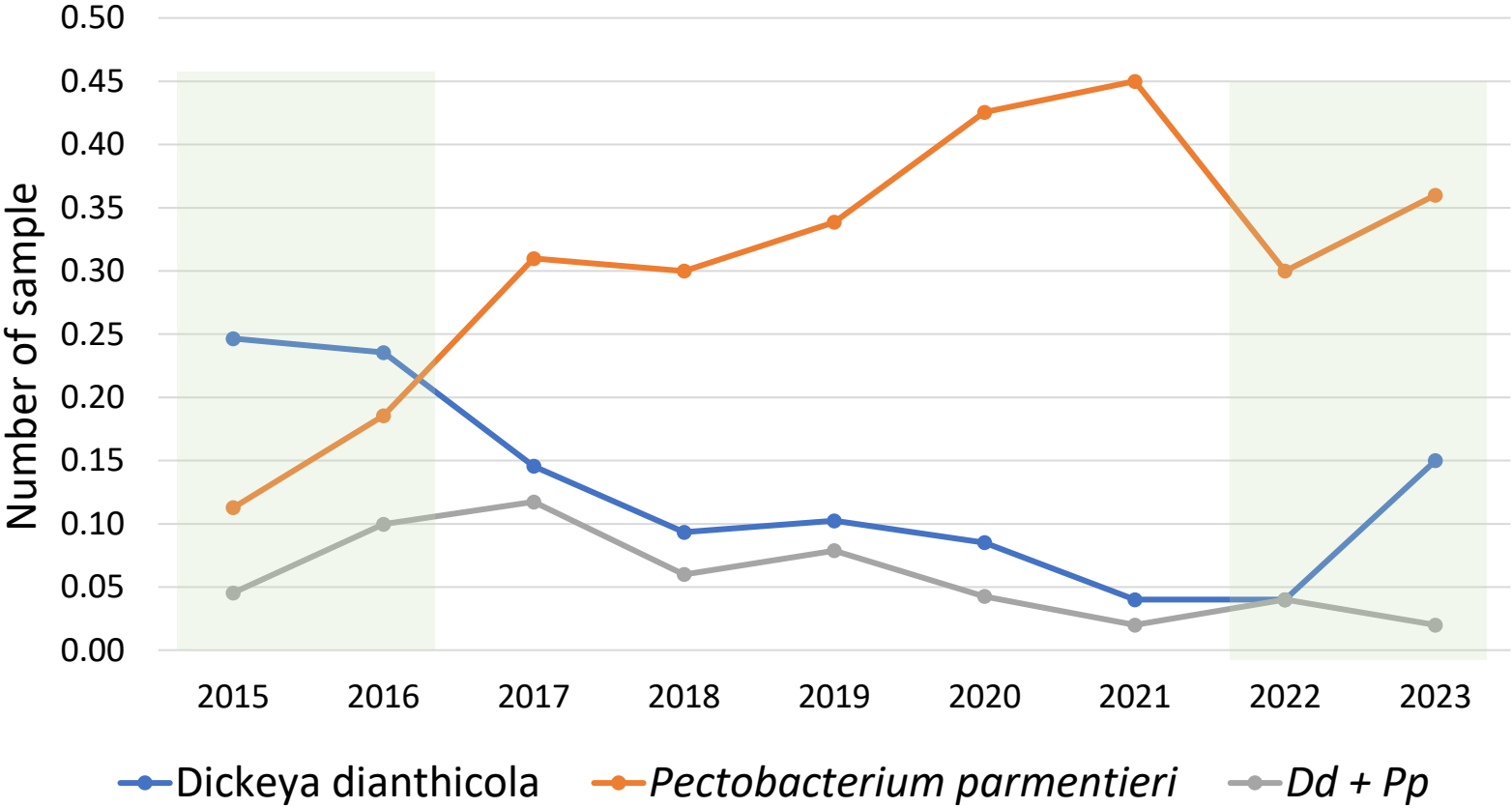
Outbreaks in history: old disease? New pathogen?



