

Genome sequence of the enterobacterial phytopathogen *Erwinia carotovora* subsp. *atroseptica* and characterization of virulence factors

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The bacterial family Enterobacteriaceae is notable for its well studied human pathogens, including *Salmonella*, *Yersinia*, *Shigella*, and *Escherichia* spp. However, it also contains several plant pathogens. We report the genome sequence of a plant pathogenic enterobacterium, *Erwinia carotovora* subsp. *atroseptica* (*Eca*) strain SCRI1043, the causative agent of soft rot and blackleg potato diseases. Approximately 33% of *Eca* genes are not shared with sequenced enterobacterial human pathogens, including some predicted to facilitate unexpected metabolic traits, such as nitrogen fixation and opine catabolism. This proportion of genes also contains an overrepresentation of pathogenicity determinants, including possible horizontally acquired gene clusters for putative type IV secretion and polyketide phytotoxin synthesis. To investigate whether these gene clusters play a role in the disease process, an arrayed set of insertional mutants was generated, and mutations were identified. Plant bioassays showed that these mutants were significantly reduced in virulence, demonstrating both the presence of novel pathogenicity determinants in *Eca*, and the impact of functional genomics in expanding our understanding of phytopathogenicity in the Enterobacteriaceae.

The bacterial family Enterobacteriaceae includes many well studied human pathogens within genera such as *Salmonella*, *Yersinia*, and *Shigella*, as well as the model commensal and pathogenic species *Escherichia coli*, and the insect pathogen *Photobacterium luminescens*. More genome sequences have been determined from this family than from any other (1–6). However, the Enterobacteriaceae also include several significant plant pathogens, and here we present the complete genome sequence of such a pathogen, *Erwinia carotovora* subsp. *atroseptica* (*Eca*).

Eca, also named *Pectobacterium carotovorum* subsp. *atrosepticum* (7), and recently, *Pectobacterium atrosepticum* (8), is a commercially important pathogen restricted to potato in temperate regions, where it causes blackleg in the field and soft rot of tubers after harvest. In contrast, the related soft rot bacteria *Erwinia carotovora* subsp. *carotovora* (*Ecc*) and *Erwinia chrysanthemi* (*Ech*) have broader host ranges, including potato, and cause disease in warmer climates (9). The soft rot erwiniae also live as epiphytes and endophytes on plants or saprophytes in soil and ground water (9, 10), although little is known about these nonpathogenic lifestyles. Moreover, the molecular bases of differences in host range and the requirements for establishing disease are largely unknown. Although soft rot pathogenesis relies primarily on the prolific production of extracellular plant cell wall-degrading enzymes (PCWDEs) that cause extensive tissue maceration (9, 11), discoveries in recent years suggest the process may be far more subtle and complex than previously thought (12).

Genome sequencing of the phytopathogens *Pseudomonas syringae* pv. *tomato* (13), *Ralstonia solanacearum* (14), *Xanthomonas campestris* pv. *campestris* and *Xanthomonas axonopodis* pv. *citri* (15), *Xylella fastidiosa* (16, 17), and *Agrobacterium tumefaciens* (18, 19), has yielded a wealth of information on novel and shared candidate phytopathogenicity determinants. Here, we describe the complete genome sequence of *Eca* strain SCRI1043 (*Eca*1043) and assess its similarity to other members of the Enterobacteriaceae and to other plant pathogenic bacteria. We describe a wide array of genes previously unknown in *Eca* and, in some cases, in the Enterobacteriaceae, which are potentially involved in pathogenicity and metabolism. In a functional genomic investigation, we provide evidence that genes in two identified clusters have a role in disease development.

Materials and Methods

Genome Sequencing and Annotation. The strain *Eca* SCRI1043 (American Type Culture Collection catalog no. BAA-672) was isolated from a potato stem with blackleg disease symptoms in 1985 in Perthshire, Scotland (the sample used to provide DNA for sequencing was frozen shortly after isolation). This strain has been used in epidemiological and molecular studies for many years and is amenable to genetic manipulation (20, 21). The initial shotgun was generated from 54,600 paired-end sequences from two libraries in pUC18 with insert sizes of 2.2–2.5 and 2.5–4.0 kb, and 25,800 paired-end reads from a 4.5- to 5.5-kb insert library in pMAQ1b by using dye terminator chemistry on ABI3700 automated sequencers, giving 8.2-fold coverage. Paired-end sequences from 500 clones from a 12- to 23-kb library in pBACe3.6 were used to generate a scaffold with 1.8-fold clone coverage. All identified repeats were bridged by using read pairs or end-sequenced PCR products.

