

Figure S1. Phylogenetic analysis of the strain BRDJ. (A) Phylogenetic tree based on 16S rRNA using the neighbor-joining method to compare BRDJ to other strains inside the *Burkholderia*. The scale bar indicates the expected changes per site substitution per nucleotide. The bootstrap values (%) based on 1000 bootstrap replicates are marked on each node. (B) Phylogenetic tree based on *recA*. The scale bar indicates the expected changes per site substitution per nucleotide. The bootstrap values (%) based on 1000 bootstrap replicates are marked on each node.

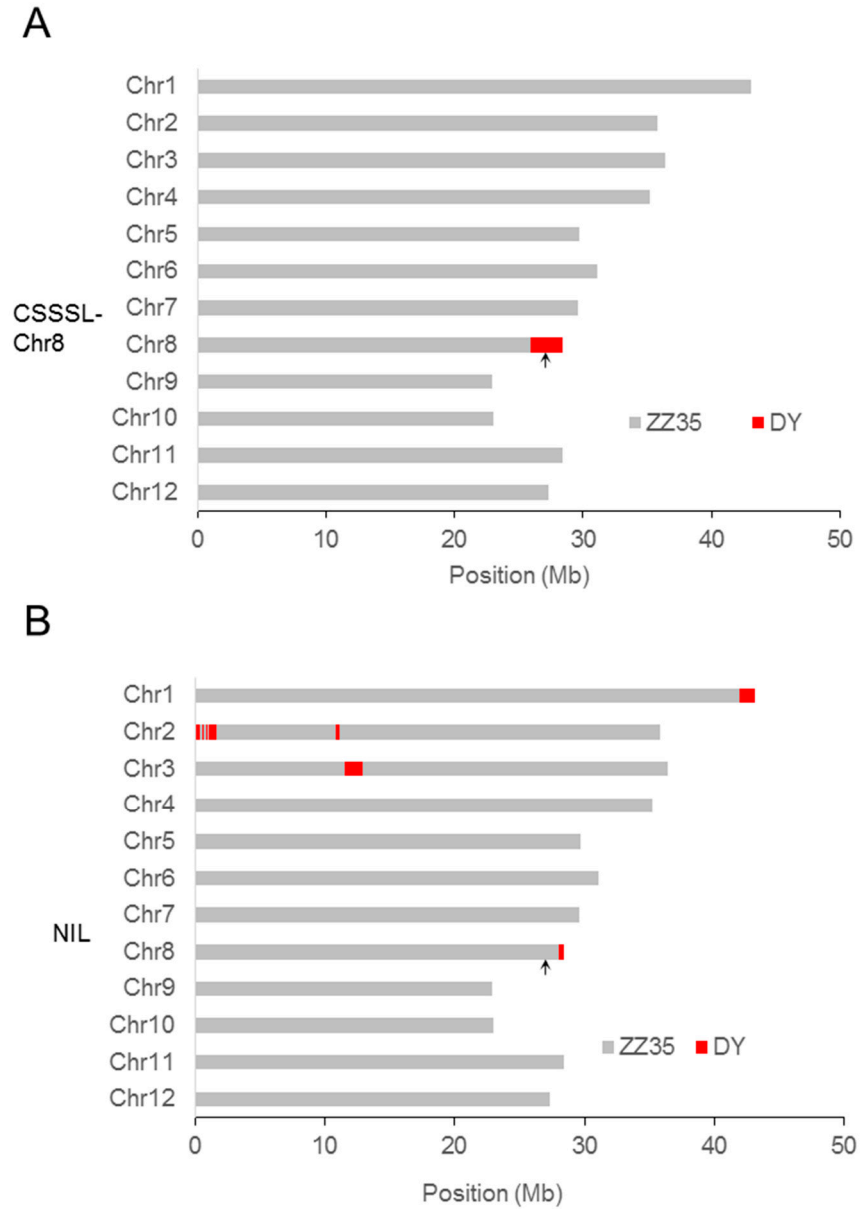


Figure S2. Diagram of chromosome composition for CSSSL-Chr8 (A) and NIL (B). NIL, near-isogenic line; CSSSL-Chr8, chromosome 8 single-segment substitution line. The arrows indicate the position of *OsCERK1^{DY}* and *OsCERK1^{ZZ35}*, respectively.