2015, Maine

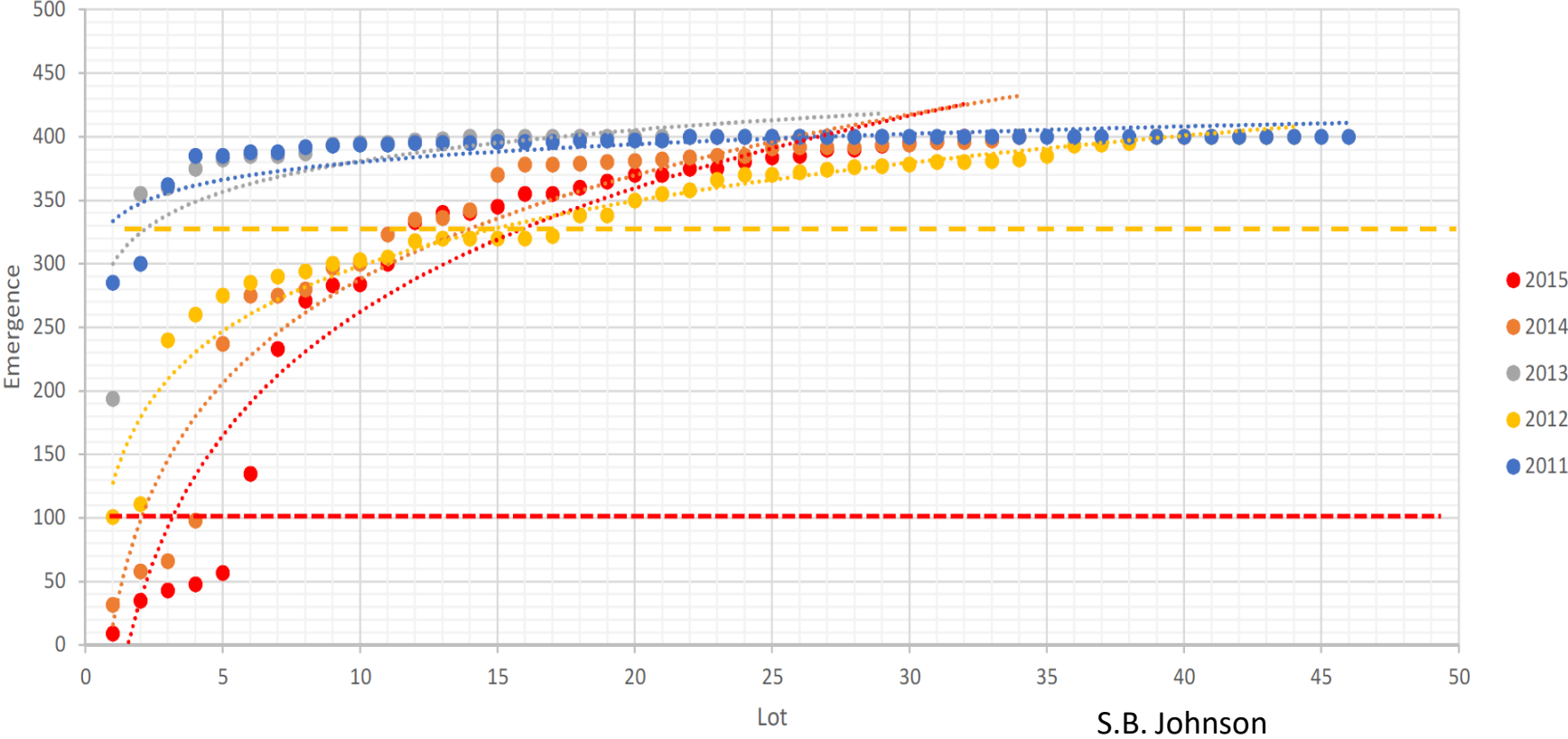


Pathogen dynamic of potato samples in the US

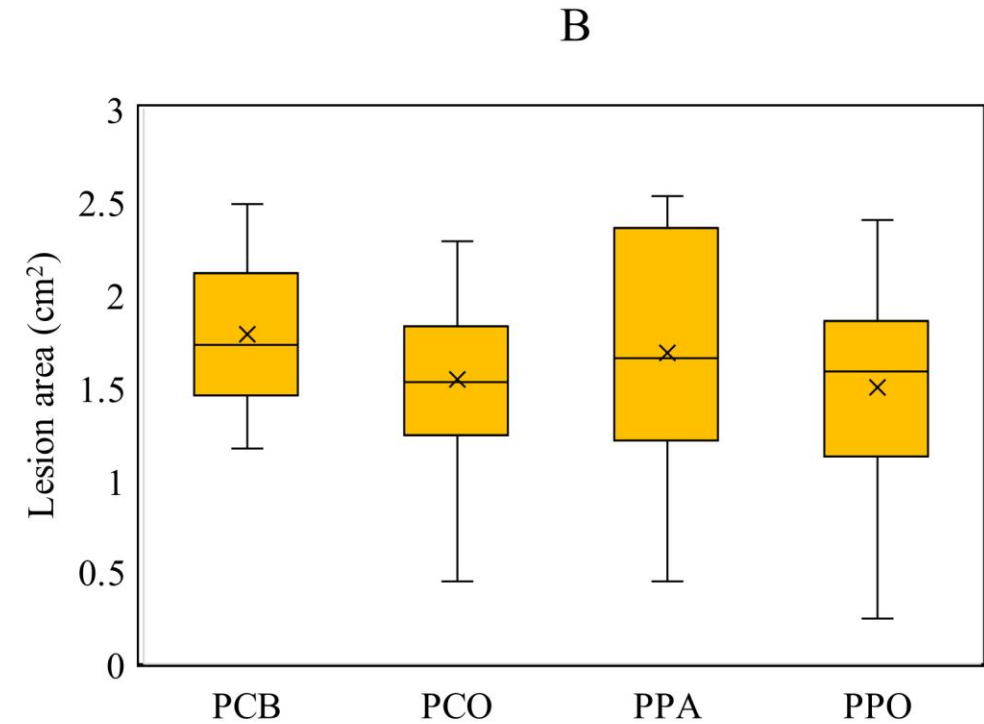
