Genomic and Functional Dissections of *Dickeya zeae* Shed Light on the Role of Type III Secretion System and Cell Wall-Degrading Enzymes to Host Range and Virulence

Ming Hu,a Yang Xue,a Chuhao Li,a Mingfa Lv,a Lianhui Zhang,a Matthew R. Parsek,a,b Guangtao Lu,c Xiaofan Zhou,a Jianuan Zhoua

aGuangdong Laboratory for Lingnan Modern Agriculture, Guangdong Province Key Laboratory of Microbial Signals and Disease Control, Integrative Microbiology Research Center, South China Agricultural University, Guangzhou, China
bDepartment of Microbiology, University of Washington School of Medicine, Seattle, Washington, United States
cState Key Laboratory for Conservation and Utilization of Subtropical Agro-Bioresources, College of Life Science and Technology, Guangxi University, Nanning, China

ABSTRACT *Dickeya zeae* is a worldwide destructive pathogen that causes soft rot diseases on various hosts such as rice, maize, banana, and potato. The strain JZL7 we recently isolated from clivia represents the first monocot-specific *D. zeae* and also has reduced pathogenicity compared to that of other *D. zeae* strains (e.g., EC1 and MS2). To elucidate the molecular mechanisms underlying its more restricted host range and weakened pathogenicity, we sequenced the complete genome of JZL7 and performed comparative genomic and functional analyses of JZL7 and other *D. zeae* strains. We found that, while having the largest genome among *D. zeae* strains, JZL7 lost almost the entire type III secretion system (T3SS), which is a key component of the virulence suite of many bacterial pathogens. Importantly, the deletion of T3SS in MS2 substantially diminished the expression of most type III secreted effectors (T3SEs) and MS2’s pathogenicity on both dicots and monocots. Moreover, although JZL7 and MS2 share almost the same repertoire of cell wall-degrading enzymes (CWDEs), we found broad reduction in the production of CWDEs and expression levels of CWDE genes in JZL7. The lower expression of CWDEs, pectin lyases in particular, would probably make it difficult for JZL7 to break down the cell wall of dicots, which is rich in pectin. Together, our results suggest that the loss of T3SS and reduced CWDE activity together might have contributed to the host specificity and virulence of JZL7. Our findings also shed light on the pathogenic mechanism of *Dickeya* and other soft rot *Pectobacteriaceae* species in general.

IMPORTANCE *Dickeya zeae* is an important, aggressive bacterial phytopathogen that can cause severe diseases in many crops and ornamental plants, thus leading to substantial economic losses. Strains from different sources showed significant diversity in their natural hosts, suggesting complicated evolution history and pathogenic mechanisms. However, molecular mechanisms that cause the differences in the host range of *D. zeae* strains remain poorly understood. This study carried out genomic and functional dissections of JZL7, a *D. zeae* strain with restricted host range, and revealed type III secretion system (T3SS) and cell wall-degrading enzymes (CWDEs) as two major factors contributing to the host range and virulence of *D. zeae*, which will provide a valuable reference for the exploration of pathogenic mechanisms in other bacteria and present new insights for the control of bacterial soft rot diseases on crops.

KEYWORDS *Dickeya zeae*, host range, comparative genomics, virulence, T3SS, T3SEs, CWDEs

*Dickeya* bacteria usually cause soft rot disease on many economically important crops and ornamental plants all over the world. As a highly diverse group, the genus contains 12 species according to current classification criteria, namely, *D. chrysanthemi*, *D. acidovorans*, *D. chrysanthemi* subsp. *tuberigenes*, *D. chrysanthemi* subsp. *lilacinus*, *D. chrysanthemi* subsp. *purpurea*, *D. chrysanthemi* subsp. *rosea*, *D. chrysanthemi* subsp. *sclerotiorum*, *D. chrysanthemi* subsp. *cicadae*, *D. chrysanthemi* subsp. *polonicum*, *D. chrysanthemi* subsp. *violaceum*, *D. chrysanthemi* subsp. *zeae*, and *D. chrysanthemi* subsp. *novae-angliae*. Among these species, *D. chrysanthemi* subsp. *lilacinus* is the most widely distributed and has been isolated from a wide range of plants, including rice, maize, soybean, and pepper. *D. chrysanthemi* subsp. *purpurea* is also a common species in *Dickeya*, and it is associated with soft rot diseases on a variety of plants, including rice, maize, potato, and sunflower. *D. chrysanthemi* subsp. *rosae* and *D. chrysanthemi* subsp. *sclerotiorum* are also important species in *Dickeya*, and they have been isolated from soft rot diseases on ornamental plants and agricultural crops, respectively. *D. chrysanthemi* subsp. *violaceum* is a less common species in *Dickeya*, and it has been isolated from soft rot diseases on rice, potato, and sunflower. *D. chrysanthemi* subsp. *novae-angliae* is the most recently described species in *Dickeya*, and it has been isolated from soft rot diseases on ornamental plants, including chrysanthemum and daisy. *D. chrysanthemi* subsp. *zeae* is a less common species in *Dickeya*, and it has been isolated from soft rot diseases on ornamental plants, including clivia and banana.
D. dadantii, D. dianthicola, D. paradisiaca, D. zeae, D. solani, D. aquatica, D. fangzhongdai, D. poaceaeaphila, D. lacustris, D. undicola, and D. oryzae (1–8). Among them, D. zeae was isolated mostly from plants in tropical and subtropical regions, especially in Southeast Asian countries (9), suggesting its preference to high temperature and humidity. On the other hand, D. solani was usually isolated from potato in temperate and frigid zones, especially across Europe (10, 11), with a wider temperature range for growth and disease development (12).

Although isolated mainly from monocotyledonous hosts in nature, D. zeae is so far known to infect 24 types of dicots and 23 types of monocots, indicating a broad host range (9). In recent years, D. zeae has caused considerable losses in crop yields in China, especially on rice and banana (13–16). At the same time, D. zeae strains from diverse sources also display considerable variations in their pathogenesis. For instance, the strains EC1 (isolated from rice) and MS2/MS3 (isolated from banana) showed different virulence on various monocot and dicots plants and exhibited 2-fold difference in their ability to inhibit rice seed germination (9, 17). Furthermore, consistent with these phenotypic variations, there are also key genomic differences between EC1 and MS2/MS3, including the zms gene cluster encoding the phytotoxic zeamines, one of the most important virulence factors unique to and shared by rice strains isolated from geographically distant regions (9, 18, 19), the biosynthetic gene cluster (C1O30_RS04995 to C1O30_RS05185) encoding a novel phytotoxin in MS2, and the pipR and pipA that are present only in MS1 and MS2 (17).

Importantly, we have recently isolated from the ornamental plant Clivia miniata three D. zeae strains which are, for the first time, found to specifically infect monocots (9). These strains were pathogenic on nearly all tested monocots (e.g., rice, banana, clivia), although their virulence was usually lower than that of other D. zeae strains, and could not infect any of the nine dicots tested (e.g., potato, tomato, radish, cabbage) (9). A distinctive characteristic of these clivia-isolated strains is the remarkably lower activity of cell wall-degrading enzymes (CWDEs) compared with that of other D. zeae (9). However, the molecular basis of the dramatic alteration in host range remains largely unknown.

To investigate determinants of the host range of D. zeae, we sequenced the genome of JZL7, one of the monocot-specific strains isolated from C. miniata, and performed comparative genomic as well as functional analyses of JZL7 and other D. zeae strains that infect both monocots and dicots. The findings of this study will facilitate our understanding of the nature and the evolution of the pathogenicity mechanisms of D. zeae.