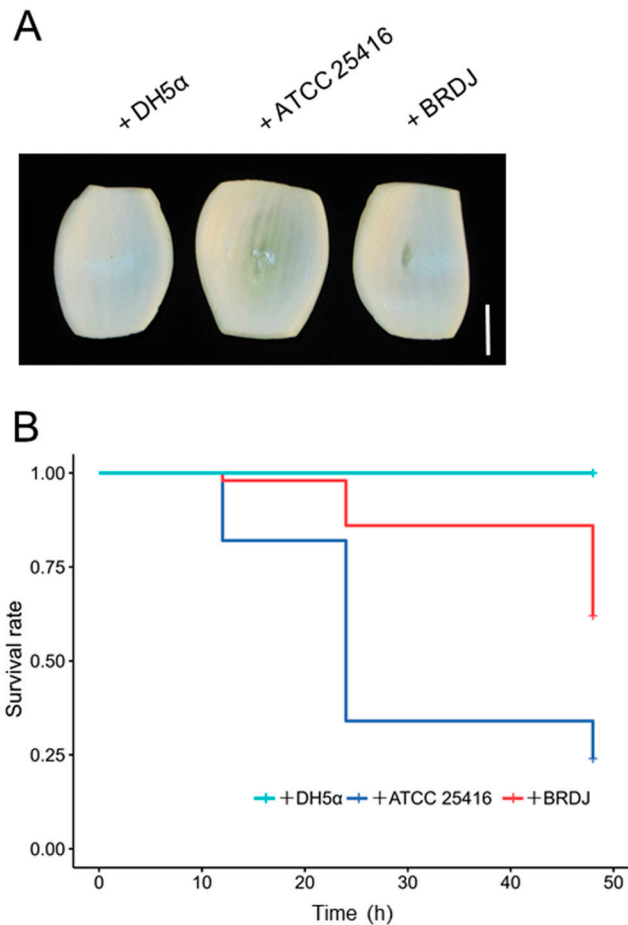


Figure S3 Pathogenicity test on onion and worm.

(A) Tissue maceration symptom of onion slices after 48 h incubation at 28°C. Onion slices were wounded by pipette tip, 10μL culture of the corresponding strain was inoculated. The experiments were performed three times. One of the representative results is shown. Scale bar, 2 cm. (B) Survival curve of *Caenorhabditis elegans* in a fast-killing assay. The experiment were repeated three times. One of the representative results is shown. The curves were plotted using the Kaplan–Meier method. The log-rank test showed a significant difference ($P < 0.0001$) between ATCC 25416 and BRDJ treatment.

Table S1. Genes linked to plant growth promoting and biocontrol activities in the strain BRDJ genome.

PGP Activities	Gene name	Gene Annotation	Chromosome Location
ACC Deaminase			
	<i>acdS</i>	1-aminocyclopropane-1-carboxylate deaminase	Chr2:409477-410493 -
Siderophores			
Pyochelin	<i>pchG</i>	pyochelin biosynthetic protein PchG	Chr2:2791298-2792350 -
	<i>pchF</i>	pyochelin synthetase	Chr2:2792347-2797821 -
	<i>pchE</i>	dihydroaeruginosic acid synthetase	Chr2:2797818-2802140 -

Table S1 Continued

PGP Activities	Gene name	Gene Annotation	Chromosome Location
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Pyoverdin	<i>pchR</i>	AraC family transcriptional regulator, transcriptional activator of the genes for pyochelin and ferripyochelin receptors	Chr2:2802351-2803250 -
	<i>pchD</i>	pyochelin biosynthesis protein PchD	Chr2:2803531-2805162 +
	<i>pchC</i>	pyochelin biosynthetic protein PchC	Chr2:2805159-2805932 +
	<i>pchB</i>	isochorismate pyruvate lyase	Chr2:2805929-2806234 +
	<i>pvdE</i>	putative pyoverdin transport system ATP-binding/permease protein	Chr3:1962159-1963904 -
	<i>pvdA, SIDA</i>	L-ornithine N5-monooxygenase	
	Phosphate Metabolism		
	<i>pstS</i>	phosphate transport system substrate-binding protein	Chr3:1457432-1458466 +
	<i>pstC</i>	phosphate transport system permease protein	Chr3:1458561-1459547 +
	<i>pstA</i>	phosphate transport system permease protein	Chr3:1459544-1460437 +
	<i>pstB</i>	phosphate transport system ATP-binding protein	Chr3:1460459-1461301 +
	<i>phoU</i>	phosphate transport system protein	Chr3:1461320-1462024 +
	<i>phoB</i>	two-component system, OmpR family, phosphate regulon response regulator PhoB	Chr3:1462057-1462758 +
	<i>phoR</i>	two-component system, OmpR family, phosphate regulon sensor histidine kinase PhoR	Chr3:1462816-1464135 +
	<i>pstS</i>	phosphate transport system substrate-binding protein	Chr3:1747532-1748254 +
	<i>phoH, phoL</i>	phosphate starvation-inducible protein PhoH and related proteins	Chr3:3272707-3273753 +
Plant Hormones	<i>iaaH</i>	indoleacetamide hydrolase	Chr1:664183-665646 -
	<i>trpB</i>	tryptophan synthase beta chain	Chr2:1160344-1161537 +
	<i>trpA</i>	tryptophan synthase alpha chain	Chr2:1162439-1163254 +

Table S1 Continued

PGP Activities	Gene name	Gene Annotation	Chromosome Location
	<i>trpC</i>	indole-3-glycerol phosphate synthase	Chr3:576638-577423 -
	<i>trpD</i>	anthranilate phosphoribosyltransferase	Chr3:577453-578484 -
	<i>trpG</i>	anthranilate synthase component II	Chr3:578498-579088 -
	<i>trpE</i>	anthranilate synthase component I	Chr3:579102-580595 -
Volatiles			
Acetoin	<i>acoR</i>	sigma-54 dependent transcriptional regulator, acetoin dehydrogenase operon transcriptional activator AcoR	Chr2:2759917-2761821 +
	<i>acoB</i>	acetoin:2,6-dichlorophenolindophenol oxidoreductase subunit beta	Chr3:2260355-2261359 -
	<i>acoA</i>	acetoin:2,6-dichlorophenolindophenol oxidoreductase subunit alpha	Chr3:2261414-2262397 -
2,3-Butanediol	<i>BDH, butB</i>	(R,R)-butanediol dehydrogenase / meso-butanediol dehydrogenase / diacetyl reductase	Chr2:127771-128892 -