The initial shotgun sequences were assembled by using PHRAP (www.phrap.org), and gap closure and finishing used GAP4 (http://staden.sourceforge.net) in combination with directed sequencing (primer walks and subcloning and shotgun sequencing of bacterial artificial chromosome clones or PCR products that spanned sequence gaps). The final sequence was composed of 106,500 reads, giving an average 10.2-fold coverage. The

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Abbreviations: *Eca*, *Erwinia carotovora* subsp. *atroseptica*; *Ecc*, *Erwinia carotovora* subsp. *carotovora*; *Ech*, *Erwinia chrysanthemi*; CDS, coding sequence; HAI, horizontally acquired genomic island; RBH, reciprocal best hit; PCWDE, plant cell wall-degrading enzyme; T3SS, type III secretion system; T4SS, type IV secretion system; LSD, least significant difference.

Data deposition: The sequence reported in this paper has been deposited in the EMBL/GenBank database (accession no. BX950851).

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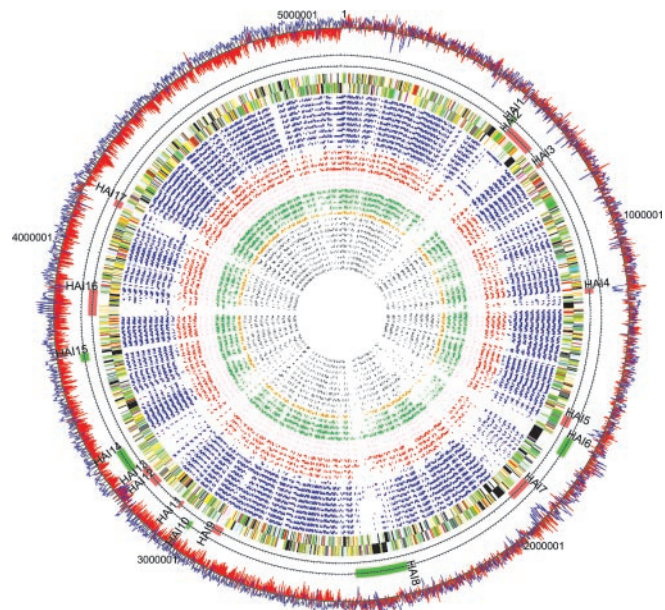


Fig. 1. Comparison of the *Eca* genome sequence with other bacterial genomes. Inner to outer tracks show the locations of RBHs found by reciprocal FASTA of *Eca* CDSs against those from 32 bacterial genomes (circular plot): Gram-positive (gray); *Shewanella oneidensis* (ochre); nonenteric animal pathogens (green); plant-associated bacteria (brown); nonenteric plant pathogens (red); and enterobacteria (blue) (Table 2). The locations of CDSs on the *Eca* genome colored by functional class (see legend to Fig. 5). Two tracks indicating HAIs listed in Table 1. Shown are islands with evidence of recent acquisition (red bars) and possible islands based on reciprocal FASTA analysis (green bars). A plot of G+C skew (red) and percent G+C content (blue).

finished sequence was compared with DNA sequences in public databases by using FASTA, BLASTX, and BLASTN (22). Potential coding sequences (CDSs) were predicted by a combination of ORPHEUS (23) and GLIMMER (24) and manual curation, and were searched for PFAM (25) domains, and compared with the protein databases by using BLASTP. ARTEMIS (26) was used to collate data and facilitate annotation. Stable noncoding RNAs were identified by comparison with the RFAM database (27). Metabolic pathways were examined by using the KEGG database (www.genome.ad.jp/kegg).

Comparative Genomics. Each CDS from the *Eca*1043 genome was used as the query in a FASTA protein search against the complete set of CDSs from each of 64 fully annotated genomes obtained from the National Center for Biotechnology Information web site (ftp.ncbi.nih.gov/genomes/Bacteria; Fig. 1, and Table 2, which is published as supporting information on the PNAS web site). Where the resulting top hit (ranked by score; hits with equivalent scores treated equally) was aligned with the query over at least 80% of its length to >30% identity, it was used as the query in a search against the *Eca* genome. Where the original CDS from *Eca*1043 was found to be the top match to this second query, the pair of sequences was termed a reciprocal best hit (RBH). For each genome, results for chromosomal and extra-chromosomal sequences were obtained independently, and were then concatenated for further analyses. The number of CDSs in each of four groups as follows: (i) *Eca* only, (ii) shared with nonenterobacteria only, (iii) shared only with other enterobacteria, and (iv) shared with enterobacteria and nonenterobacteria, was counted for each functional class (C_{func} ; see EMBL/GenBank accession no. BX950851 for feature class qualifiers) and for all CDSs, normalized to each functional class (C_{all}). The