RESULTS AND DISCUSSION

General genomic features of D. zeae strain JZL7. The genome of D. zeae strain JZL7 was sequenced on both the PacBio RSII and the Illumina HiSeq X Ten platforms, producing 196,305 long sequencing reads \( N_{50} = 8,071 \) bp; mean read length: 5,356 Kb; total size: 1.051 Gb) and 5.44 million short sequencing reads \( \text{PE150}; \text{total size: 1.789 Gb} \), respectively. A hybrid de novo assembly using both the short and long sequencing reads resulted in a high-quality and gapless assembly consisting of a single circular chromosome of 4,925,859 bp in size; no plasmids were detected (Fig. 1). BUSCO evaluation of the JZL7 genome detected 438 of the 440 genes (99.5%) in the enterobacterales_oddb10 data set, suggesting that the assembly is highly complete. The JZL7 genome contains 4,268 protein-coding genes, 75 tRNA genes, and 22 rRNA genes which belong to seven complete rRNA loci, including the unusual 16S-23S-5S-5S operon previously observed in other Dickeya genomes (Table 1) (18). JZL7 has both the largest genome and the largest repertoire of protein-coding genes among all sequenced D. zeae strains; it contains 167 more genes than Ech586, which has the second largest genome, and 443 more genes than EC1, which has the smallest genome (Table 1). On the other hand, the G+C content of JZL7 genome (53.68%) is highly similar to that of the other D. zeae genomes (53.34% to 53.65%) (Table 1).

Genomic differences between JZL7 and other D. zeae strains. To determine the evolution relationship between JZL7 and other D. zeae strains, all sequenced D. zeae and the closely related D. oryzae ZYY5 (8) genomes were used for phylogenetic analysis
based on the 3,110 single-copy core genes (present in all strains). Results showed that
the 15 D. zeae strains can be divided into two clusters (Fig. 2); the average nucleotide
identity (ANI) values are above 95% for all pairwise comparisons within each cluster
but below 95% for nearly all comparisons between clusters (Fig. 2). The first cluster
consists of seven strains, including DZ2Q, EC1, EC2, ZJU1202, and ZYY5, the five rice-
pathogenic strains, as well as CSL_RW192 and NCPPB_3531. Our results thus corrobo-
rate the recent proposal by Wang et al. (8) to classify this clade as a novel species,
Dickeya oryzae.

The second clade contains JZL7, CE1, and Ech586, as well as five other strains that
are highly similar to each other (ANI values of >97.85%), namely, MS1, MS2, MK19,
NCPPB_2538, and NCPPB_3532 (Fig. 2). We have recently shown that EC1 (first clade) and MS2 (second clade) are pathogenic toward both monocot and dicot hosts, whereas JZL7 (second clade) can infect only monocots (9). Taken together, our results suggest that the broad host range may have been the ancestral state to both \textit{D. zeae}.

**TABLE 1** Genomic features of the six \textit{D. zeae} strains with complete genome

| Features            | JZL7  | MS2   | EC1   | EC2   | CE1   | EchS86 |
|---------------------|-------|-------|-------|-------|-------|--------|
| BUSCO (complete)    | 99.5% | 99.5% | 99.8% | 99.8% | 99.5% | 99.5%  |
| No. of replicons    | 1     | 1     | 1     | 1     | 1     | 1      |
| Size (bp)           | 4,925,859 | 4,740,052 | 4,532,364 | 4,575,125 | 4,714,731 | 4,818,394 |
| G+C content (%)     | 53.68 | 53.45 | 53.43 | 53.34 | 53.65 | 53.64  |
| Genes               | 4,372 | 4,171 | 3,947 | 3,985 | 4,143 | 4,205  |
| Protein-coding genes| 4,268 | 4,068 | 3,825 | 3,879 | 4,037 | 4,101  |
| rRNAs               | 22    | 22    | 22    | 22    | 22    | 22     |
| tRNA                | 75    | 75    | 88    | 75    | 75    | 76     |
| ncRNA               | 3     | 2     | 8     | 5     | 5     | 2      |
| Pseudo genes        | 112   | 50    | 65    | 74    | 71    | 64     |
| Transposases        | 47    | 48    | 38    | 59    | 25    | 22     |
| Prophage Region     | 9     | 3     | 4     | 4     | 4     | 3      |
| Prophage Gene       | 250   | 68    | 160   | 63    | 108   | 87     |
| Genomic island Region| 35    | 24    | 21    | 25    | 19    | 30     |
| Genomic island Gene | 657   | 355   | 364   | 357   | 337   | 346    |

**FIG 2** ANI analyses of 15 \textit{D. zeae} and \textit{D. oryzae} strains. Based on their pairwise ANI values, all strains were clustered into two well-separated groups corresponding to \textit{D. zeae} (type strain: NCPPB 2538) and \textit{D. oryzae} (type strain: ZYY5), respectively. JZL7 belongs to the \textit{D. zeae} group and the ANI values between JZL7 and all other \textit{D. zeae} strains are greater than 95%.
and *D. oryzae*, while JZL7 became specialized on monocots during recent evolution.

To characterize the genomic differences between JZL7 and other *D. zeae* and *D. oryzae* strains that might underlie their divergent host specificities (Table S1), we first constructed whole-genome alignment between JZL7, CE1, Ech586, EC1, EC2, and MS2, all of which have completely sequenced genomes. Results showed that the six strains are largely conserved in their overall genome structures, with the only exceptions being a large inversion of ~1.4 Mb in the genome of Ech586 and a few smaller translocations in the genomes of EC1 and EC2 (Fig. 3). At the same time, insertions/deletions up to several tens of kilobases are frequently observed and distributed throughout the six genomes (Fig. 3).

We then performed pangenome analyses on the six strains to further examine differences in their gene contents. In total, 4,966 distinct gene families were identified, the majority of which (3,112 families; 62.67%) are shared by all six strains (Fig. 4), indicating a relatively stable core genome. On the other hand, 209 ortholog group family genes are JZL7 specific (Table S4), whereas 9 gene families are absent in JZL7 but shared by all the other five strains, which may contain genes that are critical for the pathogenicity to dicots.

Among the unique genes in the JZL7 genome, an additional set of type IV secretion system (T4SS) that consists of 14 *trb* genes was detected (Table S5). This extra T4SS in JZL7 shares high levels of nucleotide sequence similarity to the T4SS-encoding gene sets in *Ralstonia solanacearum* strains FQY_4 and GMI1000, *Pseudomonas aeruginosa* F30658, and *Pectobacterium carotovorum* subsp. *brasiliense* strain SX309. T4SS usually functions in the translocation of nucleic acids or proteins from donor to recipient by conjugation and DNA release/uptake (20). The two sets of T4SSs encoded in the JZL7 genome (Table S5) may have contributed to the abundant strain-specific genes of JZL7 (Fig. 1 and 3, Tables S6 and S7). However, given that strain JZL7 has more restricted host range than the strains EC1 and MS2 (9), we conjectured that this extra T4SS is not important for the pathogenesis of *D. zeae*.

The loss of T3SS in JZL7 partially explains its restricted host range. The more restricted host range of JZL7 (Table S1) might be due to the loss of some vital determinants of virulence or host specificity during its evolution. Accordingly, we found in our pangenome analysis 85 gene families that are shared by both EC1 and MS2 but absent
in JZL7 (Fig. 4, Table S8), including a set of 30 genes that are colocalized in the genome; they comprise the majority of the *dsp* gene cluster, which encodes multiple T3SS secreted proteins (e.g., DspE, HrpZ, and HrpW) as well as their chaperone (DspF), and the *hrp/hrc* gene cluster, which encodes a T3SS (Fig. 5, Table S8). The *hecA-hecB* genes between the *dsp* and *hrp/hrc* clusters, however, were conserved in JZL7; they encode the type V secretion system (T5SS), which contributes to the adherence to hosts (21). Exactly the same organization in this genomic region was found in CE1, the closest relative of JZL7 (Fig. 5). Interestingly, the *D. oryzae* strain EC2 also lost its *dsp* and *hrp/hrc* clusters, but it has a substantially different set of remaining genes.

