

Abstract

Potato blackleg and soft rot have caused substantial production and storage losses in the Northeastern U.S. In the past decade, the primary pathogens have shifted from *Dickeya dianthicola* to *Pectobacterium* species, such as *P. versatile* and *P. parmentieri*. The pathogenicity of these bacteria varies depending on the species. Whole genome sequencing of over a hundred bacterial isolates suggests that this shift in pathogen populations may be influenced by climate change.

Introduction

Potato blackleg and soft rot has caused significant economic losses in the Northeastern United States¹⁻³, especially in Maine since the outbreak of the disease in 2015 (Fig. 1). We have observed the pathogens in taxonomy and found that the predominant species have changed over the time. To understand the driving forces, various studies have been conducted under laboratory, greenhouse and field conditions.

The goal of this study was to investigate factors that are associated with pathogen population switch and understand the potential risk of disease epidemic with the change of predominant pathogens.

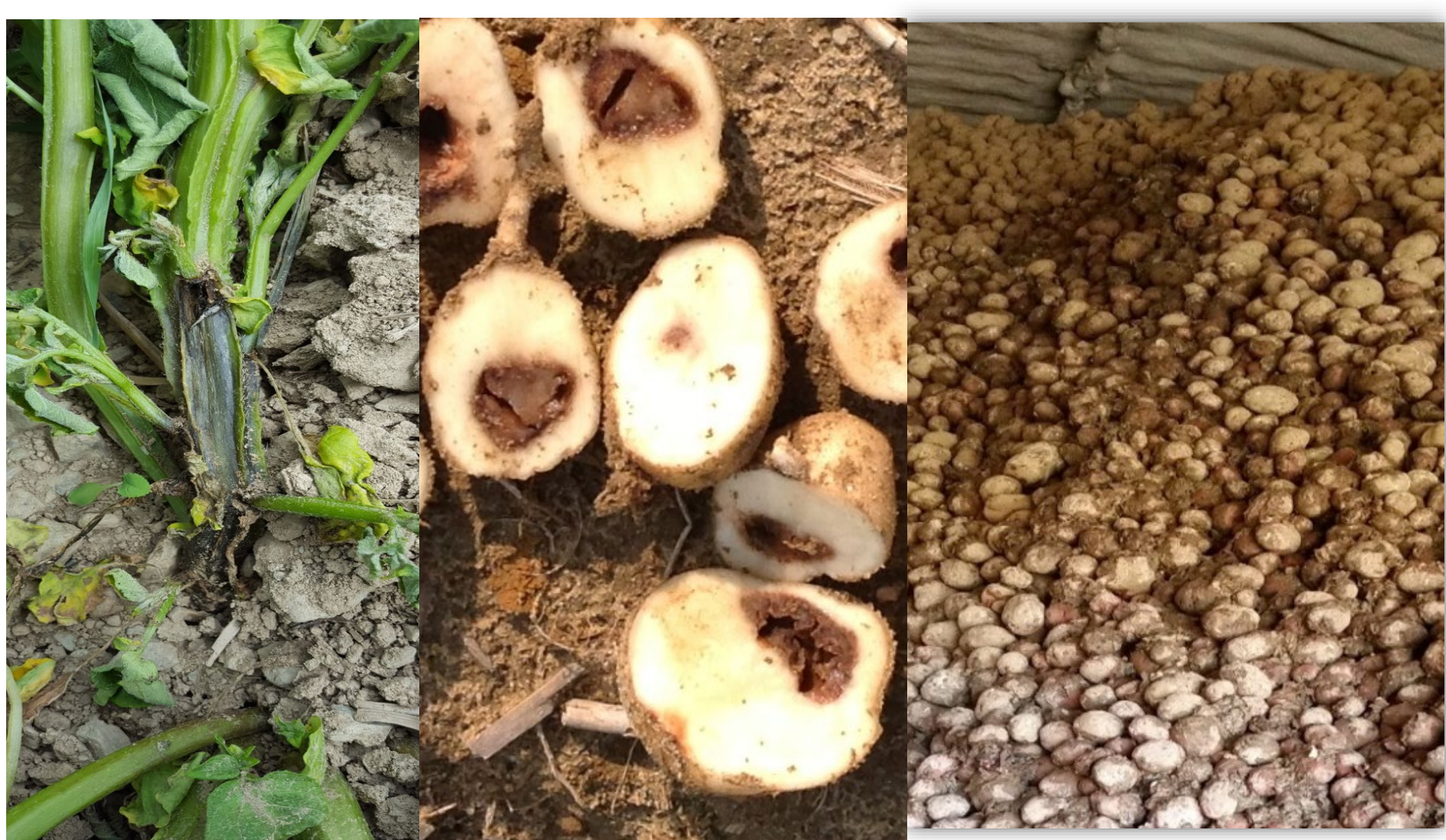


Fig. 1 Blackleg and soft rot of potato causing plant stand loss in fields and tuber rot in storage.

Dynamic population of pathogens

Potato stems and tubers exhibiting blackleg and soft rot symptoms were collected from various states in the Northeastern U.S., such as Maine. The samples were processed to obtain either a bacterial suspension (mixture of bacteria) or to isolate individual bacterial strains. DNA was extracted from both the bacterial mixtures and pure-culture isolates. The DNA from the samples was then subjected to amplicon sequencing, while the DNA from the isolates was analyzed using whole-genome sequencing.

