

Supplementary Materials

Table S1. *Dickeya solani* D s0432-1 gene classes and operons suggested as virulence determinants in the other *Dickeya* species.

Gene ID	Start codon	End codon	Gene product	Gene class
577	636066	637013	Pectin lyase	pectin-degrading and modifying enzymes
2230	2573121	2573453	Pectin degradation protein	pectin-degrading and modifying enzymes
1924	2210139	2211458	Pectate lyase	pectin-degrading and modifying enzymes
2233	2575823	2577454	Pectate disaccharide-lyase	pectin-degrading and modifying enzymes
2239	2582998	2583933	Pectin acetylerase	pectin-degrading and modifying enzymes
3026	3541120	3542298	Pectate lyase A	pectin-degrading and modifying enzymes
3027	3542733	3543947	Pectate lyase E	pectin-degrading and modifying enzymes
3028	3544474	3545652	Pectate lyase D	pectin-degrading and modifying enzymes
3029	3545730	3547385	Pectin acetylerase	pectin-degrading and modifying enzymes
3030	3547471	3548571	Pectinesterase A	pectin-degrading and modifying enzymes
2674	3087237	3088514	Pectate lyase L	pectin-degrading and modifying enzymes
2885	3379324	3380364	Endo-pectate lyase	pectin-degrading and modifying enzymes
3778	4441335	4442462	Pectate lyase/Amb allergen	pectin-degrading and modifying enzymes
3779	4443005	4444129	Pectate lyase/Amb allergen	pectin-degrading and modifying enzymes
3780	4444315	4445577	Pectate lyase	pectin-degrading and modifying enzymes
4119	4846042	4848246	Exopolygalacturonate lyase	pectin-degrading and modifying enzymes
569	625736	627034	Putative hexuronate MFS transporter ExuT	pectin catabolism and transport
570	627537	628946	Uronate isomerase 1	pectin catabolism and transport
571	629106	630557	Altronate oxidoreductase	pectin catabolism and transport
572	630576	632066	Altronate hydrolase	pectin catabolism and transport
1980	2272792	2273433	KHG/KDPG aldolase	pectin catabolism and transport
2042	2338392	2339117	Oligogalacturonate-specific porin kdgM	pectin catabolism and transport
2231	2573777	2574613	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase 1	pectin catabolism and transport
2232	2574800	2575561	2-deoxy-D-gluconate 3-dehydrogenase	pectin catabolism and transport
2233	2575823	2577454	Pectate disaccharide-lyase	pectin catabolism and transport

Table S1. Cont.

Gene ID	Start codon	End codon	Gene product	Gene class
2234	2577499	2578389	Putative ABC sugar transporter, permease	pectin catabolism and transport
2235	2578382	2579284	Oligogalacturonide ABC transporter, permease protein	pectin catabolism and transport
2236	2579298	2580425	Oligogalacturonide ABC transporter, ATP-binding protein	pectin catabolism and transport
2237	2580440	2581732	Oligogalacturonide ABC transporter	pectin catabolism and transport
2238	2581982	2582692	Oligogalacturonate-specific porin kdgM	pectin catabolism and transport
2467	2845629	2846645	2-keto-3-deoxygluconate permease	pectin catabolism and transport
3997	4701790	4702722	2-dehydro-3-deoxygluconokinase	pectin catabolism and transport
321	358659	359156	Stringent starvation protein B (ClpXP)	proteases and peptidases
600	665491	666504	Probable O-sialoglycoprotein endopeptidase	proteases and peptidases
615	677830	679773	Protease, ATP-dependent zinc-metallo	proteases and peptidases
630	697271	698269	Predicted peptidase (Collagenase-like)	proteases and peptidases
804	893331	896123	Probable zinc protease PqqL	proteases and peptidases
918	1025461	1028613	Serine protease homologue	proteases and peptidases
931	1039397	1042294	Protease III	proteases and peptidases
961	1071685	1073040	Protease rseP	proteases and peptidases
1070	1197785	1198408	ATP-dependent Clp protease proteolytic subunit 2	proteases and peptidases
1071	1198536	1199810	ATP-dependent Clp protease ATP-binding subunit ClpX	proteases and peptidases
1073	1200696	1202360	ATP-dependent protease La	proteases and peptidases
1116	1251675	1252589	Putative protease, membrane anchored	proteases and peptidases
1190	1336605	1337090	Putative metalloprotease ybeY	proteases and peptidases
1265	1419782	1421653	Secreted protease; subtilase family	proteases and peptidases
1454	1678712	1679209	Protease involved in processing C-terminal end of HycE	proteases and peptidases
1864	2136671	2136991	ATP-dependent Clp protease adapter protein ClpS	proteases and peptidases
1865	2137020	2139296	ATP-dependent Clp protease ATP-binding subunit ClpA	proteases and peptidases
1973	2264185	2265597	Metalloprotease, opacity-associated protein A family	proteases and peptidases
1982	2275106	2277157	Protease II	proteases and peptidases

Table S1. Cont.