T3SS forms a syringe-like structure to directly translocate type III secreted effectors (T3SEs) from bacterial cells into host cells and is considered a key determinant for virulence in many bacteria. It has been reported in a number of plant bacterial pathogens (e.g., *Erwinia pyrifoliae*, *Ps. syringae*, and *Xanthomonas campestris pv. campestris*) that the loss of the T3SS would severely reduce the elicitation of host defenses and thus lead to attenuated disease symptoms (22–24). Moreover, T3SS was demonstrated to be required for the full virulence of *D. dadantii* 3937 (25, 26).

To evaluate whether strain JZL7 could elicit hypersensitive response (HR) as strain MS2 harboring T3SS, we performed HR assay on *Nicotiana tabacum* K326 (27) and *Nicotiana benthamiana* (28). Results indicated that strain JZL7 could not cause HR on either of the tobacco leaves, the same as the negative-control L5S medium, whereas strain MS2 elicited a typical HR quickly in the early stage of inoculation (12 hpi) (Fig. 6). To further verify the importance of T3SS, we respectively deleted the *dsp* cluster, the
hrp/hrc cluster, and both in MS2. HR induction of Δdsp was substantially reduced in the early stage of inoculation compared with that of wild-type MS2, but little difference was found between them after 24 hpi (Fig. 6), suggesting that the T3SEs DspE, HrpZ, HrpW, and HrpK function in the initial infection of plant hosts. The T3SS structure deletion mutant Δhrp/hrc almost could not induce HR both in the early and later stages of infection, while the whole T3SS deletion mutant Δdsp/hrp/hrc significantly attenuated the HR reaction at 12 hpi but recovered part of it at 24 hpi (Fig. 6). HR is a form of programmed cell death (PCD) at the site of pathogen infection commonly controlled by interactions between pathogen avirulence gene products and plant resistance genes. Although the T3SS has been deleted from strain MS2, some avirulence genes, like the known avrL (C1O30_RS14255), are still present in the genome; thus, reduced HR could be observed by mutant infiltration. Furthermore, the components of the T3SS and the T3SEs are not the only pathogen-associated molecular patterns (PAMPs) that plant defenses are known to recognize. Flagellin, peptidoglycan, and lipopolysaccharides also contribute to triggering host innate immune response through recognizing by plant pattern recognition receptors (PRRs). To quantify the function of the T3SS, we infiltrated tobacco leaves with controlled inoculum size. Results showed that the threshold of 10⁶ MS2 CFU elicited visible HR at 12 h (Fig. 6E), which may help distinguish between true HR and other types of PCD.

To further investigate the role of T3SS in the pathogenicity and host specificity of D. zeae pathogens, we tested the pathogenicity of Δdsp, Δhrp/hrc, and Δdsp/hrp/hrc mutants in strain MS2 on monocotyledonous banana stems and clivia leaves, as well as dicotyledonous potato and radish slices. We found that the Δhrp/hrc showed 30% reduced virulence on banana and clivia seedlings (Fig. 7A and B) and 22% and 24% reduced virulence on potato and radish slices, respectively, compared with wild-type MS2 (Fig. 7C and D). The Δdsp mutant similarly showed lower (35% on potato and 36% on radish) virulence on dicots, whereas its virulence on monocots was 20% reduced on banana seedlings and 7% reduced on clivia seedlings, not significantly different from that of MS2. Notably, the deletion of the whole T3SS (Δdsp/hrp/hrc) dramatically attenuated the virulence of MS2 by more than 60% on monocots (Fig. 7A and B), to a level that is comparable to that of JZL7, and by more than 65% on dicots (Fig. 7C and D). Altogether, our results indicate that T3SS has a major role in the virulence of D. zeae.
Previous studies have revealed that tissue maceration requires type II secretion (T2SS) of CWDEs and does not involve T3SS (18). Our study revealed the contribution of T3SS to the development of soft rot symptoms, which probably results from the action by the T3SEs regulated by HrpL, as shown in Fig. S1. Unlike JZL7, however, the Δdsp/hrp/hrc mutant of MS2 still exhibited considerable virulence on dicots, suggesting that there are likely other factors contributing to the host specificity of D. zeae pathogens in addition to T3SS.

**HrpL regulates most predicted T3SEs in MS2.** In addition to the syringe structure of T3SS, genes in the dsp and hrp/hrc clusters also encode multiple transcription
We generated single-gene knockout mutants for selected regulator (HrpL, HrpS, HrpX, and HrpY) or effector (DspE, HrpK, HrpN, HrpW, and HrpZ) coding genes in MS2 and tested their pathogenicity on potato slices. Results showed that three regulator gene mutants (ΔhrpL, ΔhrpX, and ΔhrpY) and three effector gene mutants (ΔhrpK, ΔhrpN, and ΔhrpZ) exhibited significantly reduced virulence compared with that of MS2 wild type (Fig. S1). In particular, the ΔhrpL mutant showed the most dramatic reduction in virulence, which is comparable to the knockout of the entire T3SS (Δdsp/hrp/hrc) (Fig. S1).

HrpL is a sigma factor activating T3SS at different levels, including gene transcription, mRNA stability, and enzymatic activity in many plant-pathogenic bacteria, such as Erwinia, Pseudomonas,Ralstonia, and Xanthomonas (25, 29–34). In Dickeya bacteria,
however, only one effector, DspE, has been characterized alongside two harpins, HrpN and HrpW (35, 36). To investigate the regulatory role of HrpL, we first used a combination of four state-of-the-art bioinformatic tools (i.e., Bastion3, BEAN2, DeepT3, and pEffect) to identify candidate T3SEs in the genomes of MS2 and JZL7. As a result, we predicted 34 T3SEs that are present in both strains, as well as 16 and 10 T3SEs that are unique to MS2 and JZL7, respectively (Table 2). Given that hrpL is absent in JZL7, we measured the expression of all T3SE genes in MS2 wild type and ΔhrpL mutant using quantitative reverse transcriptase PCR (qRT-PCR). Results showed that the expression of 5 shared T3SE and 8 MS2-unique T3SE genes was significantly downregulated in the ΔhrpL mutant, including dspE, hrpA, hrpK, hrpS, hrpW, and hrpZ, which are all members of the dsp and hrp/hrc clusters (Fig. 8A). Chi-square tests on the fold change values of shared versus unique T3SEs showed that HrpL regulates the expression of the MS2-unique T3SE genes more strongly than the shared ones.

Previous studies in Er. amylovora, Pantoea stewartii, and Ps. syringae have characterized a conserved binding motif for HrpL, which is called the "hrp box" (GGAACC/T-N15/16-C/T/ GCACNNA) (32, 33, 36). We analyzed the promoter sequences of all predicted T3SE genes and found the typical hrp box in six of them, including the known effector DspE (36), two harpins, HrpN and HrpW, secreted through the T3SS (31), two putative effectors, HrpZ and HrpK, and a T3SS gatekeeper, HrpJ (Table 2). Three other candidate T3SE genes, C1O30_RS12170, C1O30_RS16815, and C1O30_RS19500, encoding hypothetical proteins, also contain the hrp box in their promoters, except the distances between the two conserved modules are abnormally long (69, 56, and 37 nucleotides, respectively) (Table 2). Additionally, 400 ng of HrpL was demonstrated to bind to the promoter of hrpA encoding a T3SS substrate in D. dadantii 3937 with the help of core RNA polymerase (RNAP) (34). In MS2, HrpA was not predicted as a T3SE but contains a conserved hrp box in its promoter (GGAACC-N15-CTACTTA). To verify the affinity of the HrpL to the above-mentioned hrp box-containing promoters, we carried out electrophoretic mobility shift assays (EMSAs) and found that a high concentration (5 μg) of HrpL could directly bind to the promoters of hrpA, hrpN, hrpZ, hrpK, dspE, hrpX, C1O30_RS12170, C1O30_RS16815, and C1O30_RS19500 in an hrp box-dependent manner without adding core RNAP in vitro (Fig. 8B). This is similar to the phenomenon observed in Bacillus subtilis primary sigma s^A, which by itself is able to interact with promoter DNA at the concentration of 10 μM without the assistance from core RNAP (37). The observed binding of HrpL in high concentrations to the promoters of C1O30_RS12170, C1O30_RS16815, and C1O30_RS19500 containing unusual hrp-boxes in the absence of core RNAP is not likely to be biologically relevant or evidence of function, since these atypical hrp-boxes are not functional HrpL-dependent promoters, and the expression of these three genes is not significantly affected by HrpL (Fig. 8A). To verify this, low concentrations of HrpL, in addition to RNAP, were also used to test the affinity to these promoters with typical hrp boxes. No bound band was observed for the atypical promoters, while bound bands were formed by incubation of 0.2 μg HrpL protein with hrpA promoter, and 0.4 μg HrpL protein with dspE promoter, with RNAP (Fig. 8C).