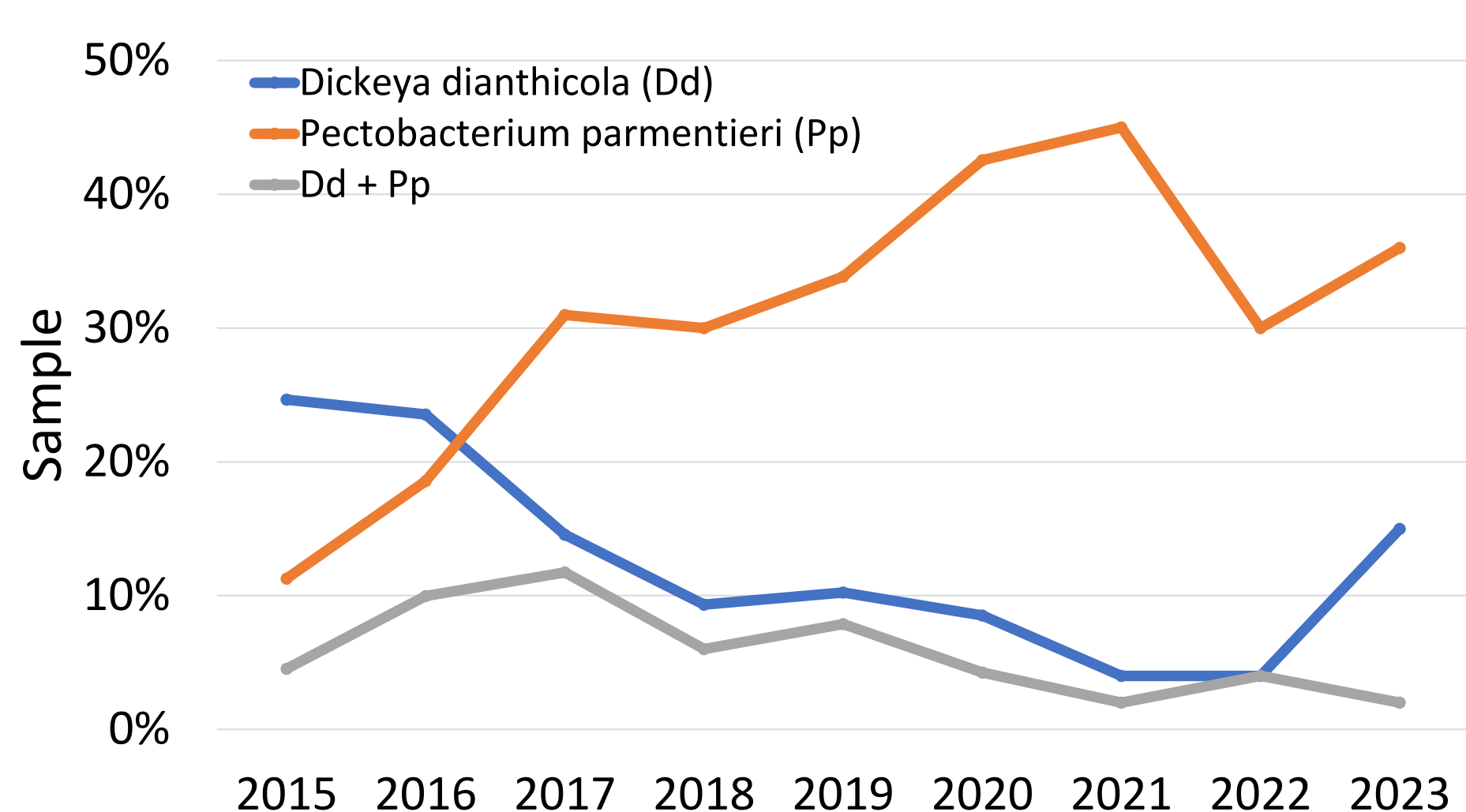


Fig. 2 Dynamics of predominant bacterial pathogen species detected from blackleg and soft rot of potato in the Northeastern United States from years 2015 to 2023. Total of 1,192 samples were analyzed.