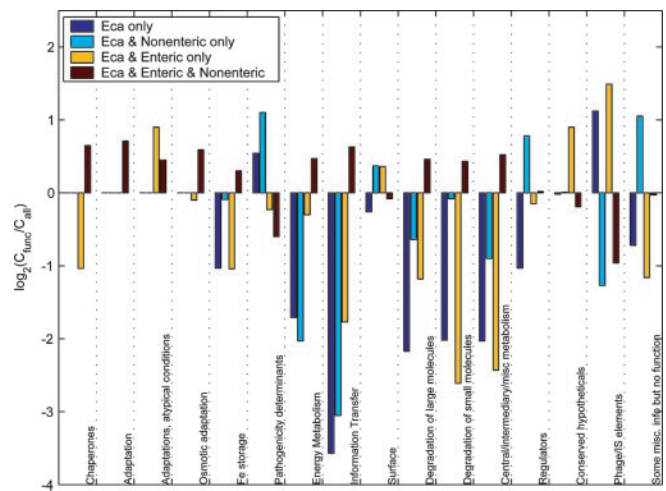


Fig. 2. Ratio of observed to expected CDSs by functional class and bacterial group distribution. The $\log_2(C_{\text{func}}/C_{\text{all}})$ ratio of CDSs from *Eca* strain SCRI1043 shared with no other species (i, dark blue), nonenteric only (ii, cyan), enteric only (iii, yellow), or enteric and nonenteric species (iv, red), by functional class.

value $\log_2(C_{\text{func}}/C_{\text{all}})$ was plotted to illustrate over- or under-representation of each group (Fig. 2).

Transposon Mutation Grid. Donor (*E. coli* S17-1[λ pir] carrying the Tn5 cassette [mTn5-*gusA*-*pgfp21*] in the pUT vector; ref. 28) and recipient (*Eca*1043) strains were mated and transconjugants recovered on M9^{Kan}. A total of 9,216 transconjugants were grown in 24 384-well microtiter plates (M9^{Kan} broth plus 4% glycerol), constituting the mutation grid. Clones from each of the 24 384-well plates were pooled and DNA extracted for PCR screening by using primers designed to anneal to the gene of interest and the end of the transposon cassette. Having identified a plate pool containing a mutant, PCR from each clone within that plate was conducted by using a 384-well PCR machine.

Primers used to identify mutants were: VIRB4F 5'-CATTACCTCAGTTATGGCTATTACAGGGC-3' (*virB4*); PKSF3 5'-CGGATCGGTGGTTCCGTC-3' (*cfaf6*); PKSR1 5'-GGAGCACTATGCTTCCTGCAC-3' (*cfaf7*); and Tn5R 5'-TATCCTCCTAGCTAGTCAGG-3' (mTn5-*gusA*-*pgfp*).

The purified PCR products were sequenced in both directions to confirm the location of the transposon. The mutations were transduced into a clean genetic background before analysis (20).

Pathogenicity Test. *Eca*1043-susceptible potato plants cv. Estima were grown in compost to a height of ≈ 20 cm. *Eca* cells were grown to log phase (overnight) in LB broth, and cells were harvested by centrifugation at $4,000 \times g$ for 10 min, washed in PBS, and resuspended in the same volume of PBS. Two dilutions (10^4 and 10^8 cells per ml⁻¹) in PBS were prepared from these suspensions, and potato plant stems were inoculated under the second fully expanded leaf by using a micropipette tip with 10 μ l of bacterial suspension (equivalent to 10^2 and 10^6 cells per inoculation site). The inoculation site was then covered with parafilm to avoid desiccation. At least 12 replicas for each strain and each inoculum level were used. The inoculated plants were kept in the glasshouse under controlled temperature conditions ($\approx 22^\circ\text{C}$) and high humidity and the presence and length (millimeters) of necrotic lesions was recorded daily for 14 days. GENSTAT for Windows, version 6.1.0.200 (Lawes Agricultural Trust), was used to determine the least significant difference (LSD; $P < 0.05$) defined as the smallest difference between any two means that can be described as being significantly different.