The expression of CWDE genes was broadly reduced in JZL7. Plant cell wall is a major barrier for the invasion of pathogenic bacteria and is composed of mainly cellulose, hemicellulose, and pectin polymers. To breach this barrier, D. zeae bacteria produce a full set of cellulases (Cels), pectinases (Pels), polygalacturonases (Pehs), and proteases (Prts), along with a glucuronoxylanase (XynA) and two rhamnogalacturonan lyases (Rhe1/2) (Table 3). Our previous study showed that JZL strains produced significantly smaller amounts of all four types of CWDEs compared to EC1 and MS2 when they were all cultivated at the same, relatively high cell density (optical density at 600 nm [OD600] = 1.8) (9).

In this study, we further compared the CWDE activities of strains JZL7 and MS2 at three different cell densities (i.e., OD600 of 0.5, 1.0, and 1.5) and observed a similar pattern that JZL7 produced a considerably smaller amount of CWDEs (Cels: 41.3%; Pehs: 50%; Pels: 34.6%; Prts: 57.2%) than MS2 at all densities (Fig. 9A). The lower CWDE
| Accession no. of: | NCBI accession no. | Product | Predicted *hrp* box (GGAACC-Nx-CCACNNA) |
|-----------------|-------------------|----------|--------------------------------------|
| C1O30_RS00560   | JZL000100         | Hypothetical protein VfmS                  | |
| C1O30_RS00675   | JZL000138         | Hypothetical protein                       | |
| C1O30_RS00680   | JZL000139         | Hypothetical protein                       | |
| C1O30_RS00895   | JZL000183         | Murein hydrolase activator EnvC            | |
| C1O30_RS01895   | JZL000383         | Type I-E CRISPR-associated protein Cse2/CasB | |
| C1O30_RS02135   | JZL000448         | Hypothetical protein                       | |
| C1O30_RS02140   | JZL000451         | Hypothetical protein                       | |
| C1O30_RS02185   | JZL000460         | Hypothetical protein                       | |
| C1O30_RS03200   | JZL000666         | Glycine dehydrogenase GcvP                 | |
| C1O30_RS03400   | JZL000710         | Hypothetical protein                       | |
| C1O30_RS04855   | JZL000906         | LOG family protein                         | |
| C1O30_RS05230   | JZL000962         | Hypothetical protein                       | |
| C1O30_RS08240   | JZL001538         | Alginate lyase family protein              | |
| C1O30_RS08785   | JZL001698         | Hypothetical protein                       | |
| C1O30_RS11185   | JZL002290         | DUF1852 domain-containing protein          | |
| C1O30_RS12170   | JZL002462         | Hypothetical protein                       | −241 GGAAC-NT69-CCACNNA −133 |
| C1O30_RS12625   | JZL002555         | Anhydro-N-acetylMuramic acid kinase AnmK   | |
| C1O30_RS13325   | JZL002697         | Flagellin FlIC                              | |
| C1O30_RS13330   | JZL002698         | Flagellar filament capping protein FlfD    | |
| C1O30_RS13375   | JZL002707         | Flagellar hook-length control protein Flk  | |
| C1O30_RS13415   | JZL002715         | Flagellar hook-filament junction protein FlgL | |
| C1O30_RS14125   | JZL002985         | Flagella biosynthesis regulator Flk        | |
| C1O30_RS14425   | JZL003042         | General secretion pathway protein GspB     | |
| C1O30_RS15345   | JZL003254         | Pectate lyase PeI                          | |
| C1O30_RS15350   | JZL003255         | Pectate lyase PeE                          | −590 GGAACA-N56-GCCACCA −522 |
| C1O30_RS15355   | JZL003256         | Pectate lyase PeID                         | |
| C1O30_RS16815   | JZL003523         | Hypothetical protein                       | |
| C1O30_RS18405   | JZL003848         | Hypothetical protein                       | |
| C1O30_RS19255   | JZL004042         | Hypothetical protein                       | |
| C1O30_RS19500   | JZL004096         | Hypothetical protein                       | +22 GGAACG-N37-TCACCA +71 |
| C1O30_RS19635   | JZL004123         | Uroporphyrinogen-III C-methyltransferase HemX | |
| C1O30_RS20330   | JZL004262         | Four-carbon acid sugar kinase family protein | |
| C1O30_RS20375   | JZL004272         | Cell envelope biogenesis protein ToIA      | |
| C1O30_RS20935   | JZL004396         | Der GTPase-activating protein Yihl          | |
| C1O30_RS00105   | JZL0020757        | Hypothetical protein                       | |
| C1O30_RS02465   | JZL0020962        | Hypothetical protein                       | |
| C1O30_RS02835   | JZL0021541        | Hypothetical protein                       | |
| C1O30_RS04030   | JZL0021114        | Hypothetical protein                       | |
| C1O30_RS04130   | JZL0021119        | Hypothetical protein                       | |
| C1O30_RS08565   | JZL0021570        | Hypothetical protein                       | |
| C1O30_RS08570   | JZL0021572        | Hypothetical protein                       | |
| C1O30_RS11100   | JZL0021796        | Type III secretion system effecter DspE    | −82 GGAACC-N15-CCACTCA −55 |
| C1O30_RS11105   | JZL0021797        | Type III effector protein HrpZ             | −110 GGAACC-N16-TCACTCA −82 |
| C1O30_RS11110   | JZL0021798        | Pectate lyase HrpW                         | −98 GGAAC-T15-GTACTCA −71 |
| C1O30_RS11125   | JZL0021801        | Type III effector protein HrpK             | −70 GGAAC-T15-CCACTCA −43 |
| C1O30_RS11560   | JZL0023957        | HrpN                                        | −125 GGAAC-T15-CCYCTCA −98 |
| C1O30_RS11660   | JZL0023962        | Type III secretion system gatekeeper HrpJ  | −73 GGAAC-N15-CCYCTCA −46 |
| C1O30_RS11685   | JZL0021846        | Type III secretion protein HrpP            | |
| C1O30_RS15015   | JZL0021841        | Hypothetical protein                       | |
| C1O30_RS16137   | JZL0021842        | Hypothetical protein                       | |
| C1O30_RS16140   | JZL0021843        | Hypothetical protein                       | |
| C1O30_RS16145   | JZL0021844        | Hypothetical protein                       | |
| C1O30_RS16160   | JZL0021845        | Hypothetical protein                       | |
| C1O30_RS16165   | JZL0021846        | Hypothetical protein                       | |
| C1O30_RS16196   | JZL0021847        | Hypothetical protein                       | |
| C1O30_RS16266   | JZL0021848        | Hypothetical protein                       | |
| C1O30_RS16271   | JZL0021849        | Hypothetical protein                       | |
| C1O30_RS16287   | JZL0021850        | Hypothetical protein                       | |
| C1O30_RS16284   | JZL0021851        | Hypothetical protein                       | |
FIG 8 The T3SEs regulated by the HrpL regulator. (A) qRT-PCR of the predicted T3SEs in the genome of MS2. The expression of the predicted T3SE encoding genes (listed in Table 2), including 34 genes shared in both MS2 and JZL7 genomes and 15 genes present uniquely in the MS2 genome, as well as the regulatory genes hrpX, hrpY, hrpS, and hrpL, were measured by qRT-PCR. Expression of the housekeeping gene atpD was used as a reference. The y axis indicates the values log2(fold change of ΔhrpL mutant relative to wild-type MS2). Red bar indicates expression levels higher in the mutant, while blue indicates those lower in the mutant. Red stars indicate the target genes whose promoters were verified to be interacted by HrpL protein in the panel (Continued on next page)
activities of JZL7 might be due to either a much smaller repertoire of CWDE encoding genes or a greatly reduced expression of the same set of genes. Our genome comparison revealed a highly conserved set of 34 CWDE genes shared by both JZL7 and MS2 (84.96% to 98.69% DNA sequence identity) and very few strain-specific genes, including two beta-glucosidase-encoding genes (bglC and bglD) in JZL7 and one pectin lyase-encoding gene (pnl) in MS2 (Table 3). Interestingly, recent studies showed that pnl was drastically upregulated during early disease development in Pectobacterium carotovorum but not so in D. dadantii (38). Here, in D. zeae, we found that neither the complementation of pnlMS2 in JZL7 nor the deletion of pnl in MS2 altered the virulence of respective strains on dicotyledonous tissues (i.e., potato and radish slices) (Fig. S2).