Gene ID	Start codon	End codon	Gene product	Gene class
2011	2304912	2306762	Protease 4	proteases and peptidases
2054	2350979	2352025	Peptidase S49 domain protein	proteases and peptidases
2256	2599586	2600470	Protease HtpX	proteases and peptidases
2363	2720709	2722730	Carboxy-terminal protease for penicillin-binding protein 3	proteases and peptidases
2418	2780886	2781704	Putative protease YdgD	proteases and peptidases
2605	3013563	3015293	Protease La	proteases and peptidases
2898	3395866	3396540	Peptidase S14, ClpP	proteases and peptidases
2957	3467517	3468893	Peptidase U32	proteases and peptidases
2992	3507479	3508528	Grimelysin	proteases and peptidases
3755	4415406	4416215	Predicted metal-dependent membrane protease	proteases and peptidases
3772	4432761	4434722	Subtilisin DY	proteases and peptidases
3814	4484951	4485775	Rhomboid protease glpG	proteases and peptidases
3928	4630261	4630791	ATP-dependent protease subunit HslV	proteases and peptidases
3929	4630801	4632132	ATP-dependent protease ATPase subunit HslU	proteases and peptidases
2109	2410964	2412397	Serralysin	proteases and peptidases
2110	2412831	2414270	Serralysin	proteases and peptidases
2111	2414421	2415866	Serralysin	proteases and peptidases
2116	2421119	2422552	Serralysin	proteases and peptidases
115	138081	140768	Cellulose 1,4-beta-cellobiosidase	cellulases
4000	4706324	4707322	Endoglucanase (Endo-1,4-beta-glucanase Y)	cellulases
2811	3280597	3281388	Necrosis-inducing protein	necrosis-inducing protein toxin
2813	3283379	3285271	Putative avirulence protein avrL	avirulence protein
2814	3285415	3287262	Putative avirulence protein avrM	avirulence protein
4001	4707335	4707802	Cellulose synthase operon protein D	cellulose synthesis
4002	4707805	4711755	Cellulose synthase operon C domain protein	cellulose synthesis
4004	4714277	4716367	Cellulose synthase (UDP-forming)	cellulose synthesis

Table S1. Cont.

Gene ID	Start codon	End codon	Gene product	Gene class
4005	4716477	4717292	Cellulose synthase operon protein YhjQ homolog	cellulose synthesis
1314	1478791	1479660	Periplasmic hemin-binding protein	sequestration or storage of iron
1315	1479657	1480646	Hemin transport system permease HmuU	sequestration or storage of iron
1316	1480639	1481433	Hemin transport system ATP-binding protein	sequestration or storage of iron
1317	1481658	1484129	Outer membrane porin, receptor for ferric enterobactin	sequestration or storage of iron
1365	1543100	1543945	Ferrous iron permease efeU	sequestration or storage of iron
1431	1648625	1650760	Hydroxamate-type ferrisiderophore receptor	sequestration or storage of iron
1594	1839386	1840213	Chelated iron ABC transporter, permease protein YfeD	sequestration or storage of iron
1595	1840215	1841069	Chelated iron ABC transporter, permease protein YfeC	sequestration or storage of iron
1596	1841062	1841958	ABC chelated iron transporter, ATP-binding subunit yfeB	sequestration or storage of iron
1597	1841955	1842905	Iron (Chelated) ABC transporter, periplasmic-binding protein YfeA	sequestration or storage of iron
1697	1948195	1949211	Iron(III) ABC transporter, periplasmic iron(III)-binding protein	sequestration or storage of iron
1698	1949246	1950838	Iron(III)-transport system permease protein	sequestration or storage of iron
1699	1950835	1951869	Iron(III)-transport ATP-binding protein	sequestration or storage of iron
2269	2615883	2618204	Ferrous iron transport protein B	sequestration or storage of iron
2270	2618227	2618454	Putative ferrous iron transport protein A	sequestration or storage of iron
2507	2889968	2890714	FeS assembly ATPase SufC	sequestration or storage of iron
2508	2890803	2892302	Component of SufBCD complex	sequestration or storage of iron
2509	2892317	2892748	Iron-sulfur cluster assembly scaffold protein	sequestration or storage of iron
2815	3287674	3288723	Ferrienterobactin-binding periplasmic protein	sequestration or storage of iron
2817	3290278	3291324	FepD protein	sequestration or storage of iron
2818	3291337	3292386	Ferric enterobactin transport system permease protein fepG	sequestration or storage of iron
2819	3292424	3293221	Ferric enterobactin transport system ATP-binding protein ViuC	sequestration or storage of iron
3011	3525770	3526093	Iron-binding protein iscA	sequestration or storage of iron
3012	3526119	3526505	FeS cluster assembly scaffold	sequestration or storage of iron
3017	3530265	3531389	ABC type periplasmic iron siderophore/cobalamin binding protein	sequestration or storage of iron

Table S1. Cont.