Table 1. Putative HAIs and their phenotypic traits

CDS identifiers	Island no.	Acquisition evidence	Putative phenotype(s)
ECA0499–0510	HAI1	FASTA analysis*	Capsular polysaccharide biosynthesis
ECA0516–0614	HAI2	Integrase and tRNA	Polyketide phytotoxin biosynthesis (<i>cfa</i>) Agglutination/adhesion
ECA0665–0678	HAI3	Phage genes	
ECA1054–1067	HAI4	Integrase Low-percent GC region	
ECA1416–1443	HAI5	Low-percent GC region	Exopolysaccharide and O-antigen biosynthesis
ECA1466–1488	HAI6	FASTA analysis*	Nonribosomal peptide phytotoxin
ECA1598–1679	HAI7	Integrase and tRNA Low-percent GC region	Type IV secretion (<i>virB</i>) Integrated plasmid Agglutination/adhesion
ECA2045–2182	HAI8	FASTA analysis*	Type III secretion (<i>hrp</i>) Agglutination/adhesion (<i>hecAB</i>)
ECA2598–2637	HAI9	Phage genes	P2 family prophage
ECA2694–2705	HAI10	FASTA analysis*	Phenazine antibiotic biosynthesis (<i>ehp</i>)
ECA2750–2759	HAI11	Phage genes Integrase and tRNA	
ECA2850–2879	HAI12	Integrase and tRNA	Rhs and its accessory element VgrG
ECA2889–2921	HAI13	Integrase and tRNA Low-percent GC region	Putative integrated plasmid
ECA2936–3000	HAI14	FASTA analysis*	Nitrogen fixation (<i>nif</i>)
ECA3262–3270	HAI15	FASTA analysis*	Agglutination/adhesion (<i>aggA</i>)
ECA3378–3460	HAI16	Integrase and tRNA	
ECA3695–3742	HAI17	Phage genes	Prophage

*Absence in other enteric bacteria determined by reciprocal FASTA analysis.

LSD was derived from the residual mean square of the analysis of variance from means averaged across all days.

Results and Discussion

Genome Composition. The genome of *Eca*1043 is a single circular chromosome of 5,064,019 bp with a G + C content of 50.97%, 4,491 predicted CDSs, seven rRNA operons, 76 tRNAs, and 25 predicted stable noncoding RNAs. There are 183 bacteriophage genes, including two complete prophages with similarity to phage sequences in other enterobacteria and, in one case, in other plant pathogens (Table 1). Fifty-two of the 4,491 CDSs are pseudogenes (including 22 phage or transposase genes). This figure is similar to the established enterobacteria such as *E. coli* CFT073 (62 CDSs) and *Salmonella enterica* serovar Typhimurium (39 CDSs), but is relatively low compared with the recently diverged enterobacteria such as *S. enterica* serovar Typhi (204 CDSs) (3) and *Yersinia pestis* (149 CDSs) (4). The positions of 11 putative horizontally acquired genomic islands (HAIs) having some of the hallmarks of recent gene transfer events, such as atypical percent G+C, location at or near tRNA genes, and the presence of pathogenicity and/or phage/plasmid genes, were determined (Fig. 1 and Table 1).

Comparative Genomics and Evolution. Reciprocal FASTA analysis of the *Eca*CDS set was performed against 64 published bacterial genome sequences, including 15 enterobacteria, and all available plant pathogenic and plant-associated bacteria (Fig. 1, Table 2, and for a linear version of the diagram see Fig. 5, which is published as supporting information on the PNAS web site). The largest numbers of RBHs were with other enterobacteria, and 2,982 (66.4%) CDSs have RBHs in at least one member of this family. This analysis helped to confirm the locations of the 11 HAIs (see above). Moreover, from regions of the genome lacking RBHs to other enterobacterial genomes, six additional candidate HAIs, possibly representing older acquisition events, were identified (Fig. 1 and Table 1).

The full set of RBHs was used to determine CDSs in *Eca*1043

that were shared with (i) no other genomes, (ii) nonenterobacterial genomes only, (iii) enterobacterial genomes only, or (iv) both enterobacterial and nonenterobacterial genomes. The distribution of CDSs among groups *i–iv* by major functional class, relative to the overall distribution of CDSs across the groups, is shown in Fig. 2. As expected, CDSs involved in core bacterial functions, such as energy metabolism, had a greater proportion of RBHs in group *iv*. The distribution of pathogenicity determinants was of particular interest and this analysis focused on CDSs with a probable direct involvement in pathogenesis, e.g., those coding for toxins, type III secretion system (T3SS) proteins, PCWDEs, etc. (148 CDSs; Table 3, which is published as supporting information on the PNAS web site). CDSs encoding pathogenicity determinants comprised a greater proportion of RBHs in groups *i* and *ii*. Because many of these CDSs lie within predicted HAIs, this finding may indicate the impact of horizontal gene transfer on the evolution of *Eca* as a plant pathogen.