Dynamic

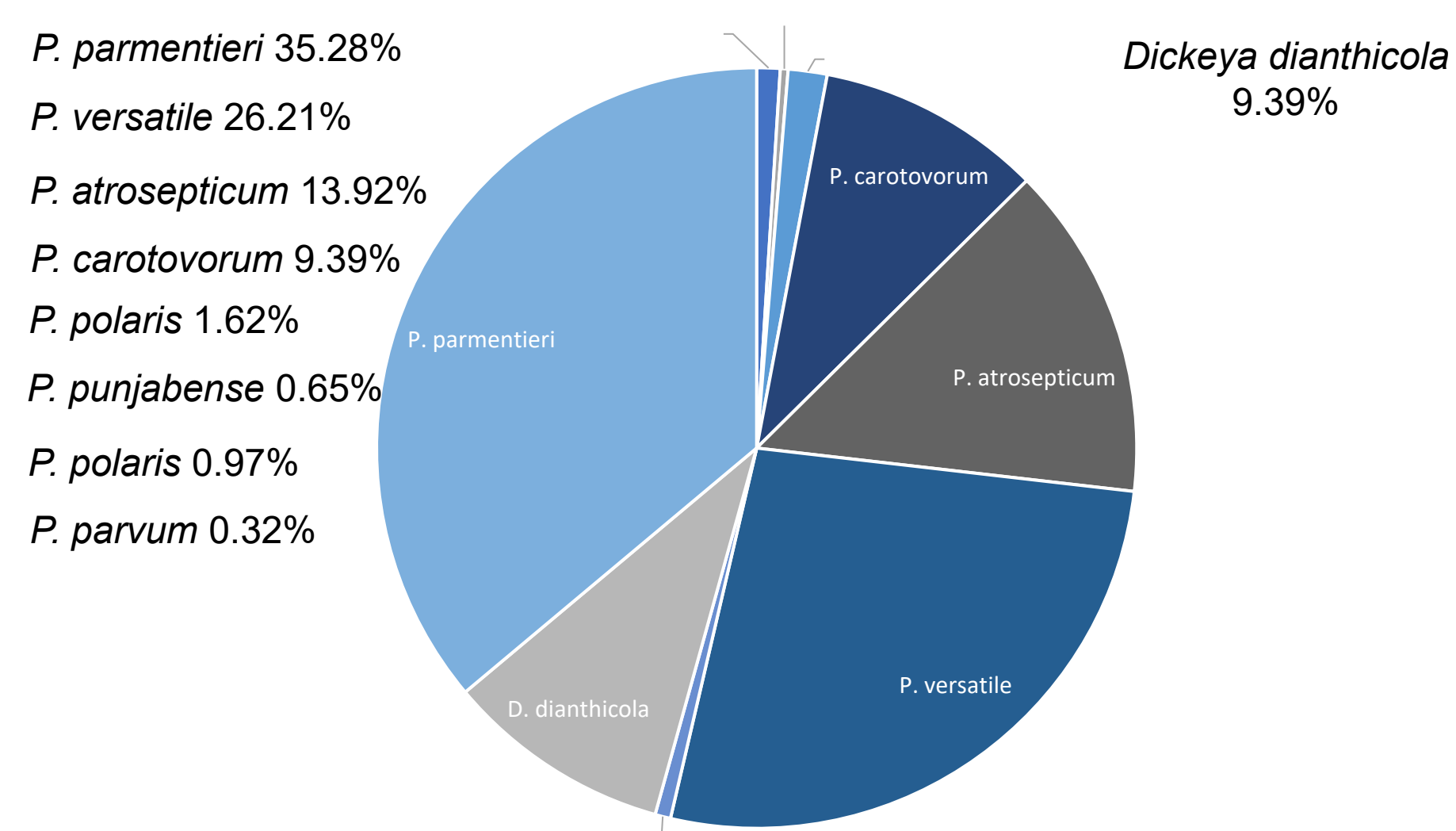


Fig. 3 Composition of bacterial pathogen species causing blackleg and soft rot of potato.