**FIG 8 Legend (Continued)**

below. (B) EMSA of the T3SEs with predicted hpr box. The promoter DNA fragments of the genes C1O30_RS12170, C1O30_RS16815, C1O30_RS19500, dspE, hprZ, hprK, and hprN and the known HrpL-regulated gene hrpA, which contain the predicted hpr box in Table 2, were amplified and labeled by biotin and then performed for EMSA with different concentrations of the expressed and purified HrpL protein. Fragments without hpr box (non GGAACC-Nx-CCACNNA motif) in the hprA and C1O30_RS12170 promoters, designated nmhrpA and nm12170, respectively, were amplified and used for EMSA reaction to confirm the importance of the presence of hpr box. For specific competition, a 100 nM unlabeled DNA fragment was incubated with 1 µg HrpL protein for 15 min before addition of a 25 nM labeled DNA fragments. (C) E. coli core RNAP (0.5 U) was incubated on ice for 20 min with 0.2 or 0.4 µg of purified HrpL protein. The remaining steps were as described above.

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### TABLE 3 Genes encoding the CWDEs in genomes of Dickeya zeae

| Gene   | Accession no. of: | EC1       | Ech586    | MS2       | JZL7       | Identity between MS2 and JZL7 |
|--------|------------------|-----------|-----------|-----------|-----------|-------------------------------|
| celZ   | W909_12595       | DdS86_1489| C1O30_RS13580| JZL002780| 96.94     |
| celY   | W909_19635       | DdS86_4057| C1O30_RS20545| JZL004313| 97.07     |
| bgxA   | W909_01965       | DdS86_0376| C1O30_RS502015| JZL000410| 97.56     |
| bgxB   | W909_07850       | DdS86_2493| C1O30_RS508765| JZL001697| 95.72     |
| bgLB   | W909_11710       | DdS86_1660| C1O30_RS512705| JZL002602| 95.14     |
| nagZ   | W909_12020       | DdS86_1600| C1O30_RS513010| JZL002663| 94.38     |
| bgLC   | W909_16350       | DdS86_5611| JZL003612 |
| bgLD   | W909_16355       | DdS86_5612| JZL003612 |
| celH   | W909_16359       | DdS86_3407| C1O30_RS17155| JZL003621| 97.89     |
| lfaA   | W909_11990       | DdS86_1606| C1O30_RS12980| JZL002657| 95.71     |
| pni    | W909_02890       | C1O30_RS502835|         |
| pelN   | W909_08805       | DdS86_2245| C1O30_RS509885| JZL001947| 97.72     |
| pelL   | W909_12600       | DdS86_1488| C1O30_RS513585| JZL002781| 96.36     |
| pelI   | W909_14095       | DdS86_2937| C1O30_RS514580| JZL003127| 84.96     |
| pelA   | W909_14860       | DdS86_3083| C1O30_RS515345| JZL003289| 96.11     |
| pelE   | W909_14870       | DdS86_3084| C1O30_RS515350| JZL003291| 96.50     |
| pelD   | W909_14875       | DdS86_3085| C1O30_RS515355| JZL003292| 97.84     |
| pelC   | W909_18430       | DdS86_3788| C1O30_RS519205| JZL004051| 96.63     |
| pelB   | W909_18435       | DdS86_3789| C1O30_RS519210| JZL004052| 97.61     |
| pelZ   | W909_18440       | DdS86_3790| C1O30_RS519215| JZL004053| 92.89     |
| pelW   | W909_10230       | DdS86_1962| C1O30_RS511330| JZL002317| 98.16     |
| pelX   | W909_20195       | DdS86_4161| C1O30_RS521105| JZL004439| 97.03     |
| paeX   | W909_10260       | DdS86_1956| C1O30_RS511360| JZL002324| 95.61     |
| paeY   | W909_14880       | DdS86_3086| C1O30_RS515360| JZL003293| 91.08     |
| pemA   | W909_14885       | DdS86_3087| C1O30_RS515365| JZL003294| 97.07     |
| pelN   | W909_15935       | DdS86_3319| C1O30_RS516710| JZL003524| 96.93     |
| pelK   | W909_19025       | DdS86_3904| C1O30_RS519785| JZL004171| 96.91     |
| rhiE1  | C1O30_RS04480     | C1O30_RS504839| JZL000839| 98.00     |
| rhiE2  | W909_09610       | DdS86_2097| C1O30_RS510600| JZL002175| 97.29     |
| synA   | W909_10005       | DdS86_2011| C1O30_RS510505| JZL002266| 94.12     |
| prtX   | W909_09760       | DdS86_2059| C1O30_RS510785| JZL002216| 95.49     |
| prtC   | W909_09765       | DdS86_2058| C1O30_RS510790| JZL002217| 97.71     |
| prtB   | W909_09770       | DdS86_2057| C1O30_RS510795| JZL002218| 96.53     |
| prtG   | W909_09795       | DdS86_2052| C1O30_RS510820| JZL002223| 96.30     |
| prtF   | W909_09775       | DdS86_2056| C1O30_RS510800| JZL002219| 97.51     |
| prtE   | W909_09780       | DdS86_2055| C1O30_RS510805| JZL002220| 97.09     |
| prtD   | W909_09785       | DdS86_2054| C1O30_RS510810| JZL002221| 96.89     |
We then measured the expression of the shared CWDE genes in the two strains using semiquantitative PCR. Results showed that the ratios (JZL7 versus MS2) of cumulative expression levels of genes encoding Cels, Pehs, RhiEs, XynA, Pels, and Prts are 0.56 (430.579:774.477), 0.22 (26.663:119.403), 0.21 (1.714:8.168), 0.47 (13.404:28.810), 0.62 (632.929:1,023.790), and 0.11 (143.640:1,346.054), respectively. In addition, *Dickeya* exports Prts via T1SS encoded by the *prtD*, *prtE*, and *prtF* genes after recognizing a C-terminal signal sequence in their substrates (18, 39, 40). The expression level of T1SS genes in strain JZL7 is 0.66 of those in strain MS2 (Fig. 9B). Furthermore, 15 of the 34 shared CWDE genes had significantly lower expression levels in JZL7 than in MS2, including *lfaA*, *celH*, *celY*, *celZ*, *pehK*, *pehX*, *rhiE1*, *xynA*, *pelD*, *pelL*, *pelN*, *pelX*, *pemA*, *prtX*, and *prtC* (Fig. 9B).

