



Editorial: Genome-Wide Analyses of *Pectobacterium* and *Dickeya* Species

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Editorial on the Research Topic

Genome-Wide Analyses of *Pectobacterium* and *Dickeya* Species

Pectobacterium and *Dickeya*, emerging pathogens and key genera included in the Soft Rot Pectobacteriaceae family (SRP; formerly known as pectinolytic *Erwinia* spp.) (Adeolu et al., 2016), are among the top 10 bacterial plant pathogens that limit crop yields and threaten global food security worldwide (Mansfield et al., 2012). Species within both genera are globally distributed (Mansfield et al., 2012; Ma et al., 2019; Boluk et al., 2021) and cause significant damage to both monocots and dicots, particularly to potato with potential global losses in production (Agrios, 2006), and an estimated cost of US\$50–100 million annually in vegetables, fruits, and ornamental plants (Perombelon and Kelman, 1980; Pérombelon, 2002; Ma et al., 2007). Species in both genera have been isolated from infected plant tissues, soil, and water (Glasner et al., 2008; Hugouvieux-Cotte-Pattat et al., 2019; Oulghazi et al., 2019) as well as from alternative non-agricultural plant hosts (Fikowicz-Krosko et al., 2017; Fikowicz-Krosko and Czajkowski, 2018). The pectinolytic bacteria rapidly adapt to new hosts, raising serious concerns for potential damage to new crops (Boluk et al., 2020, 2021; Klair et al., 2021).

Recently, several new *Pectobacterium* and *Dickeya* species were reported; *Pectobacterium* is currently divided into 19 recognized species with the addition of *P. parvum* in 2020 (Pasanen et al., 2020), and *Dickeya* is divided into 12 species, including the recent addition of *D. oryzae* (Wang et al., 2020).

High levels of virulence associated with these SRPs involves the secretion of plant cell wall degrading enzymes (PCWDEs) primarily through a type II secretion system (T2SS), enabling them to digest their hosts more extensively than any other microbes in both field and storage conditions (Hugouvieux-Cotte-Pattat et al., 2014; Li et al., 2018; Arizala and Arif, 2019; Fan et al., 2020). Pathogenicity determinants play a significant role in host adaptation and virulence (Boluk et al., 2021). PCWDEs and other virulence factors, such as the type III effector protein DspE and necrosis inducing protein Nip, are used to macerate plant tissue and promote plant cell death, providing nutrients for the multiplication and colonization of these necrotrophic pathogens (Kim et al., 2011; Babujee et al., 2012; Charkowski et al., 2012; Haque et al., 2017; Fan et al., 2020). The T1SS, T2SS, T6SS, some PCWDEs and proteases, the ECA cluster, achromobactin, flagellar genes, single virulence locus, the *pilW* and *pilABC* genes, Flp/Tad, carotovoricin, DsbA oxidoreductase, and the majority of virulence regulators were anticipated critical genes/gene clusters for all *Pectobacterium* species, while T3SS, T4SS, T5SS, phytotoxins, type IV pilus, capsular polysaccharide, lipopolysaccharides, exopolysaccharides, iron uptake systems, phenazine, carbapenem, and colicin-like bacteriocins were observed in some species. Differences among

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antimicrobial compounds and toxin and antitoxin systems surrounding the CRISPR-Cas systems were observed in others (Glasner et al., 2008; Charkowski et al., 2012; Arizala and Arif, 2019; Przepiora et al., 2022).

Despite the severe disease impact of *Pectobacterium* and *Dickeya* species, not many comprehensive studies of SRPs have been conducted to ascertain evolutionary relationships among strains or the role of horizontal gene transfer (HGT) in speciation and adaptation to a new niche. Likewise, the impact of phages and prophages on the ecology and virulence of *Pectobacterium* and *Dickeya* still needs to be assessed in detail to understand the role of these virus-bacteria interactions in natural and agricultural settings (Czajkowski, 2016, 2019).