Gene ID	Start codon	End codon	Gene product	Gene class
3018	3531393	3532475	Inner membrane permease of iron/siderophore ABC transporter	sequestration or storage of iron
3019	3532472	3533263	Siderophore ABC transporter, ATP-binding subunit	sequestration or storage of iron
3074	3598602	3598946	Iron--sulfur cluster insertion protein erpA	sequestration or storage of iron
3077	3600786	3602807	Ferrichrome ABC transporter, permease protein	sequestration or storage of iron
3078	3602804	3603715	Ferrichrome-binding periplasmic protein	sequestration or storage of iron
3079	3603727	3604527	ATP-binding component of hydroxymate-dependent iron transport	sequestration or storage of iron
3097	3621422	3622486	Ferric iron ABC transporter ATP-binding protein	sequestration or storage of iron
3098	3622494	3624101	Iron-uptake permease inner membrane protein	sequestration or storage of iron
3265	3808904	3809959	Iron-chelating periplasmic-binding protein	sequestration or storage of iron
3266	3809964	3812144	Ferric siderophore receptor	sequestration or storage of iron
2822	3297464	3306064	Synthetase CbsF	chrysobactin siderophore
2823	3306116	3306334	MbtH-like protein	chrysobactin siderophore
2824	3306446	3307753	Enterochelin esterase	chrysobactin siderophore
2825	3308068	3310272	Ferrichrysobactin receptor	chrysobactin siderophore
2826	3310356	3311543	Isochorismate synthase	chrysobactin siderophore
2827	3311540	3313168	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase	chrysobactin siderophore
2828	3313172	3314047	Phosphopantetheine attachment site protein	chrysobactin siderophore
2829	3314044	3314802	2,3-dihydroxybenzoate-2,3-dehydrogenase	chrysobactin siderophore
1518	1744837	1746951	TonB-dependent ferric achromobactin receptor	achromobactin siderophore
1527	1757602	1758624	Achromobactin transport system permease protein CbrB	achromobactin siderophore
1528	1758617	1759666	Achromobactin transport system permease protein CbrC	achromobactin siderophore
1529	1759675	1760523	Achromobactin ABC transporter ATP-binding component cbrD	achromobactin siderophore
744	830486	830779	Ferredoxin (2Fe-2S)	ferredoxin
2739	3199463	3200479	Hydrogenase 2 4Fe-4S ferredoxin-type component	ferredoxin
3008	3522889	3523224	Ferredoxin, 2Fe-2S type, ISC system	ferredoxin
3025	3539420	3540610	Flavohemoprotein (Haemoglobin-like protein)	ferredoxin

Table S1. Cont.

Gene ID	Start codon	End codon	Gene product	Gene class
3045	3568860	3569120	Predicted 4Fe-4S cluster-containing protein	ferredoxin
3636	4242585	4246094	Pyruvate-flavodoxin oxidoreductase	ferredoxin
3936	4638330	4639076	Ferredoxin--NADP reductase	ferredoxin
1987	2279613	2280122	Cytoplasmic ferritin (FtnA)	ferritin
3730	4393060	4393533	Bacterioferritin (bfr)	ferritin
1319	1485816	1486301	Non-specific DNA-binding protein Dps/ferroxidase	ferritin
1738	1999319	1999822	DNA protection during starvation protein	ferritin
1987	2279613	2280122	Cytoplasmic ferritin	ferritin
2599	3002162	3004714	Glucans biosynthesis glucosyltransferase H (OpgH)	periplasmic glucans synthesis
2600	3004707	3006275	Glucans biosynthesis protein G (OpgG)	periplasmic glucans synthesis
2455	2830083	2831843	Peptide transport periplasmic protein	antimicrobial peptide
2456	2831840	2832805	ABC peptide transporter, permease subunit sapB	antimicrobial peptide
2457	2832792	2833682	Peptide transport system permease protein SapC	antimicrobial peptide
441	495477	496136	Type-1Aa cytolytic delta-endotoxin	insect-specific Cyt-like toxin
442	496208	496819	Type-1Ba cytolytic delta-endotoxin	insect-specific Cyt-like toxin
443	496915	497514	Type-2Aa cytolytic delta-endotoxin	insect-specific Cyt-like toxin
444	497585	498220	Delta-endotoxin CytB	insect-specific Cyt-like toxin
85	102786	103478	Indigoidine synthesis protein IdgB	indigoidine synthesis
86	103691	108157	Blue-pigment synthetase	indigoidine synthesis
2112	2416100	2417488	Alkaline protease secretion outer membrane protein AprF	Type I secretion
2113	2417501	2418847	Proteases secretion protein prtE	Type I secretion
2114	2418861	2420588	Alkaline protease secretion ATP-binding protein aprD	Type I secretion
2115	2420605	2420916	Metalloprotease inhibitor I38	Type I secretion
2281	2631417	2632613	Putative HrcS protein (Fragment)	type II secretion
2835	3318834	3319685	Bacterial Peptidase A24 N-domain protein	type II secretion
2836	3319870	3320358	EtpM protein	type II secretion

Table S1. Cont.