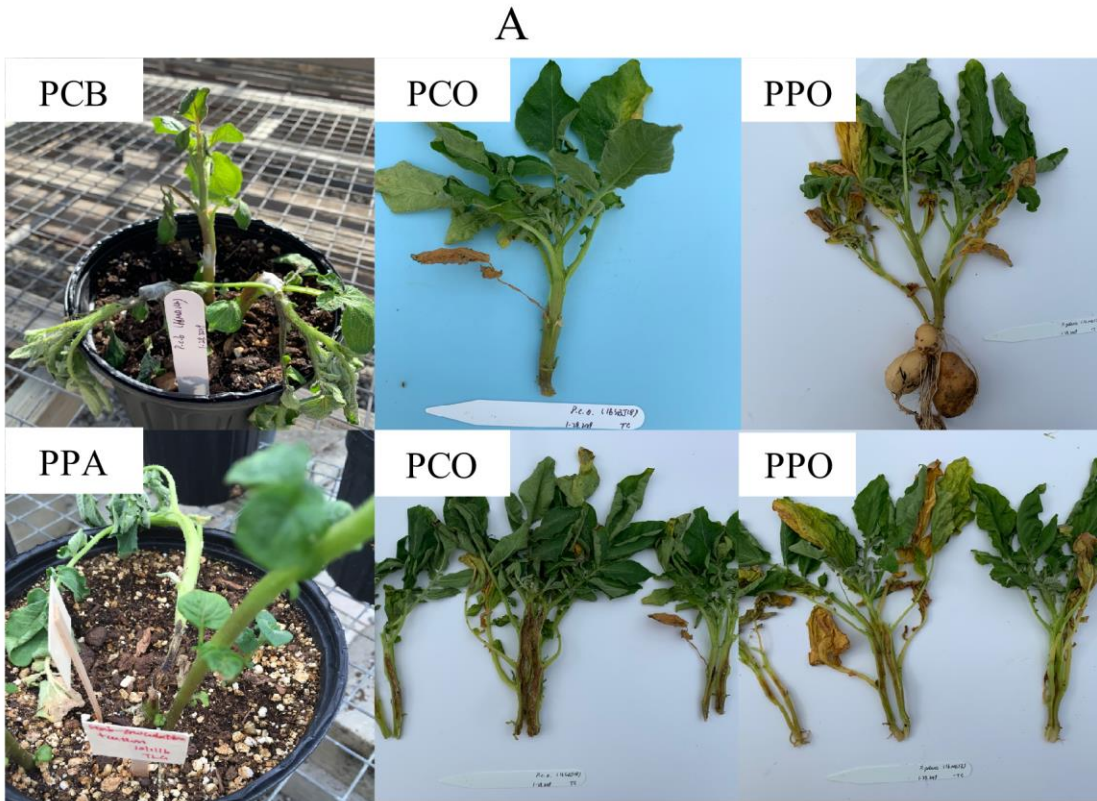


Low emergence of potatoes is associated with seed contamination

Reba Emergence 2011-2015



Pathogenicity of *Pectobacterium* spp.