Rapidly developing sequencing technology (Illumina, Ion Torrent, Pacific Biosciences and Oxford Nanopore) has led to a sharp decrease in sequencing costs and has enabled genome sequencing of plant bacterial strains on a vast scale. Genomics analyses play a dominant role in elucidating bacterial taxonomy, phylogeny, and evolutionary biology and provide insights into distinct niche adaptation (McAdam et al., 2014; Cai et al., 2018; Arizala and Arif, 2019). Comparative genomics of recently evolved or emerging pathogens provide insights into the regions/islands acquired by closely related strains, enabling them to adapt to a new host/environment (Zhang et al., 2020). The number of new “omics datasets—such as genome sequencing, RNA-seq, pan-genomics, and metabolomics—are increasing rapidly. New bioinformatics pipelines and software have also become available, and with the increasing numbers of datasets and bioinformatics pipelines and software, we can accelerate the progress made in comparative and functional bacterial genomics (Chen et al., 2017; Karp et al., 2019).

In this special issue, six articles were published. Czajkowski et al. in their article “Genome-wide identification of *Dickeya solani* transcriptional units upregulated in response to plant tissues from a crop-host *Solanum tuberosum* and a weed-host *Solanum dulcamara*”, identified 210 mutant of *D. solani* IPO2222 exhibited plant tissue-dependent expression. The selected 13 genes were differentially expressed in potato (*Solanum tuberosum*) and/or *Solanum dulcamara* (bittersweet nightshade) stem, leaf, and root tissues. These results imply that necrotrophic bacterium *D. solani* can recognize its hosts during the early stages of infection and modify its behavior accordingly. In the next article “The PhoPQ two-component system is the major regulator of cell surface properties, stress responses, and plant-derived substrate utilization during development of *Pectobacterium versatile*-host plant pathosystems” by Kravchenko et al. it was revealed that PhoP, part of PhoPQ two compartment system, regulates at least 115 genes involved in degradation, transport, and metabolism of plant-derived carbon sources, bacterial cell envelope, and stress resistance, and concluded that PhoPQ is a crucial system regulating multiple virulence-related genes controlling the development of *P. versatile*-host plant pathosystem. Article “*Pectobacterium brasiliense* 1692 chemotactic responses and the role of methyl-accepting chemotactic proteins in ecological fitness” by Tanui et al.

identified 34 methyl-accepting chemotactic proteins (MCPs) in *P. brasiliense* Pb 1692. Four out of 34 MCPs were further characterized and found that these MCPs contribute toward the biology and fitness of Pb 1692 during potato infection. Pun et al. in their article “Phloretin, an apple phytoalexin, affects the virulence and fitness of *P. brasiliense* by interfering with quorum-sensing” described that biofilm formation, secretion of plant cell wall-degrading enzymes, and production of acyl-homoserine lactone (AHL) signaling molecules were significantly inhibited by exposing *P. brasiliense* to phloretin, and impaired virulence mechanisms. The results support that phloretin inhibits Expl activity. Genomic biology of two unique strains of *Dickeya zea* was described in the article “Genomic and phenotypic biology of novel strains of *D. zea* isolated from pineapple and taro in Hawaii: insights into genome plasticity, pathogenicity, and virulence determinants” by Boluk et al.. The analyses revealed truncated type III and IV secretion systems (T3SS and T4SS) in the taro strain. Both strains, from pineapple and taro, however, were pathogenic, lacking the zeamine biosynthesis gene cluster, a key player in virulence in other *Dickeya* species. In the last article “Transcriptome analysis revealed overlapping and special regulatory roles of RpoN1 and RpoN2 in motility, virulence, and growth of *Xanthomonas oryzae* pv. *oryzae*” by Yu et al. it was found that deletion of *rpoN1* or *rpoN2* in *X. oryzae* pv. *oryzae* led to significant dysfunction of bacterial swimming motility, flagellar assembly, and virulence, and identified 127 overlapping differentially expressed genes (DEGs) regulated by both RpoN1 and RpoN2.

In conclusion, this special issue compiled research articles covering comparative and functional genomics analysis of SRP bacteria. The articles published in this issue added scientific knowledge to fill information gaps related to pathogenicity determinants, genetic exchange, and evolution of this devastating group of pathogens, and enhanced our ability to combat soft rot diseases that unequivocally impact food security.

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All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

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