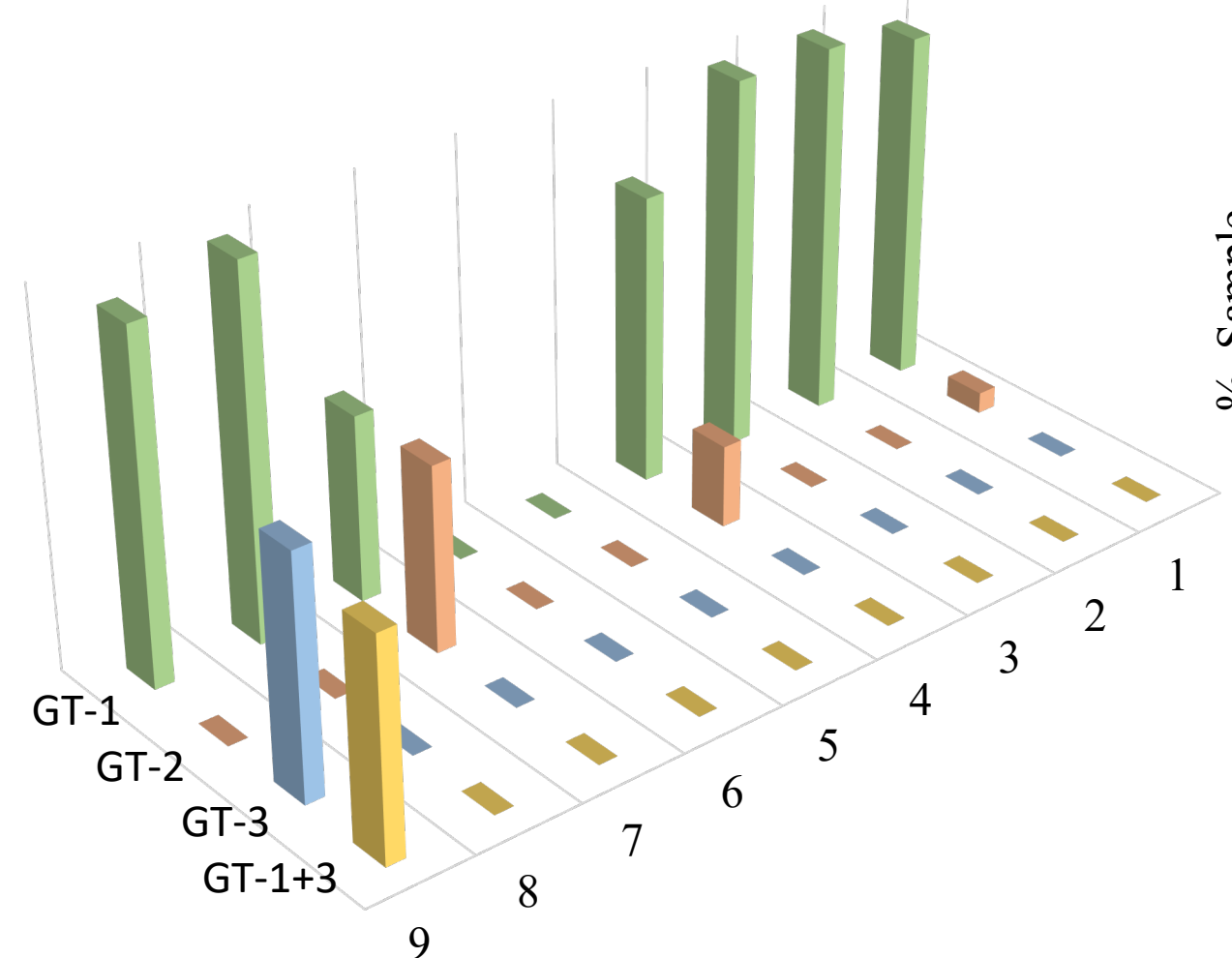


Fig. 4 Genotypes (GT-1, -2, -3, and -1+3) of *Dickeya dianthicola* detected from blackleg and soft rot of potato.

Multiple pathogenic species were detected, responsible for disease. *Dickeya dianthicola* was predominant in 2015 and 2016 but declined in prevalence in subsequent years. In contrast, *Pectobacterium parmentieri* increased over time, emerging as a primary pathogen (Fig. 2). Similarly, *Pectobacterium versatile* showed a significant increase (Fig. 3). Regarding *D. dianthicola*, genotype 1 was the dominant strain responsible for the outbreak. Over time, genotype 2 became noticeable (Fig. 4).

Bacterial interactions

Pathogenic bacteria were inoculated either individually or as a mixture of two species into potato tubers through a puncture wound. After 4 days of incubation at different temperatures, disease lesions were measured.

Lesions were smaller at 8° C but significantly larger at 28° C. The largest lesions occurred when a mixture of *Dickeya dianthicola* and another bacterial species was used for inoculation (Fig. 5). This indicates that *D. dianthicola* is highly infectious and its pathogenicity can be further enhanced by co-infection with other bacterial species. The newly emerged *Pectobacterium versatile* was found to be more aggressive than *D. dianthicola*, highlighting its potential as a significant risk under changing climate conditions.