Gene ID	Start codon	End codon	Gene product	Gene class
2837	3320355	3321557	General secretion pathway protein L	type II secretion
2838	3321554	3322615	General secretion pathway protein K	type II secretion
2839	3322612	3323352	General secretion pathway protein J	type II secretion
2840	3323349	3323726	General secretion pathway protein I	type II secretion
2841	3323730	3324269	EtpH	type II secretion
2842	3324272	3324733	General secretion pathway protein G	type II secretion
2843	3324767	3325993	General secretion pathway protein F	type II secretion
2844	3325995	3327491	EtpE	type II secretion
2845	3327488	3329668	Uncharacterized protein	type II secretion
2846	3329622	3330440	General secretion pathway protein C	type II secretion
2847	3331668	3332288	General secretion pathway protein B	type II secretion
2848	3332323	3332724	Lipoprotein, PulS/OutS family	type II secretion
3446	4023742	4024185	Putative major pilin subunit	type II secretion
3447	4024191	4025627	Putative integral membrane protein involved in biogenesis of fimbriae	type II secretion
3448	4025637	4026842	Outer membrane protein export (MTB) system (Type II secretion system)	type II secretion
3790	4454642	4455946	Protein transport protein hofQ	type II secretion
3827	4499979	4501949	Glycogen debranching enzyme 1	type II secretion
2184	2511847	2512299	AvrF	type III secretion and effectors
2185	2512336	2517213	AvrE	type III secretion and effectors
2186	2517435	2518484	Type III effector protein	type III secretion and effectors
2187	2518614	2520239	Uncharacterized protein	type III secretion and effectors
2188	2520253	2520585	Potential HrpW-specific chaperone	type III secretion and effectors
2189	2520814	2521488	Oxidoreductase, short chain dehydrogenase/reductase family protein	type III secretion and effectors
2190	2521526	2523241	Pathogenicity locus protein hrpK	type III secretion and effectors
2277	2629038	2629436	Probable phospholipase C (PlcA)	type III secretion and effectors
2278	2629592	2630626	Hairpin protein N (Fragment)	type III secretion and effectors

Table S1. Cont.

Gene ID	Start codon	End codon	Gene product	Gene class
2279	2630787	2631197	HrpV	type III secretion and effectors
2280	2631194	2631382	HrpT	type III secretion and effectors
2281	2631417	2632613	Putative HrcS protein (Fragment)	type III secretion and effectors
2282	2632634	2633485	Uncharacterized protein	type III secretion and effectors
2283	2633478	2633912	HrpG	type III secretion and effectors
2284	2633899	2634126	HrpF family protein	type III secretion and effectors
2285	2634411	2634815	Putative uncharacterized protein yafO	type III secretion and effectors
2286	2634812	2635105	Putative antitoxin of the YafO-YafN toxin-antitoxin system	type III secretion and effectors
2287	2635323	2636372	Extracellular phospholipase C	type III secretion and effectors
2288	2636912	2638072	Putative uncharacterized protein orf3	type III secretion and effectors
2289	2638083	2639396	HopAJ2 protein	type III secretion and effectors
2290	2639401	2639511	Uncharacterized protein	type III secretion and effectors
2291	2639658	2640260	HrpE	type III secretion and effectors
2292	2640389	2640865	HrpD	type III secretion and effectors
2293	2640985	2641770	HrcJ	type III secretion and effectors
2294	2641854	2642219	HrpB protein	type III secretion and effectors
2295	2642300	2642503	Hrp pili protein hrpA	type III secretion and effectors
2297	2643639	2643827	Uncharacterized protein	type III secretion and effectors
2301	2647382	2648551	HrpJ	type III secretion and effectors
2302	2648555	2650657	HrcV	type III secretion and effectors
2303	2650669	2651640	HrpQ protein	type III secretion and effectors
2304	2651640	2653019	HrcN protein	type III secretion and effectors
2305	2653006	2653485	HrpO	type III secretion and effectors
2306	2653482	2654006	HrpP	type III secretion and effectors
2307	2654003	2655187	HrcQ	type III secretion and effectors
2308	2655184	2655837	Type III secretion protein HrcR	type III secretion and effectors

Table S1. Cont.

Gene ID	Start codon	End codon	Gene product	Gene class
2309	2655845	2656105	HrcS	type III secretion and effectors
2310	2656113	2656916	HrcT	type III secretion and effectors
2311	2656956	2658035	HrcU	type III secretion and effectors
1634	1882602	1883618	TriJ protein	type IV secretion
1635	1883608	1883928	Uncharacterized protein	type IV secretion
1636	1883941	1884816	Inner membrane protein channel for type IV secretion	type IV secretion
1637	1884813	1885703	P-type conjugative transfer protein VirB9	type IV secretion
1638	1885703	1886386	TriG protein	type IV secretion
1639	1886607	1887635	TriE protein	type IV secretion
1640	1887647	1887871	Eex	type IV secretion
1641	1887883	1888599	PilX5	type IV secretion
1642	1888625	1891372	TriC protein	type IV secretion
1643	1891382	1891657	Putative conjugal transfer protein TriB	type IV secretion
1644	1891677	1892324	Pilx1 protein	type IV secretion
3001	3516227	3516982	Type IV pilus bioproteinsis/stability protein PilW	type IV secretion
371	422108	422587	Similar to Hcp protein	type VI secretion and effectors
770	855989	856474	Type VI secretion system effector, Hcp1 family	type VI secretion and effectors
784	867534	871880	Rhs core protein with extension	type VI secretion and effectors
786	872313	874166	Putative Rhs accessory genetic element	type VI secretion and effectors
787	874279	874797	Hcp protein	type VI secretion and effectors
813	905844	906323	Hcp-like protein	type VI secretion and effectors
1329	1496595	1497113	Hcp protein	type VI secretion and effectors
1330	1497278	1499314	VgrG protein	type VI secretion and effectors
1330	1497278	1499314	VgrG protein	type VI secretion and effectors
1331	1499324	1500136	Uncharacterized protein	type VI secretion and effectors
1332	1500133	1500693	Putative phospholipase	type VI secretion and effectors