To investigate further the possible acquisition of pathogenicity determinants from nonenterobacterial genomes (represented by group *ii*) CDSs from *Eca* making RBHs only with nonenterobacterial genomes were identified (Fig. 6, which is published as supporting information on the PNAS web site). This finding revealed a number of interesting relationships, most striking of which were the RBHs for putative pathogenicity determinants shared between *Eca* and the phytopathogen *P. syringae* pv. *tomato* DC3000 (referred to as *P. syringae* throughout the text). These relationships correspond to two *P. syringae* pathogenicity gene clusters: the *hrp* (T3SS) gene cluster (HAI8) (also shared with *Pseudomonas aeruginosa*), and the *cfa* gene cluster (within HAI2) involved in phytotoxin synthesis (29). Several organisms, including the plant-associated *Pseudomonas putida* and three animal pathogenic *Vibrio* species, share genes from a cluster (HAI15) that includes *aggA*, which is involved in adherence to plant roots in *P. putida* (30). Other RBHs include *avrXca*, which is involved in avirulence in *X. campestris* pv. *raphani* (31), and VirB/type IV secretion genes (HAI7) in *A. tumefaciens* (32); the latter also being present in *X. axonopodis* pv. *citri* and *Sinorhiz-*

zobium meliloti. Finally, plant pathogens, plant-associated bacteria, and more distantly related bacteria, including *Bacillus* and *Streptomyces* spp., make RBHs to CDSs encoding several PCWDEs. These data provide evidence for horizontal transfer of putative pathogenicity determinants (HAIs 2, 7, 8, and 15) during the evolution of *Eca1043*.

Survival in Diverse Environments. The gene content of *Eca1043* suggests that all major metabolic pathways are intact, and that it has the ability to use a range of different nutrients for adaptation to diverse environments. There are 36 putative methyl-accepting chemotaxis protein genes, more than in other sequenced enterobacterial genomes, e.g., 11 in *S. enterica* serovar Typhi and 10 in *Yersinia enterocolitica*, or in most other sequenced phytopathogens, e.g., 20 in *X. campestris* pv. *campestris*, 22 in *X. axonopodis* pv. *citri*, and 20 in *R. solanacearum* (www.genome.ad.jp/kegg). Similarly, 80 (2% of CDSs) putative ABC transport uptake systems were identified, compared with only 44 (1% of CDSs) in *E. coli* K12. The genome also contains 336 (7% of CDSs) putative regulators, compared with 178 (4% of CDSs) in *E. coli* K12 (1). Many regulators may have been acquired through horizontal gene transfer (Fig. 2), and a number are also directly implicated in virulence (Table 3). Interestingly, other phytopathogens also possess large numbers of putative regulators (8% and 12% of CDSs in *R. solanacearum* and *P. syringae*, respectively), which may reflect similarities in lifestyle. These findings suggest that *Eca1043* is able to respond to a wide range of nutrient sources, or other environmental cues, in keeping with its variety of lifestyles and habitats.

Eca1043 appears to have unexpected metabolic traits of potential advantage for survival in the soil or rhizosphere, including the potential to fix nitrogen (*nif* genes, HAI14) and catabolize opines (e.g., *occQMPJ*). Such traits have not been recognized in the soft rot erwiniae, and are absent in other sequenced enterobacterial genomes, but are important in other bacteria for colonization of plants (33–35). In addition, HAI10 carries genes similar to those for phenazine antibiotic production in the closely related plant pathogen *Pantoea agglomerans* (*ehp* genes) (36), which may provide a competitive advantage in soil or on the host.

Pathogenicity Determinants. The *Eca1043* genome carries many factors previously implicated in the pathogenesis of soft rot erwiniae (12), but many more putative pathogenicity genes novel to this group of pathogens have now been revealed. A total of 393 CDSs with a possible involvement in pathogenicity, including the 148 CDSs used in the comparative genomic analyses and other CDSs related to processes such as adhesion, iron acquisition, and motility, are listed in Table 3, and key findings are summarized below.

The main virulence determinants in *Eca* are PCWDEs that cause extensive tissue maceration during the latter stages of infection (11). *Eca1043* has 20 putative pectinase genes, 11 of which were previously unknown in *Eca*. Two of these genes are most similar to genes from *A. tumefaciens* and *Bacillus* spp. Seven CDSs may encode other PCWDEs, including cellulases, four of which are novel to the erwiniae. In addition to known *Ecc* regulators that control the PCWDEs and other virulence factors (Table 3), the genome contains other candidate virulence regulators. The LuxR homologue ECA1561 encodes a putative novel cognate binding protein of *N*-acyl homoserine lactones. Homologues of some of the previously identified quorum sensing-related genes are present in the genome, including *expI*, encoding the *N*-acyl homoserine lactone synthetase, and the contiguous putative regulator *expR*. Strain SCRI1043 does not make a carbapenem antibiotic (G.P.C.S., unpublished work) and the corresponding biosynthetic genes are absent. It therefore seems unlikely that ECA1561 encodes a functional homologue

of CarR, the LuxR-type regulator of carbapenem biosynthesis previously identified in some *Ecc* strains. The function of the cryptic ECA1561 is currently unknown but one possibility would be a role as a “missing link” in the quorum-sensing control of PCWDEs (11).