The broadly reduced expression of CWDE genes observed here was consistent with the aforementioned lower CWDE activities in JZL7 and may provide a basis for the strain’s lack of virulence on dicots. Specifically, monocots and dicots differ in the composition and structure of their primary cell walls; the former contain mainly cellulose and rarely pectin, while the latter consist of both (41). In this study, we showed that several pectin lyase-encoding genes were either lost (e.g., *pnl*) or expressed at remarkably lower levels (e.g., *pelD*, *pelL*, *pelN*, *pelX*, and *pemA*) in JZL7 (Fig. 9B). The resulting reduction in Pel activity might considerably compromise the ability of JZL7 to degrade cell wall and invade dicot hosts, which, together with the loss of T3SS, might abolish the pathogenicity of JZL7 on dicots. To verify whether the significantly lower expression of CWDEs is due to the lower expression of some important regulators controlling...
CWDE activity, we measured the expression of the genes encoding CWDE regulators, such as Fis, SlyA, VfmE, PecS, PecT, and KdgR, in both MS2 and JZL7 by RT-PCR. Results showed that none of these genes was differentially expressed between MS2 and JZL7 (Fig. S3).

Other 13 genes were newly found to encode pathogenicity-related proteins in *D. zeae* MS2. In order to identify additional factors related to the virulence of *D. zeae* pathogens on dicots, we obtained knockout mutants in MS2 for most of the genes absent in JZL7 but shared by MS2 and EC1 (apart from the T3SS and T3SE genes, which have already been examined above; Table S8). Pathogenicity tests showed that deletion of C1O30_RS01370-01390, C1O30_RS02130, C1O30_RS02370, C1O30_RS02510, C1O30_RS03460, C1O30_RS04230, C1O30_RS04475, C1O30_RS05105, C1O30_RS06880, C1O30_RS07840, C1O30_RS08725, C1O30_RS12525, and C1O30_RS14540 significantly reduced the virulence of MS2 on potato slices (Fig. 10). Among them, C1O30_RS01370-1390, C1O30_RS02510, C1O30_RS03460, C1O30_RS04230, C1O30_RS04475, C1O30_RS05105, C1O30_RS06880, C1O30_RS07840, C1O30_RS08725, C1O30_RS12525, and C1O30_RS14540, respectively, carry a dimethyl sulfoxide reductase anchor subunit gene cluster (*dmsC, dmsB, dmsA, dmsD*), and a SDR family oxidoreductase) and encode a GNAT family N-acyltransferase, LysE family transporter, a PAS domain-containing protein (helix-turn-helix transcriptional regulator), an SDR family oxidoreductase, an HAMP domain-containing protein, an FMN-binding negative transcriptional regulator, a glycosyltransferase, DUF2335 domain-containing protein, and a diguanylate cyclase, while all the others encode hypothetical proteins (Table S8). All these genes were first reported to be involved in *Dickeya* pathogenesis and, thus, represent prominent targets of future studies.

Recently, an *saxA* gene encoding isothiocyanate hydrolase was found to enable a potato-specific *Pectobacterium parmentieri* strain to increase the ability to macerate *Arabidopsis*, suggesting its significant role in defining the host range (42). We searched the homologs of this interesting gene in the genomes of *D. zeae* and found 4 and 6 copies of *saxA*, respectively, present in the genomes of MS2 and JZL7. Thus, we ruled out the possibility of SaxA as a host range determinant.

**Pathogenic mechanism of *Dickeya* and other soft rot *Pectobacteriaceae*.** In this study, we sequenced the genome of *D. zeae* JZL7 and carried out in-depth comparative and functional analyses with other *D. zeae* strains. The results not only provide insights into the unique pathogenicity and host specificity of JZL7 but also help to better understand the pathogenic mechanism of soft rot *Pectobacteriaceae* pathogens (e.g., *Dickeya, Erwinia*, and *Pectobacterium*) in general.

*Xanthomonas, Ps. syringae*, and many other bacterial phytopathogens adopt the “stealth” model of pathogenicity whereby they make use of an extensive battery of type III secreted effector proteins and phytopoxins for successful infection. These effectors act to suppress or manipulate host defenses as the bacterial population grows to numbers that are sufficient to induce disease symptoms (43–47). Additionally, many studies have demonstrated that T3SEs could alter the physiology of host cells in a way...
that is beneficial for the pathogens. In Xanthomonas, a mutation in the T3SS impairs the ability to inject T3SEs in the host plant and, as a consequence, abolishes pathogenicity and multiplication in planta (48). Among pathogenicity determinants shown to display heterogeneous distribution between strains are T3SEs. Furthermore, in Xanthomonas and Ps. syringae, diversity in T3SE repertoires from different hosts revealed determinants of host specificity (45, 49, 50).

Soft rot Pectobacteriaceae pathogens also possess in their genomes the molecular machineries required for the stealth mode of infection, such as T3SS, T4SS, phytotoxins, and so on. Functional studies have also demonstrated the importance of T3SS in soft rot Pectobacteriaceae (SRP) pathogens. For instance, T3SS is important for the full virulence of D. dadantii 3937 (25, 26) and required for pellicle formation and cell aggregation (51, 52). However, T3SS or T3SE has not been reported in SRP as a determinant of host range, and the role of T3SS in the virulence of necrotrophic SRP and other bacterial pathogens appears quite complex.

In our study, we knocked out the whole T3SS gene clusters dsp/hrp/hrc in D. zeae MS2, which resulted in significantly reduced virulence on both monocotyledonous and dicotyledonous hosts (Fig. 7), demonstrating its role as an important virulence factor in the course of disease. However, Δdsp/hrp/hrc was not virulence free on either monocots or dicots, suggesting that T3SS alone does not determine host range in D. zeae. In addition, Er. pyrifoliae, Pe. carotovorum, Pectobacterium wasabiae, and Ps. syringae strains lacking a functional T3SS have been reported to infect plants (22, 23, 53, 54). In Ps. syringae, nonpathogenic isolates are separate from the pathogenic ones due to the deficiency of T3SS and T3SEs (23). In contrast, T3SS-deficient Pe. wasabiae strains are still virulent (53). More strikingly, human-pathogenic Ps. aeruginosa isolates from patients with chronic lung infections are typically T3SS deficient, even though 90% of environmental isolates carry a T3SS (55). These T3SS-deficient pathogens may have alternative ways of modifying the host plant at the initiation of infection.

It has often been assumed that the mechanisms of infection used by SRP are distinctly different from those used by other bacteria like Xanthomonas and Ps. syringae (56). In addition to the above-mentioned stealth model, SRP pathogens also share a “brute-force” model of pathogenicity; they produce many CWDEs to physically attack the plant cell walls and their surrounding apoplast, which thus promotes soft rotting (45, 57). It is unquestionable that brute force has made the SRP highly successful pathogens, and the CWDEs are critical factors in both the pathogenicity and host range of SRP. We compared the concentrated enzymatic activities of soft rot D. zeae MS2 and JZL7 and found that broadly reduced expression of CWDE genes might be a major cause for the significantly lower virulence of JZL7 on dicots (Fig. 9). Importantly, the brute-force and stealth models seem to operate in parallel in SRP pathogens, as the production of CWDEs remained unaffected in the T3SS mutants of MS2 (Fig. S4), which might explain their remaining soft rot symptoms on potato and radish slices (Fig. 7C and D).

Bacterial phytopathogens employ various approaches to infect and kill their host(s). Plant-pathogen interaction is a multifaceted process, mediated by the pathogen- and plant-derived molecules. Secreted as well as translocated molecules, derived from the pathogens, are the key factors, which determine their pathogenicity and allow successful colonization of pathogens on the host. On the other hand, plant-derived molecules are involved in the recognition of pathogen and triggering of the defense response. In the future, to learn more about the latent stage of Dickeya infection and host range, we should consider factors including both CWDEs and T3SEs.

MATERIALS AND METHODS

Bacterial strains and growth conditions. The bacterial strains and plasmids used in this study are listed in Table S1. Escherichia coli strains were grown at 37°C in Luria-Bertani (LB) medium. D. zeae and its derivatives strains were cultivated at 28°C in LB medium, minimal medium (MM), or LS5 medium (58, 59). Antibiotics were added to the media at the following final concentrations when required: streptomycin 50 μg/mL, kanamycin 50 μg/mL, tetracycline 15 μg/mL, and ampicillin 100 μg/mL.
Genome sequencing and assembly. Genomic DNA was extracted from D. z ease strain JZL7 in LB medium: culture using MasterPure DNA purification kit (Epicentre, Madison), which was then subjected to quality control by agarose gel electrophoresis and quantified by Qubit. The genome sequencing was performed at Health Time Gene (Shenzhen, China) using both the PacBio RS II and the Illumina Hiseq X Ten platforms.