Table S1. Cont.

Gene ID	Start codon	End codon	Gene product	Gene class
1333	1500693	1501460	Ankyrin	type VI secretion and effectors
1334	1501620	1502588	Putative uncharacterized protein	type VI secretion and effectors
1335	1502585	1503502	Putative uncharacterized protein	type VI secretion and effectors
1336	1503522	1508504	YD repeat protein	type VI secretion and effectors
1336	1503522	1508504	YD repeat protein	type VI secretion and effectors
1337	1508507	1508896	Putative uncharacterized protein	type VI secretion and effectors
1338	1509749	1510093	Uncharacterized protein	type VI secretion and effectors
1339	1510210	1510596	Putative uncharacterized protein	type VI secretion and effectors
1340	1510890	1511156	Uncharacterized protein	type VI secretion and effectors
1341	1511116	1511916	Putative N-formylglutamate amidohydrolase	type VI secretion and effectors
1342	1512722	1513879	Probable amidohydrolase/peptidase	type VI secretion and effectors
1343	1514852	1515355	ImpB	type VI secretion and effectors
1344	1515387	1516865	Uncharacterized protein ImpC	type VI secretion and effectors
1345	1516872	1517303	Type VI secretion system lysozyme-related protein	type VI secretion and effectors
1346	1517306	1519072	Protein ImpG/VasA	type VI secretion and effectors
1347	1519036	1520049	Uncharacterized protein ImpH/VasB	type VI secretion and effectors
1348	1520052	1521281	Type VI secretion system FHA domain-containing protein	type VI secretion and effectors
1349	1521281	1521802	Type VI secretion lipoprotein, VC_A0113 family	type VI secretion and effectors
1350	1521805	1523142	Uncharacterized protein ImpJ/VasE	type VI secretion and effectors
1351	1523159	1523935	ImpK/VasF outer membrane protein	type VI secretion and effectors
1352	1523951	1526551	Type VI secretion ATPase, ClpV1 family	type VI secretion and effectors
1354	1528092	1528655	Type VI secretion-associated protein, VC_A0118 family	type VI secretion and effectors
1355	1528667	1530106	Type VI secretion-associated protein, VC_A0119 family	type VI secretion and effectors
1356	1530132	1533629	Type VI secretion protein IcmF	type VI secretion and effectors
1357	1533681	1535114	ImpA domain protein	type VI secretion and effectors

Table S1. Cont.

Gene ID	Start codon	End codon	Gene product	Gene class
1658	1902811	1903329	Hcp protein	type VI secretion and effectors
1658	1902811	1903329	Hcp protein	type VI secretion and effectors
1659	1903442	1905304	Putative Rhs accessory genetic element	type VI secretion and effectors
1661	1905840	1910027	Putative membrane-bound sugar-binding protein	type VI secretion and effectors
3395	3955198	3956988	Similar to unknown protein and some similarities with VgrG protein	type VI secretion and effectors
3496	4077924	4078403	Type VI secretion system effector, Hcp1 family	type VI secretion and effectors
3496	4077924	4078403	Type VI secretion system effector, Hcp1 family	type VI secretion and effectors
195	223640	223894	Sec-independent protein translocase protein tatA/E homolog 1	twin arginine translocation
196	223898	224470	Twin arginine-targeting protein translocase TatB	twin arginine translocation
197	224474	225241	Sec-independent protein translocase, TatC subunit	twin arginine translocation
709	792076	793680	Transporter with twin-arginine translocation signal	twin arginine translocation
82	99734	100234	Regulatory protein PecS	regulation
113	136147	136899	Transcriptional activator protein expR	regulation
114	136865	137503	N-acylhomoserine lactone synthase YpeI	regulation
267	306191	306487	DNA-binding protein fis	regulation
278	316144	318090	Regulatory protein CsrD	regulation
695	773642	774034	Global regulatory protein RsmC	regulation
711	794800	795255	MarR family transcriptional regulator MfbR	regulation
721	806008	806772	Pectin degradation repressor protein kdgR	regulation
1122	1260968	1263829	Sensor histidine kinase/response regulator RcsC	regulation
1123	1263891	1264541	Capsular synthesis regulator component B (RscB)	regulation
1201	1351527	1351973	Negative regulator Fur	regulation
1353	1526554	1528092	VasH	regulation
1978	2269899	2270798	Hex regulon repressor	regulation
2020	2314757	2315773	Response regulator of RpoS ExpM	regulation
2042	2338392	2339117	Oligogalacturonate-specific porin kdgM	regulation

Table S1. Cont.