In *Ech*, PCWDE production and full pathogenicity are linked to production of the siderophores chrysoabactin and achromobactin, which scavenge iron from the iron-poor environment of the host (37, 38). Although *Ecc* strains produce chrysoabactin and aerobactin siderophores, they have no obvious role in potato disease, suggesting that other iron acquisition systems may be involved (39). Little is known about iron acquisition in *Eca*. However, *Eca1043* has genes for the achromobactin uptake and transport system (*cbrABCD*) and enterobactin synthesis (*entAFBECD*). The latter has not previously been identified in the erwiniae but is a well characterized siderophore in *E. coli* and *Salmonella* spp (40). Two additional putative siderophore-independent systems similar to ferric citrate uptake in *E. coli* (*fecIRABCD*), and to the HasA heme-binding protein and its cognate secretion system in *Serratia marcescens* (41), are also identified in the erwiniae. Genes involved in hemin storage (*hmsHFRS*) are also present, although a second operon containing *hmsT* present in *Y. pestis* is absent in *Eca1043* (42).

Several *Ech* genes involved in defense against the plant oxidative burst or antimicrobial peptides are present in *Eca1043* (12). However, there are additional putative defenses against active oxygen species: catalase peroxidase (*katB*), paraquat-inducible genes (*pqiAB*), a broad specificity flavoprotein reductase (similar to *P. putida xenA*; ref. 43), and peroxide resistance genes (similar to *X. campestris* pv. *phaseoli ahpC*, *ohr*, and *ohrR*; refs. 44 and 45).

Eca1043 is the only enterobacterium sequenced to date that possesses all six known Gram-negative protein secretion systems. To our knowledge, the only other bacterium identified with representatives of all these systems is another plant pathogen, *X. axonopodis* pv. *citri* (15). The known type I and II systems, which secrete PCWDEs and other pathogenicity determinants (11), are present together with types III, IV, and V (autotransporter), and two-partner secretion and additional putative type I systems (Table 3). Also revealed in the genome are the twin arginine-targeting pathway *tat* genes, which offer an alternative route to *sec*-dependant export for folded proteins to reach the periplasm. Such proteins include virulence factors in some species (46, 47), although no *Eca* proteins have yet been identified that use this system.

A complete T3SS, recently identified in *Eca* SCRI1039 (48), and carrying putative effector, helper, and avirulence genes similar to those in *Erwinia amylovora*, *Ecc*, and *Ech* (12), is also present in *Eca1043* (HAI8), but carries eight additional CDSs absent in these closely related pathogens. Elsewhere in the genome there are T3SS-associated genes resembling *srfABC* in *Salmonella* spp. *SrfC* is similar to *HopPtoL* in *P. syringae*, encoding putative T3SS-delivered effector proteins (49, 50). In contrast to the broad host range phytopathogens *P. syringae* and *R. solanacearum* (13, 14, 51), large numbers of candidate type III (Hrp) effectors have not so far been identified in *Eca1043*. If confirmed, this finding may reflect the narrow host range of *Eca* and/or its lack of a “race structure;” i.e., strains that are incompatible on specific potato host genotypes have not been found.

A surprise finding was a gene cluster within HAI7 that resembles both a plasmid conjugation system in *E. coli* and the pathogenicity-related type IV secretion system (T4SS) locus in *A. tumefaciens* (32). Although this may simply be an integrated plasmid, and not directly related to pathogenicity, recent discoveries show that conjugation machinery can also deliver virulence proteins (52), and that similar loci are present in two