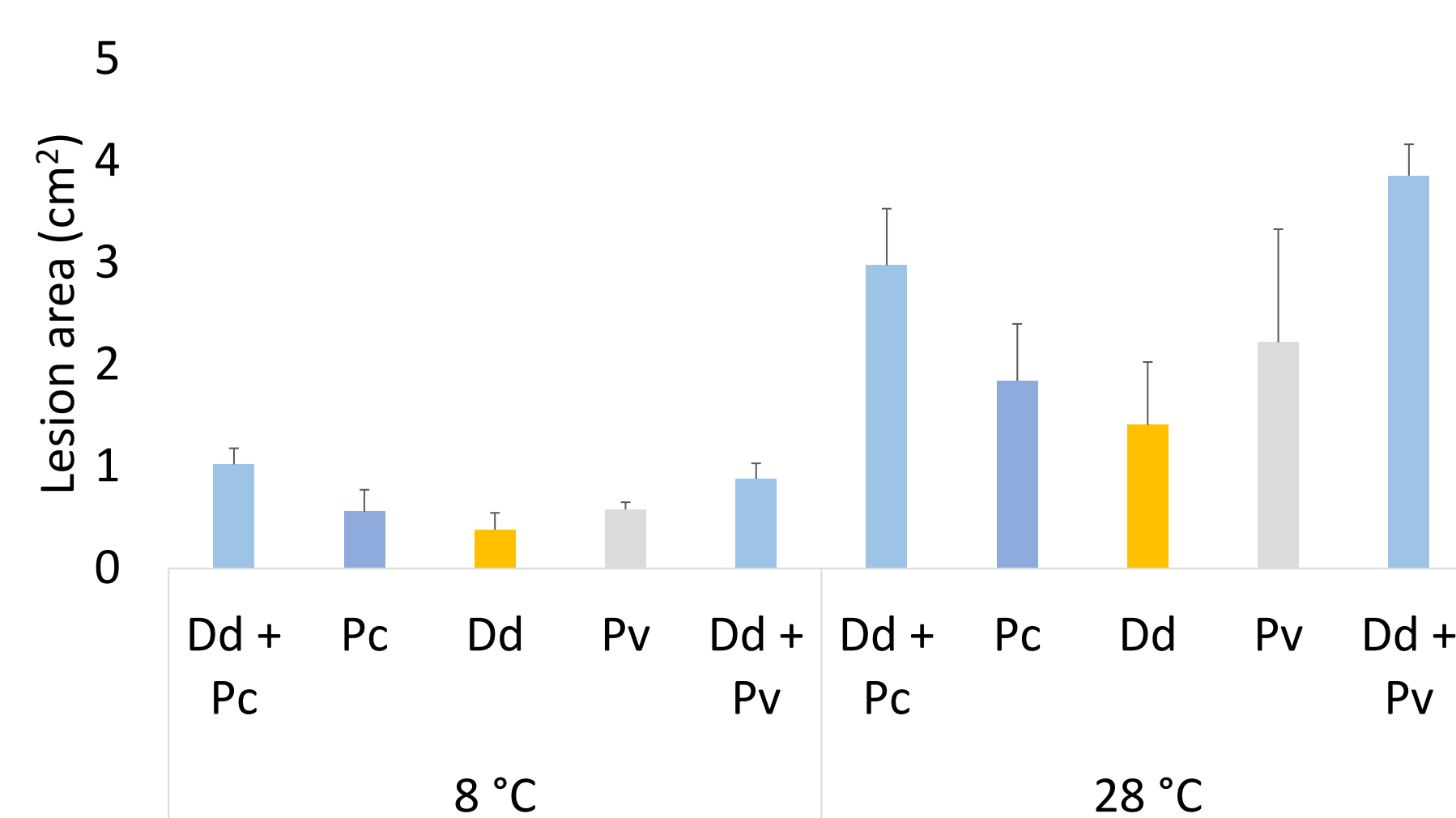


Fig. 5 Interactions between species of *Dickeya dianthicola* (Dd), *Pectobacterium parmentieri* (Pp), and *P. parvum* (Pv) measured by disease lesion sizes on potato tubers.

Plant infection

Potato tubers were inoculated with *Dickeya dianthicola* at three time points: January, March, and May in 2021 and 2022. These infected tubers were mixed at ratios (0, 50%, and 100%) with uninfected tubers and subsequently planted in the field. Results indicated that the earlier the tubers were inoculated, the higher the disease incidence observed in the field (Fig. 6).

Whole-genome sequencing analyses were conducted on *Pectobacterium parmentieri* strains worldwide. The results revealed that the majority of *P. parmentieri* strains in the U.S. form a unique cluster distinct from international strains, indicating they are indigenous (Fig. 7). This suggests unique evolutionary pressures or limited introduction of foreign strains into the U.S.