Gene ID	Start codon	End codon	Gene product	Gene class
2254	2597128	2597919	KdgR	regulation
2257	2600926	2603097	Diguanylate cyclase with PAS/PAC and GAF sensors	regulation
2264	2610546	2611214	Two-component response regulator of virulence determinant PhoP	regulation
2265	2611270	2612721	Virulence sensor histidine kinase phoQ	regulation
2296	2642672	2643655	HrpS	regulation
2298	2644098	2644739	HrpY	regulation
2299	2644773	2646239	HrpX	regulation
2300	2646505	2647059	HrpL	regulation
2485	2864704	2865141	Transcriptional regulator slyA 1	regulation
2665	3078279	3078860	Flagellum biosynthesis transcription activator (FlhC)	regulation
2666	3078860	3079210	Transcriptional activator FlhD	regulation
2695	3138500	3139156	ExpA protein	regulation
2758	3223622	3224437	PecT HexA	regulation
3043	3565429	3566946	Diguanylate cyclase with PAS/PAC and GAF sensors	regulation
3044	3567721	3568356	EAL domain containing protein involved in flagellar function	regulation
3129	3658530	3659045	S-ribosylhomocysteine lyase 1 LuxS	regulation
3133	3662807	3662992	Carbon storage regulator homolog RsmA	regulation
3245	3787478	3788470	RNA polymerase sigma factor RpoS	regulation
3273	3820376	3823141	Signal transduction histidine-protein kinase BarA ExpS	regulation
3305	3862095	3864044	Bifunctional 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase	regulation
3400	3963238	3965712	Response regulator receiver modulated diguanylate cyclase/phosphodiesterase	regulation
3555	4149855	4150670	Hth-type transcriptional regulator pir	regulation
3767	4427445	4428077	Catabolite activator protein (CRP)	regulation
3819	4490476	4491177	Cyclic diguanylate phosphodiesterase (EAL) domain protein	regulation
3820	4491209	4491967	Diguanylate phosphodiesterase	regulation
4003	4711767	4714280	Cyclic di-GMP-binding protein, Cellulose synthase operon protein B	regulation

Table S2. *Dickeya solani*-specific ORFs not present in other *Dickeya* or *Pectobacterium* species used in the genome comparison. The ORFs present in predicted horizontally acquired genomic islands are marked with grey color.

Gene ID	Improved annotation	COG description	Closest homolog	BlastX coverage	Identity/Similarity at protein level
185	Permease, drug/metabolite transporter family	Permeases of the drug/metabolite transporter (DMT) superfamily	<i>Rahnella aquatilis</i>	99%	65%/78%
397	Transcriptional regulator Icc related protein	Predicted phosphohydrolases	<i>Vibrio cholerae</i>	99%	41%/59%
398	Putative uncharacterized protein	null	<i>Glaciecola arctica</i>	98%	56%/73%
399	Putative uncharacterized protein	null	<i>Glaciecola arctica</i>	98%	52%/71%
401	Uncharacterized protein	null	null		
412	Putative type I restriction-modification system, M subunit	Type I restriction-modification system methyltransferase subunit	<i>Pectobacterium wasabiae</i> SCC3193	99%	95%/96%
413	Type I restriction-modification	Restriction endonuclease S subunits	<i>Shewanella frigidimarina</i>	94%	48%/65%
414	Type I site-specific restriction-modification system, R subunit	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases	<i>Pectobacterium wasabiae</i> SCC3193	99%	96%/98%
535	Putative uncharacterized protein	null	<i>Escherichia coli</i>	99%	56%/73%
639	Putative HsdS	Restriction endonuclease S subunits	<i>Escherichia coli</i>	99%	81%/89%
640	Type I restriction enzyme	Type I restriction-modification system methyltransferase subunit	<i>Shigella flexneri</i>	99%	88%/94%
641	Type I restriction enzyme, R subunit	Type I site-specific restriction-modification system, R (restriction) subunit and	<i>Escherichia coli</i>	99%	84%/90%
647	Transcriptional regulator, TetR family	Transcriptional regulator	<i>Burkholderia graminis</i>	91%	85%/90%

Table S2. Cont.