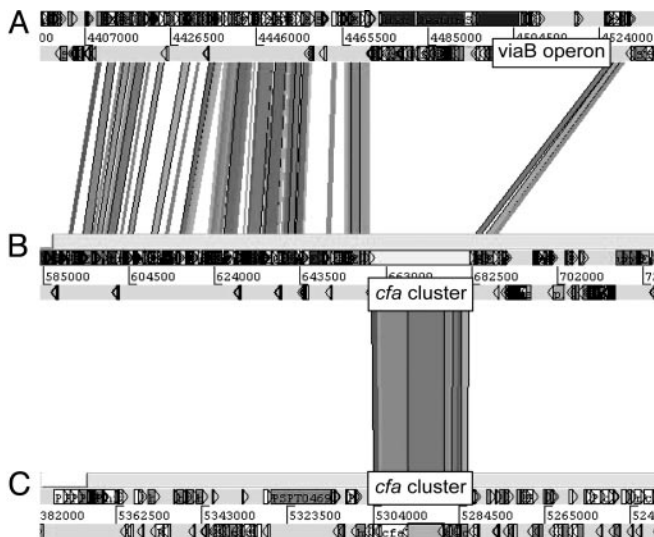


Fig. 3. Screen shot adapted from Artemis Comparison Tool (www.sanger.ac.uk/Software/ACT). (A–C) RBHs between the SPI-7-like regions of *S. enterica* serovar Typhi (A) and *Eca* SCR1043 (B), and the genomic region containing the *cfa* gene cluster of *P. syringae* pv. *tomato* (C). The locations of the *cfa* gene cluster and the *viaB* operon are indicated. Shaded lines between the genomes represent RBHs.

other phytopathogens (15, 16). We thus investigated its possible role in virulence (see below).

The *Eca*1043 genome has a number of genes associated with agglutination and cell attachment, similar to those in both plant and animal pathogens and plant-associated bacteria. These genes include two putative two-partner secretion systems (e.g., *hecAB* and *HAI8*) found in all sequenced necrogenic plant pathogens, which may offer a common mechanism of host attachment (13, 53, 54). Another cluster (*HAI15*) includes genes encoding a large hemagglutinin-like protein (4,588 aa) and a putative adhesion protein (*aggA*; ref. 55). Other CDSs (e.g., within *HAI2*) appear to encode type IV pili and other fimbrial proteins similar to those in other enterobacteria and plant-associated bacteria, which in plant pathogens such as *R. solanacearum* are involved in adhesion to the host plant (56). *Eca*1043 also has CDSs similar to polysaccharide biosynthesis genes (*HAI1*) that more closely resemble those of distantly related (often plant-associated) bacteria than those of other enterobacteria. Flagellar motility is also recognized as contributing to the pathogenicity of *Eca* (57) and a large number of genes similar to those in other enterobacteria are devoted to this function.

Additional CDSs potentially encoding secreted pathogenicity proteins include those that resemble eukaryotic genes (putative lipases and a carbonic anhydrase), an avirulence gene from *X. campestris* pv. *raphani* (*avrXca*; ref. 31), and a necrosis-inducing gene from *Fusarium oxysporum* (*nep1*; ref. 58). The latter two are required for full virulence of *Eca*1043 (G.P.C.S., unpublished work).

The largest genes in the *Eca*1043 genome (*HAI6*) appear to encode a nonribosomal peptide (NRP) synthetase system. These genes are similar to that producing the *P. syringae* pv. *syringae* phytotoxin syringomycin (*syxE*), which induces necrosis by forming transmembrane pores and causing electrolyte leakage (29). Interestingly, these genes are not present in *P. syringae* pv. *tomato* DC3000 (13), and NRP phytotoxins have not previously been identified in enterobacterial plant pathogens. However, similar genes have been found in *R. solanacearum* (14) and *X. axonopodis* pv. *citri* (15).