Percentage of potato tubers inoculated with *D. dianthicola*

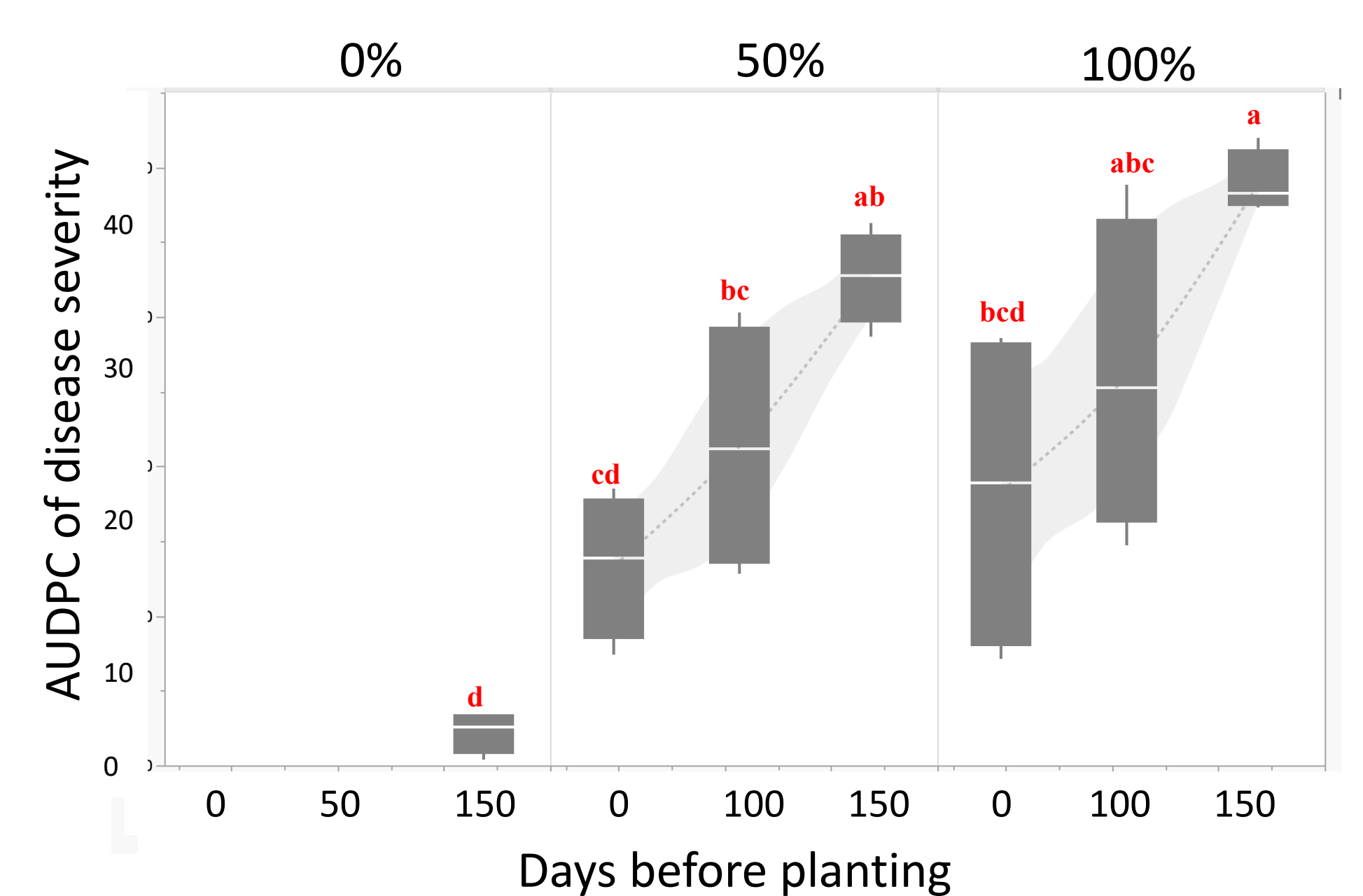


Fig. 6 Impact of *Dickeya dianthicola* infestation time and length of storage on blackleg and soft rot of potato in fields measured by area under disease progress (AUDPC).