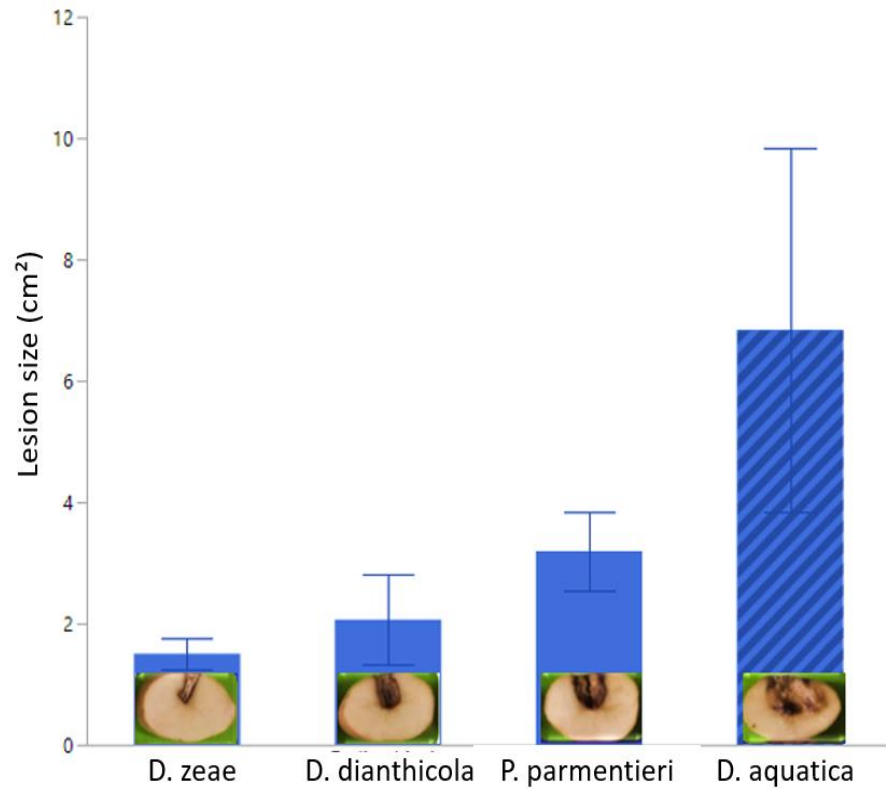
PCO: *P. carotovora* subsp. *odoriferum*, PCB: *P. brasiliense*, PPO: *P. polaris*, PPA: *P. parmentieri*

Bacteria surviving in water could be a source of inoculum

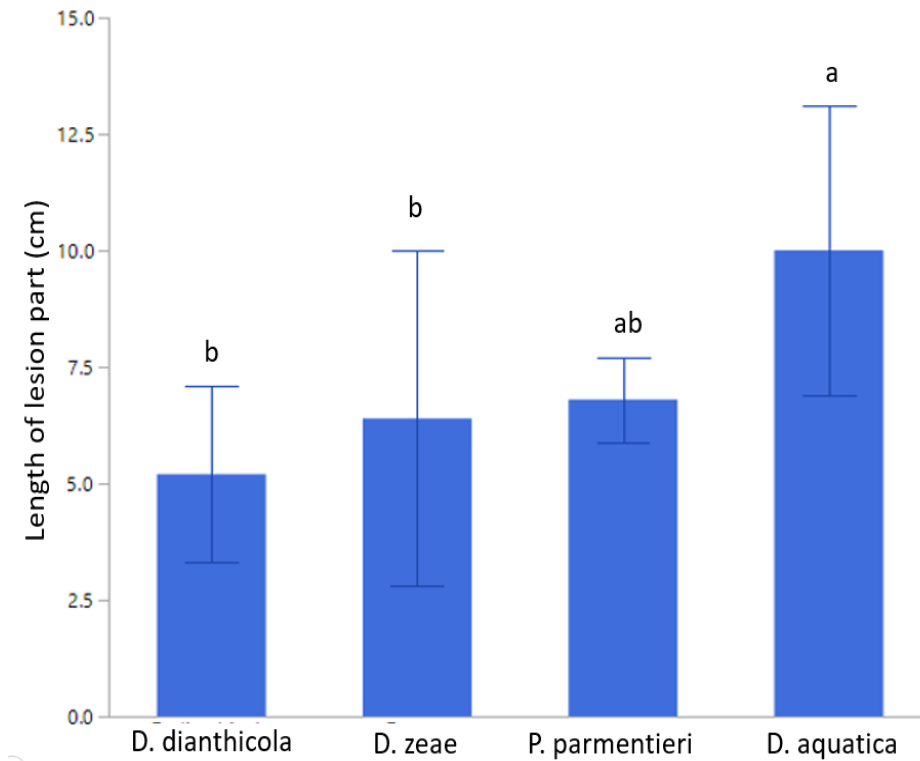
- Maine
 - 40.5% water samples were *Dickeya* spp.
 - *D. dadantii*
 - *D. zeae*
 - *D. dianthicola*
 - *D. aquatica*
 - *Pectobacterium*
 - *P. brasiliense*
 - *P. carotovorum*
 - *P. atrosepticum*
 - *P. parmentieri*
- *Dickeya* spp. were also found in water in Massachusetts and Canada