HAI2 shows a high level of conservation of both sequence and

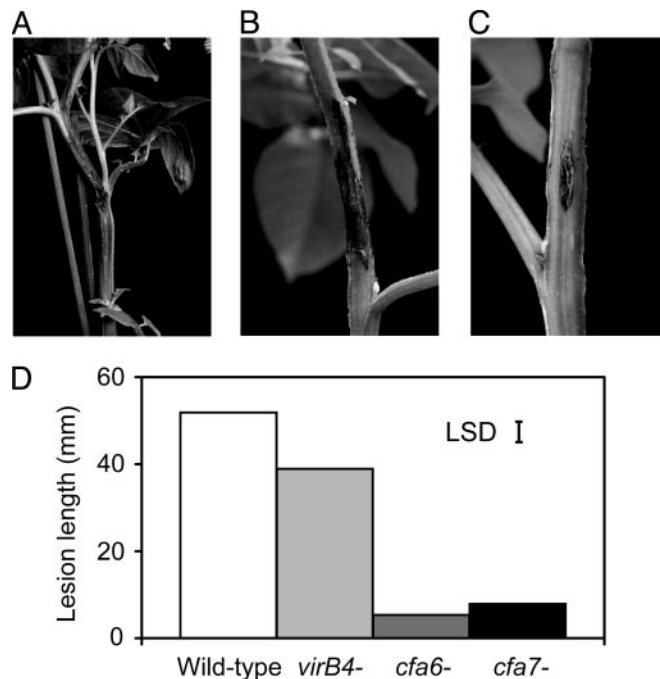


Fig. 4. Mutations in putative type IV secretion and polyketide phytotoxin synthesis genes affect disease development. Lesion development on potato plant stem over a 14-day period after inoculation of *Eca* strain SCR1043 wild-type and mutant strains at 10^4 cells per inoculation site. (A) Wild type. (B) Mutant *Eca*1043 *virB4*::Tn5. (C) Mutant *Eca*1043 *cfa6*::Tn5. (D) Bar graph showing length of rot (millimeters) for wild-type and mutants *Eca*1043*virB4*::Tn5, *Eca*1043*cfa6*::Tn5, and *Eca*1043*cfa7*::Tn5. LSD = LSD of means across all days (value 4.82).

gene order to the SPI-7 pathogenicity island in *S. enterica* serovar Typhi (Fig. 3). The presence of similar islands in distantly related bacteria, such as *P. aeruginosa* and *X. axonopodis* pv. *citri*, has led to the suggestion that this island is a mobile element (59). However, the *viaB* operon in SPI-7, encoding the *S. enterica* serovar Typhi Vi exopolysaccharide pathogenicity determinant, is absent in *Eca*1043 (Fig. 3). This finding is perhaps unsurprising because SPI-7 has a mosaic structure across *S. enterica* isolates and may have arisen as a result of several independent insertion events (59). Interestingly, at an equivalent location to the *viaB* operon in SPI-7, *HAI2* contains genes highly similar to the *cfa* gene cluster in *P. syringae* (Fig. 3). The *cfa* genes in *P. syringae* encode synthetases of the polyketide component (coronafacic acid) of the coronatine phytotoxin, a molecular mimic in plant-signaling pathways (29). However, genes encoding synthetases of the second component of coronatine, coronamic acid, are absent. The *Eca*1043 *cfa*-like cluster and *S. enterica* *viaB* operon could be “islands within an island,” and their similar locations in SPI-7-like loci may indicate a recombination “hot spot.” Polyketide phytotoxins have not previously been identified in enterobacterial plant pathogens but are important pathogenicity determinants in *P. syringae*. This cluster was thus investigated for its role in virulence (see below).

Functional Genomics. As two major findings from the *Eca*1043 genome sequence and comparative genomics study, the putative T4SS and *cfa*-like polyketide phytotoxin clusters were selected to investigate their role in virulence. For this purpose, an arrayed set of transposon insertion mutants (mutation grid) was constructed. By PCR screening of pooled clones from the grid, mutants carrying insertions within these clusters (*ECA*1620, *virB4*, T4SS, and *ECA*0602–0603, *cfa6*, and *cfa7*) were isolated,

and were inoculated into potato stems. The *virB4* mutant showed a statistically significant reduction in virulence ($P < 0.05$), whereas virulence was greatly reduced in the *cfa6* and *cfa7* mutants ($P < 0.05$; Fig. 4). Although only a preliminary indication in the absence of other experiments, such as measuring bacterial growth, the reduced virulence in the *virB4* mutant suggests that the putative T4SS does appear to be more than simply integrated conjugation machinery and may have been recruited for delivery of virulence factors. Moreover, although only one of the two gene clusters required for coronatine synthesis in *P. syringae* is present in *Eca1043*, this cluster appears to play a major role in disease development, possibly through the production of an alternative polyketide phytotoxin.

Conclusions. Here, we report the complete genome sequence of a plant pathogen from the Enterobacteriaceae, a family noted for its human pathogens. The sequence has revealed a metabolic plasticity that fits a lifestyle adapted to different environments in and around the plant host. It contains all of the known Gram-negative protein targeting systems and many PCWDEs, which is consistent with a lifestyle as a “rotter,” whereas factors

such as the T3SS imply more subtle interactions with its host. However, the genome has also revealed putative pathogenicity determinants novel to *Eca1043*, to other soft rot erwiniae and, in many cases, to the enterobacteria. Many of these determinants lie within putative HAIs and resemble genes in other plant pathogens, suggesting horizontal exchange of genomic islands during the evolution of plant pathogens. Finally, we carried out functional analyses on two gene clusters in what appear to be recently acquired islands in *Eca1043*, providing evidence that a T4SS and a polyketide phytotoxin act as virulence determinants in nontumorigenic and non-*Pseudomonas* phytopathogens, respectively. A wider functional genomics program used to identify all components contributing to the pathogenic lifestyle of this important bacterial plant pathogen is warranted for future study.

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