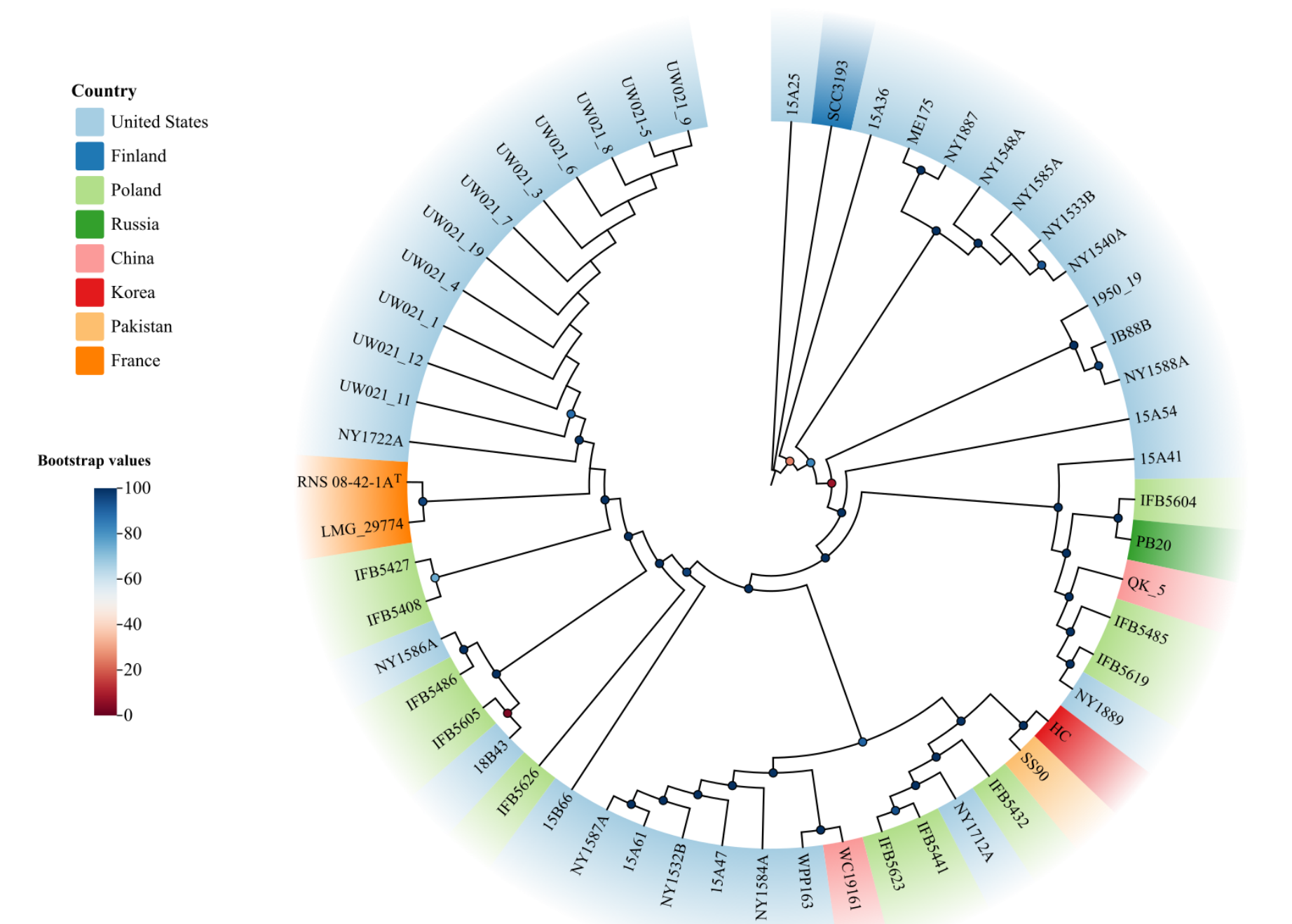


Fig. 7 Whole genome sequence analysis on *Pectobacterium parmentieri* strains from various regions in the world.

References

- Ge, T. et al. 2021. Plant Disease 105: 1976-1983. DOI: 10.1094/PDIS-10-20-2138-RE.
- Ma, X. et al. 2024. Frontiers in Microbiology 15:1403121. DOI: 10.3389/fmicb.2024.140312.1
- Ge, T. et al. 2021. Microorganisms 9: 316. DOI: 10.3390/microorganisms9020316.
- Curland, R.D. et al. 2021. Microorganisms 9: 1733. DOI: 10.3390/microorganisms9081733.

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