For the PacBio sequencing, genomic DNA was treated into fragments in 10 kb by g-TUBE first. The fragments were damage-repaired and end-repaired. Both sides of the DNA fragments were, respectively, connected with hairpin adapter to get a dumbbell structure, which is known as SMRTbell. After annealing, the SMRTbell was fixed at the bottom of the ZMW polymerase and was sequenced last. Adapter trimming and quality filtering were performed by using fastp (version 0.20.0) (60) with default parameters.

For the Illumina sequencing, genomic DNA was randomly broken, and 350 bp fragments were purified and end-repaired using T4 DNA polymerase, Klenow DNA polymerase, and T4 PNK. The fragments were added with an “A” base at the 3’ terminal and ligated with the adaptor with a “T” base at its terminal. The library was sequenced on the Hiseq X Ten platform to generate PE150 reads. A hybrid genome assembly with both the PacBio long-reads and Illumina short-reads was carried out using Unicycler v0.4.7 (default parameters) (61).

Genome annotation. The genome annotation of JZL7 was carried out using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v2019-11-25 (standalone version) (62). Functional annotations of all proteins predicted in JZL7 were conducted using eggNOG-mapper v1.0.3 (for GO) (63), KofamKOALA v2020-08-04 (for KEGG) (64), and COGsoft v201204 (for COG) (65). The genome and annotated protein sequences of other Dickeya strains analyzed in this study were all obtained from the NCBI RefSeq and GenBank databases (Table S2). Genomic islands and prophages were predicted using the webserver of IslandViewer 4 (http://www.pathogenomics.sfu.ca/islandviewer/) (66) and PHASTER (http://phaster.ca/) (67), respectively. Genes encoding type I to VI secretion system-related proteins were identified using TXSScan v1.0.2 (68). Type III secreted effectors (T3SEs) were predicted by using a combination of four bioinformatics approaches, including the webserver of Bastion3 (https://bastion3.erc.monash.edu/) (69) and standalone versions of BEAN2 v2.0 (70), DeepT3 (71), and pEffect (72); a protein is classified as T3SE only if it is predicted by at least three of the four approaches. The circular visualization of JZL7 genome characteristics was created by Circos (73). Prediction of hrp box was performed by searching the promoter sequences (2,000 bp upstream the start codon) of the candidate T3SE-coding genes in MS2 genome using the following regular expressions: GGAAC[CT]ATCG[1,100][CTG][CTA][CATG][CT]A (forward) and T[AG][ATC][AG][AGCT]{1,100}[AG]GTTCC (reverse).

Comparative genomic analyses. Pairwise average nucleotide identity (ANI) values between all D. z ease and D. oryzae strains were calculated using pyani v0.2.10 (with the “-m Anlib” option) (74). The whole-genome alignment of CE1, EC1, EC2, EchS86, JZL7, and MS2 was constructed using Mauve v2.4.0 (75). The pangenome analysis of CE1, JZL7, and MS2 was carried out using OrthoFinder v2.4.0 (76). To build the phylogenetic tree, we generated multiple DNA sequence alignment for each of the 3,110 single-copy core genes (present in all strains) using Mafft v7.453 (77). All single-gene alignments were then concatenated, and a phylogenetic inference was conducted using IQ-TREE v1.6.12 (78). Reliability of the inferred topology was assessed by ultrastar bootstrap with 1,000 replicates.

Generation of in-frame deletion mutants. For generation of in-frame deletion mutants of D. z ease MS2, triparental mating was performed using the methods described previously (15). For instance, to knock out the hrp/hrc gene cluster of T3SS in strain MS2, the upstream and downstream fragments of hrp/hrc gene cluster were amplified using the primer pairs of hrp/hrc-1 accompanied with hrc-hrc-2, and hrc-hrc-3 accompanied with hrp/hrc-4, respectively (Table S3), and purified with AxyPrep DNA gel extraction kit (Axygen Biotech Co., Hangzhou, China). The fragments were ligated with the BarnHI and Spe digested suicide plasmid pkNG101 using ClonExpress MultiS kit (Vazyme Biotech Co., Nanjing, China) and transformed into E. coli CC118 competent cells. In triparental mating, the donor and receptor cells were mixed with the helper strain E. coli RK2013 (grown in LB medium containing kanamycin) in a ratio of 2:1:1 on LB plate and incubated at 28°C overnight. The transformants were grown on minimal medium (MM) agar plates (13) containing streptomycin sulfate. Single colony culture was then spread on MM agar plate containing 5% sucrose to exclude the suicide plasmid. The resultant deletion mutants were confirmed by PCR using the detection primer pair of hrp/hrc-F and hrp/hrc-R and DNA sequencing. In the same way, we correspondingly deleted the important T3SS transcriptional regulation genes hpx, hpy, hps, and hpl, and the candidate T3SE genes dspE, hpx2, hpxW, hpxK, and hpxN, the pectin lyase-encoding gene pni, and, compared to JZL7, some genes specific to MS2. In addition, the Δdsp/hrp/hrc mutant was also generated by deleting the dsp gene cluster based on the obtained Δhrp/hrc mutant. The primers are listed in Table S3.

Measurement of bacterial growth curves. Bacterial strains were grown in LB medium overnight at 28°C, adjusted to an OD600 of 1.5, and diluted into fresh LB and LS5 medium in a 1:100 ratio, respectively (9). Aliquots of 500-μL dilutions were transferred into 2.0-ml tubes. Bacteria were grown with shaking at 200 rpm under 28°C, and cell density was measured every 2 h. The experiment was repeated three times in triplicate.

HR assay. Bacteria were grown in LS5 medium (pH 5.5) (59) until they reached an OD600 of 1.0. Leaves of Nicotiana tabacum variant K326 (27) and N. benthamiana (28) were, respectively, inoculated on the back by pressing a sterilized puncher (5 mm) dipped with bacterial culture and incubated at 28°C. The area of HR lesions on leaves was measured using Image J 1.52a 12 and 24 h postinoculation (hpi) (79). To quantify the function of the T3SS, we infiltrated leaves of N. tabacum K326 with 100 μL of MS2 bacterial dilutions in LS5 medium (OD600 of 0.5, containing approximately 106 CFU/mL), and 100 μL
each of LSS medium, Δhp/hrp/hrc, and JZL7 (10⁷ CFU/mL) was also infiltrated as a negative control. Each assay was repeated three times in triplicate.

Pathogenicity tests on monocotyledonous and dicotyledonous plants. Strains were cultured to the logarithmic phase until an OD₆₀₀ of 1.2 was reached in LB medium, and pathogenicity tests were carried out on monocotyledonous and dicotyledonous hosts. For monocots, every 100 μL of bacterial culture was injected into the basal stem of banana and the base of clivia leaf. For dicotyledonous plants, potato and radish tubers were surface-sterilized with 70% ethanol, cut evenly about 5 mm in thickness, and then placed onto moistened filter paper in a tray. Bacterial cells of 2 μL were applied to the center of the tuber slices. All plants were kept in a growth chamber with controlled conditions of 28 ± 2°C, 75% ± 15% relative humidity, and 24 h white light (7,350 lx) illumination until symptoms appeared, except that the bananas were incubated at 30°C with 12-h alternating light-dark cycles for 7 days and then disease was assessed using a modified virulence scoring (17, 80). Same volume of LB medium was inoculated as a negative control. Visible macerate areas on clivia leaves and potato and radish slices were measured using Image J 1.52a. Each assay was repeated three times in triplicate.