Pathogenicity assay

➤ Poking Method

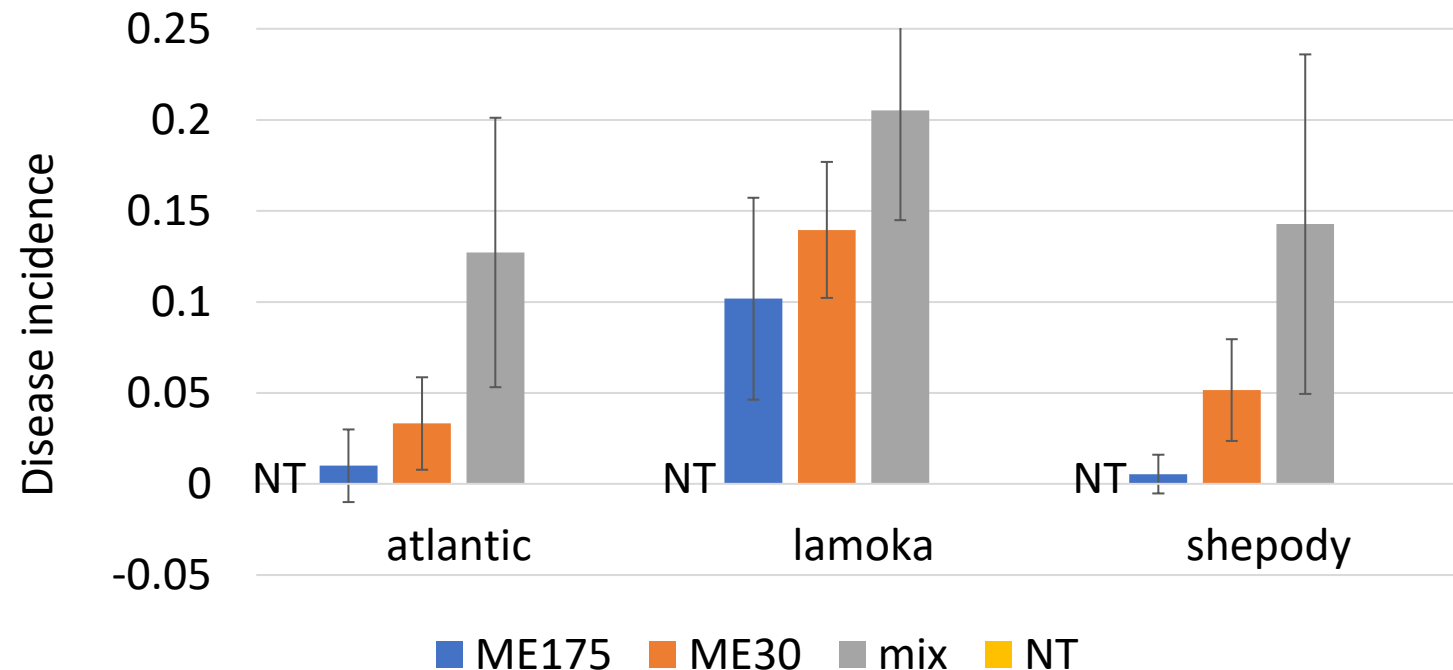


➤ Stem injection



Blackleg of potato inoculated with *Dickeya dianthicola* OR/AND *Pectobacterium parmentieri*

Ge et al. 2021. *Microorganisms* 9: 316.



- *D. dianthicola* is more aggressive than *P. parmentieri*
- Co-infection of *D. dianthicola* and *P. parmentieri* aggravate disease severity

- **ME175**: *P. parmentieri*; **ME30**: *D. dianthicola*; mix: two species combined; **NT**: non-inoculated

Interspecies interactions via plant infection

	P. parmentieri	P. versatile	P. carotovorum
Dickeya dianthicola	Synergy @ high temp Antagonism @opt temp	Synergy @ opt. temp	Synergy @ high temp Antagonism @opt temp
Pectobacterium parmentieri	-	Antagonism	Synergy @ resistant var
P. versatile		-	Synergy @ high temp Antagonism @opt temp

Conclusions

1. *Dickeya dianthicola* genotype I was the predominant strain associated with the outbreak of 2015
2. Multiple species of *Dickeya* and *Pectobacterium* cause potato blackleg and soft rot, and their interactions determine the disease epidemic
3. Water can be a potential source of inoculum of PBSR

Acknowledgements

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Thank you