Gene ID	Improved annotation	COG description	Closest homolog	BlastX coverage	Identity/Similarity at protein level
716	Putative ABC-type amino-acid transporter periplasmic solute-binding protein	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	<i>Brenneria sp.</i>	93%	83%/90%
718	ABC-type glutamine transport system, permease component	ABC-type amino acid transport system, permease component	<i>Brenneria sp.</i>	99%	81%/91%
720	Endoribonuclease-domain protein	Putative translation initiation inhibitor, yjgF family	<i>Pseudomonas psychrotolerans</i>	100%	87%/95%
722	D-serine deaminase (D-serine dehydratase) protein	null	<i>Brenneria sp.</i>	97%	71%/80%
772	ISTde1, transposase	Predicted transposase	<i>Alteromonas macleodii</i>	98%	83%/90%
906	Nuclear receptor binding factor related protein	NADPH:quinone reductase and related Zn-dependent oxidoreductases	<i>Ralstonia solanacearum</i>	99%	45%/62%
978	Probable efflux transporter protein, acriflavin resistance protein family	Cation/multidrug efflux pump	<i>Sinorhizobium fredii</i>	99%	73%/87%
979	Efflux transporter	Membrane-fusion protein	<i>Sinorhizobium fredii</i>	99%	47%/66%
980	Putative component of multidrug efflux system (RND family)	Membrane-fusion protein	<i>Sinorhizobium meliloti</i>	99%	49%/72%
981	Putative NADPH nitroreductase protein	Nitroreductase	<i>Ralstonia solanacearum</i>	100%	66%/80%
1265	Secreted protease; subtilase family	null	<i>Xanthomonas translucens</i>	99%	49%/64%
1369	Phosphopantetheinyl transferase component of siderophore synthetase	Phosphopantetheinyl transferase component of siderophore synthetase	<i>Collimonas fungivorans</i>	85%	42%/56%

Table S2. Cont.

Gene ID	Improved annotation	COG description	Closest homolog	BlastX coverage	Identity/Similarity at protein level
1372	DevC protein	ABC-type antimicrobial peptide transport system, permease component	<i>Serratia sp.</i>	99%	71%/83%
1374	Polyketide-type polyunsaturated fatty acid synthase	Polyketide synthase modules and related proteins	<i>Xenorhabdus bovienii</i>	93%	55%/69%
1375	Polyunsaturated fatty acid synthase	Polyketide synthase modules and related proteins	<i>Serratia plymuthica</i>	98%	65%/76%
1376	PfaD family protein	Glutamate-1-semialdehyde aminotransferase	<i>Serratia plymuthica</i>	98%	77%/85%
1377	3-ketoacyl-(acyl-carrier-protein) reductase)	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	<i>Serratia sp.</i>	99%	79%/88%
1378	Thioester reductase	Putative dehydrogenase domain of multifunctional non-ribosomal peptide synthetases	<i>Serratia sp.</i>	95%	67%/80%
1384	ABC transporter ATP binding protein	ABC-type multidrug transport system, ATPase component	<i>Serratia plymuthica</i>	99%	73%/87%
1385	ABC transporter permease	ABC-type multidrug transport system, permease component	<i>Xenorhabdus bovienii</i>	99%	67%/81%
1392	Cog0684, demethylmenaquinone methyltransferase protein	Demethylmenaquinone methyltransferase	<i>Sinorhizobium fredii</i>	95%	81%/93%
1393	Uncharacterized protein	Aspartate/tyrosine/aromatic aminotransferase	<i>Alicyclophilus denitrificans</i>	73%	77%/84%
1432	Iron transport system regulatory protein FitR	Transcriptional regulators	<i>Pantoea sp.</i>	98%	60%/76%
1473	Uncharacterized HTH-type transcriptional regulator ycaN	Transcriptional regulator	<i>Xylella fastidiosa</i>	99%	77%/87%

Table S2. Cont.

Gene ID	Improved annotation	COG description	Closest homolog	BlastX coverage	Identity/Similarity at protein level
1478	Carboxymuconolactone decarboxylase family protein	Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit	<i>Rhizobium leguminosarum</i>	100%	77%/85%
1479	Putative amidohydrolase/decarboxylase	Predicted metal-dependent hydrolase of the TIM-barrel fold	<i>Rhizobium leguminosarum</i>	96%	76%/85%
1622	Modification methylase HgiDII	Site-specific DNA methylase	<i>Serratia odorifera</i>	98%	99%/99%
1646	NAD(P)H dehydrogenase YwrO	Putative NADPH-quinone reductase (modulator of drug activity B)	<i>Klebsiella oxytoca</i>	99%	71%/81%
1648	L-arabinonolactonase	Gluconolactonase	<i>Shewanella sp.</i>	98%	70%/79%
1662	Leucine Rich repeat protein	null	<i>Salmonella enterica</i>	97%	65%/84%
2161	Superfamily I DNA and RNA helicase and helicase subunit	Superfamily I DNA and RNA helicases and helicase subunits	<i>Pseudomonas fluorescens</i>	99%	62%/76%
2346	Conserved hypothetical protein	null	<i>Pseudomonas sp.</i>	100%	82%/89%
2853	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	Superfamily II DNA/RNA helicases, SNF2 family	<i>Hafnia alvei</i>	99%	64%/79%
2854	Conserved uncharacterized protein	null	<i>Enterobacter radicincitans</i>	100%	90%/94%
2855	Uncharacterized 24.6 kDa protein in ccpA 3'region; ORF2	Outer membrane protein and related peptidoglycan-associated (lipo)proteins	<i>Enterobacter radicincitans</i>	100%	97%/97%
2871	Aspartate aminotransferase A protein	Aspartate/tyrosine/aromatic aminotransferase	<i>Acinetobacter ursingii</i>	100%	71%/84%
2872	Dimethylmenaquinone methyltransferase	Demethylmenaquinone methyltransferase	<i>Acinetobacter ursingii</i>	100%	75%/86%

Table S2. Cont.