RNA purification. The bacterial cultures used for RNA extraction were the ones described below for CWDE activity measurement. Since the same strain shared basically the same enzymatic activity in different cell densities (OD₆₀₀ of 0.5, 1.0, and 1.5), the bacterial cultures of strains MS2 and JZL7 at an OD₆₀₀ of 1.5 were selected for RNA extraction. On the other hand, to determine whether the predicted T3SE expression is induced by the HrpL regulator, we grew strains MS2 and ΔhrpL in LSS medium (pH 5.5) (59) for RNA extraction until an OD₆₀₀ of 1.0 was reached. The RNA was extracted using the SV total RNA isolated system kit (Promega, Madison, WI, USA), further purified using the RNA clean kit (Qiagen, Hilden, Germany), and treated with DNase I to degrade any possible DNA contamination. Quantity of RNA was first measured using a NanoDrop 2000c (Thermo Fisher Scientific, MA, USA), and the integrity of RNA was detected by agarose gel electrophoresis.

RT-PCR analysis. For each RNA sample for CWDE activity measurement, two dilutions (5 and 50 ng) were reverse transcribed into cDNAs using FastKing gDNA dispensing RT mix (Tiangen Biotech, Co., Ltd., Beijing, China), and the concentration of each resultant cDNA was quantitatively equilibrated according to the expression quantities of reference gene inB of strains MS2 and JZL7. PCR was performed using the primers listed in Table S3, and gene expression (signal intensity) of each gene was determined using the software Image Lab (Bio-Rad, USA). The experiment was repeated three times in triplicate.

RNA isolation and purification. The open reading frame (ORF) that encodes HrpL protein was amplified from MS2 genomic DNA using primers pET32a-hrpL-F and pET32a-hrpL-R containing BarHI and HindIII restriction enzyme sites (Table S3). The PCR product was purified and ligated to the BamHI/HindIII-digested pET32a vector harboring a thioredoxin (TRX)-His6 tag at its N terminus. pET32a-hrpL was then transformed into the E. coli strain BL21(DE3) competent cells (TransGen Biotech Co., Beijing, China) and confirmed by sequencing. To express the HrpL protein, a single colony of BL21(pET32a-hrpL-L) was grown in LB medium containing 100 μg/μL of ampicillin overnight and transferred into 1 L of fresh LB medium in a 1:100 ratio to grow until reaching an OD₆₀₀ of 0.6. Then, 1 mM IPTG (isopropyl β-D-thiogalactopyranoside) was added to the culture to induce protein expression at 18°C for 16 h. Bacterial cells were harvested by centrifuging at 5,000 rpm at 4°C for 30 min and suspended in 20 mL of phosphate-buffered saline (PBS). The cells were lysed with sonication and centrifuged at 12,000 rpm at 4°C for 30 min. The supernatant was treated with DNase I to degrade any possible DNA contamination. Quantity of RNA was detected by agarose gel electrophoresis.

Electrophoretic mobility shift assay. Electrophoretic mobility shift assay (EMSA) was performed as described previously (58). DNA probes were prepared by PCR amplification using primers listed in Table S3. The purified PCR fragments were labeled with [γ-³²P]ATP using T4 polynucleotide kinase (New England Biolabs, Beverly, MA, USA) following the manufacturer's protocol. The labeled DNA fragments were separated by 6% non-denaturing polyacrylamide gel electrophoresis (SDS-PAGE) and visualized by autoradiography. The molecular weight of the target protein was determined by SDS-PAGE. The gel was stained with Coomassie brilliant blue R-250 and destained with water.

Protein expression and purification. The HrpL protein was expressed in E. coli strain BL21 with the pET32a system (Novagen, Madison, WI, USA). The plasmid pET32a-hrpL-L was transformed into E. coli strain BL21(DE3) (Novagen, Madison, WI, USA) and cultivated at 37°C in LSS medium containing 100 μg/mL of ampicillin. The bacterial cells were harvested by centrifugation at 5,000 rpm at 4°C for 30 min and suspended in 20 mL of phosphate-buffered saline (PBS). The cells were lysed with sonication and centrifuged at 12,000 rpm at 4°C for 30 min. The supernatant was treated with DNase I to degrade any possible DNA contamination. Quantity of RNA was detected by agarose gel electrophoresis.

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Beijing, China) (82) was incubated on ice for 20 min with 200 or 400 ng of purified HrpL protein (34). The remaining steps were as described above.

Measurement of CWDE activities. The activities of CWDEs were measured according to the methods described previously (9). Specifically, pectate lyase (Pel) assay medium (10 g/L polygalacturonic acid, 10 g/L yeast extract, 8 g/L agarose, 0.38 μM CaCl₂, and 100 mM Tris-Cl) (pH 8.5)), polygalacturonase (Peh) assay medium (5 g/L polygalacturonic acid, 2 g/L sucrose, 2 g/L (NH₄)₂SO₄, and 15 g/L agar (pH 5.5)), cellulase (Cel) assay medium (1.0 g/L carboxymethyl ethyl cellulose, 3.8 g/L Na₃PO₄, and 8.0 g/L agarose (pH 7.0)), and protease (Prt) assay medium (10 g/L skimmed milk, 5 g/L Bacto tryptone, 2.5 g/L yeast extract, 5 g/L NaCl, and 15 g/L agar) were prepared, and 30 mL of each medium was added into a 10 by 10 cm square plate. Wells in 5 mm diameter were made, and 20 μL of bacterial cells (OD₆₀₀ of 0.5, 1.0, or 1.5) was applied to the wells. Plates were incubated at 28°C until Pel and Peh assay plates were treated with 1 M HCl after 14 h, and Cel assay plate was stained with 0.1% Congo red for 15 min after 14 h and decolored with 1 M NaCl twice. The protease activity was measured without any further treatment after 24 h. The experiment was repeated three times with duplicates.

Introduction of pnt gene in strain JZL7. To create the complementing plasmid, sequence of pnt open reading frame (ORF) with 19 bp before the start codon harboring a ribosome-binding site (RBS) was amplified and cloned from strain MS2 into the EcoRI/BamHI-digested pLAFR3 vector using pEASY-Uni seamless cloning and assembly kit (TransGen Biotech Co., Beijing, China) and transformed into E. coli DH5α competent cells. Plasmid construct was confirmed by DNA sequencing and introduced into strain JZL7 by conjugal triparental mating. The primers used here are listed in Table S3.

Statistical analysis. All the experiments were repeated three times in duplicate or triplicate. GraphPad Prism 8.4.1 (GraphPad Software, San Diego, California) was used to performed unpaired two-tailed t test (83), and the data of D. zeae strain JZL7 were normalized to those of strain MS2. * indicates P < 0.05, ** indicates P < 0.01, *** indicates P < 0.001, and **** indicates P < 0.0001. Analysis of variance (ANOVA) was used between D. zeae MS2 and its mutants. The values are means of three replicates, and the error bars are standard deviations. Statistical analysis was performed on each group of data, and significantly different values (ANOVA P < 0.05) are indicated by different letters.

To investigate association between the frequency of fold change (>0.5≤0.5) and that of unique/shared T3SEs of MS2, the Pearson χ² statistic was computed (Pearson’s chi-square test, χ² = 8.77, degrees of freedom (df) = 4, χ² = 7.88, χ² = 10.83, and χ² < χ² < χ² = 0.0005. P value was less than 0.005.

Data availability. Both the original genome sequencing data and the genome assembly were deposited in the NCBI Sequence Read Archive (SRA) database under the accession number PRJNA656647. The JZL7 genome sequence has been deposited in GenBank under accession number CP060263.1.

SUPPLEMENTAL MATERIAL

Supplemental material is available online only.

SUPPLEMENTAL FILE 1, PDF file, 1.5 MB.

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J.Z. conceived the study, J.Z. and M.H. drafted the manuscript, M.H., Y.X., and M.L. performed the experiments, X.Z., C.L., and M.H. analyzed the genome sequences and experimental data, J.Z., X.Z., L.Z., G.L., and M.R.P. revised the manuscript. All authors read and approved the final manuscript.

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