Gene ID	Improved annotation	COG description	Closest homolog	BlastX coverage	Identity/Similarity at protein level
2972	Benzoate degradation transcriptional regulator	Transcriptional regulator	<i>Cupriavidus necator</i>	98%	40%/60%
2974	Putative Ribonuclease E inhibitor RraA/Dimethylmenaquinone methyltransferase	Demethylmenaquinone methyltransferase	<i>Herbaspirillum seropedicae</i>	92%	61%/75%
2975	Dimethylmenaquinone methyltransferase	Demethylmenaquinone methyltransferase	<i>Cupriavidus necator</i>	95%	56%/75%
2980	Probable NADPH quinone oxidoreductase	NADPH:quinone reductase and related Zn-dependent oxidoreductases	<i>Pseudomonas psychrotolerans</i>	100%	74%/83%
2983	AtfA_1	Predicted acyltransferases	<i>Serratia sp.</i>	98%	44%/64%
3985	Putative demethylmenaquinone methyltransferase	Demethylmenaquinone methyltransferase	<i>Pelosinus fermentans</i>	98%	57%/75%
3986	CatR	Transcriptional regulator	<i>Cupriavidus necator</i>	95%	52%/72%

Table S3. Predicted horizontally acquired genomic islands present in *Dickeya solani* D s0432-1.

Gene ID	Start-stop codons	Size (bp)	ORFs	Description	Highest BlastN coverage	Prediction method
106-115	127938-140768	12831	10	NRPS, fatty acids breakdown and AHL	100% <i>D. dadantii</i> 3937	PAI-IDA
209-217	236910-250266	13357	9	Ribosomal DNA and potassium transport system	99% <i>D. dadantii</i> 3937	SIGI-HMM and PAI-IDA
244-260	279841-300071	20231	17	Ribosomal DNA and ABC-type amino acid transporter	99% <i>D. dadantii</i> 3937	SIGI-HMM
384-416	434339-472878	38540	33	Ribosomal DNA and Type I restriction-modification system	46% <i>D. chrysanthemi</i> 1591	PAI-IDA
507-532	562474-591786	29313	26	Capsular polysaccharide operon	72% <i>D. dadantii</i> 3937	SIGI-HMM and PAI-IDA
747-772	833028-859172	26145	26	ABC-type sugar transport system and T6SS effectors	68% <i>D. dadantii</i> 3937	PAI-IDA
971-993	1085034-1109939	24906	23	Multidrug efflux system RND	31% <i>D. dadantii</i> 3937	SIGI-HMM and PAI-IDA
1373-1385	1551051-1596720	45670	13	PKS/FAS/NRPS cluster and ABC transporters (region 3 in Figure 2)	11% <i>Serratia</i> sp. AS13	PAI-IDA
1416-1431	1633830-1650760	16931	16	ABC-type dipeptide transport and multidrug resistance	77% <i>D. dadantii</i> 3937	IslandPick and PAI-IDA
1511-1516	1737476-1742862	5387	7	ABC-type phosphate/phosphonate transport system	66% <i>D. dadantii</i> 3937	SIGI-HMM
1600-1632	1844919-1881493	36575	33	ABC-type amino acid transport system	62% <i>D. dadantii</i> 3937	PAI-IDA
1719-1726	1974352-1984501	10150	8	Sugar metabolism	100% <i>D. dadantii</i> 3937	SIGI-HMM
1906-1913	2190139-2197831	7693	8	Citrate metabolism	100% <i>D. dadantii</i> 3937	SIGI-HMM
2146-2164	2459309-2481903	22595	19	Transposase and integrase	56% <i>D. dadantii</i> 3937	PAI-IDA
2627-2666	3040936-3079210	38275	40	Flagella and chemotaxis related genes	100% <i>D. dadantii</i> 3937	PAI-IDA
2822-2856	3297464-3346949	49486	35	T2SS and uncharacterized proteins	79% <i>D. dadantii</i> 3937	PAI-IDA

Table S3. *Cont.*

Gene ID	Start-stop codons	Size (bp)	ORFs	Description	Highest BlastN coverage	Prediction method
2959-2971	3469779-3485315	15537	13	Thiamine biosynthesis and multidrug resistance	55% D. dadantii 3937	PAI-IDA
3390-3403	3951700-3971993	20294	14	Uncharacterized proteins	98% D. dadantii 3937	PAI-IDA
3637-3654	4246194-4321047	74854	18	PKS cluster (region 2 in Figure 2)	97% D. paradisiaca 703	PAI-IDA
3690-3711	4369549-4384720	15172	22	Ribosomal proteins	100% D. dadantii 3937	SIGI-HMM and PAI-IDA