Isoprene	<i>butA, budC</i>	meso-butanediol dehydrogenase / (S,S)-butanediol dehydrogenase / diacetyl reductase	Chr3:2262475-2263251 -
	<i>ilvC</i>	ketol-acid reductoisomerase	Chr3:2824437-2825453 -
	<i>ilvH, ilvN</i>	acetolactate synthase I/III small subunit	Chr3:2825558-2826049 -
	<i>ilvB, ilvG, ilvI</i>	acetolactate synthase I/II/III large subunit	Chr3:2826161-2827843 -
	<i>ilvD</i>	dihydroxy-acid dehydratase	Chr3:3020573-3022246 +
	<i>ilvE</i>	branched-chain amino acid aminotransferase	Chr3:3215940-3216857 +
	<i>ilvA, tdcB</i>	threonine dehydratase	Chr3:3322555-3324078 +
	<i>ispH, lytB</i>	4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase	Chr2:3423723-3424478 +
	<i>gcpE, ispG</i>	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase	Chr3:2231962-2233212 -
	<i>ispF</i>	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	Chr3:2374823-2375308 -
	<i>ispD</i>	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	Chr3:2375337-2375984 -

Table S1 Continued

PGP Activities	Gene name	Gene Annotation	Chromosome Location
Biocontrol			
Chitinase		chitinase	Chr3:2009034-2010389 -
Phenazine	<i>phzG</i>	dihydrophenazinedicarboxylate synthase	Chr1:891157-891795 -
	<i>phzF</i>	trans-2,3-dihydro-3-hydroxyanthranilate isomerase	Chr1:891833-893041 -
	<i>phzE</i>	2-amino-4-deoxychorismate synthase	Chr1:893086-895017 -
	<i>phzD</i>	trans-2,3-dihydro-3-hydroxyanthranilic acid synthase	Chr1:895014-895637 -
	<i>phzA_B</i>	phenazine biosynthesis protein	Chr1:895661-896146 -
	<i>rhII, phzI, soll,</i>	acyl homoserine lactone synthase	Chr2:2466342-2466875 +
	<i>cepl, tofl</i>		
Pyrrolnitrin	<i>pmA, rebH, ktzQ</i>	tryptophan 7-halogenase	Chr1:235213-236829 +
	<i>pmB</i>	monodechloroaminopyrrolnitrin synthase	Chr1:236829-237914 +
	<i>ctcP, cts4, pmC</i>	tetracycline 7-halogenase / FADH2 O2-dependent halogenase	Chr1:237973-239673 +
	<i>pmD</i>	aminopyrrolnitrin oxygenase	Chr1:239698-240810 +

Table S2. Animals and plants pathogenicity-related genes in the strain BRDJ genome.

Host species	Gene Name	Identity	Gene Function	Mutant Phenotype	Disease Name	Chromosome Location
Plants						
<i>Allium cepa</i>	PidS	84.6	Sensor histidine kinase / two-component regulatory system	reduced virulence	Panicle blight	Chr3:110284-111750-
	PidR	98.7	Response regulator/ two-component regulatory	reduced virulence	Panicle blight	Chr3:111887-112579-
	qsmR	82.3	IcIR-type transcriptional regulator	reduced virulence	Bacterial panicle blight of rice	Chr3:1344746-1345570-

	flhD	90	Flagellar transcriptional regulator	reduced virulence	Bacterial panicle blight of rice	Chr3:225050-225352+
<i>Medicago sativa</i>	BceR	83.3	response regulator	unaffected pathogenicity	Nosocomial infections	Chr1:1017605-1018252+
	BceR	100	response regulator	unaffected pathogenicity	Nosocomial infections	Chr2:1839081-1839728-

Table S2 Continued

Host species	Gene Name	Identity	Gene Function	Mutant Phenotype	Disease Name	Chromosome Location
<i>Oryza sativa</i>	tofR	77.8	Produce toxoflavin	reduced virulence	Panicle blight	Chr2:2464820-2465539-
	GyrA	93.8	DNA gyrase	chemistry target: resistance to chemical	Bacterial grain rot	Chr3:1176426-1178981+
	aroA	88.7	3-phosphoshikimate 1-carboxyvinyltransferase	reduced virulence	Panicle blight	Chr3:1183145-1184449+
	raxP	70.1	Sulfate adenylyltransferase required for Ax21 activity	increased virulence	Bacterial blight	Chr3:2728642-2729526+
	aroB	86.1	3-dehydroquinate synthase	reduced virulence	Panicle blight	Chr3:406616-407695+
<i>Pyrus communis</i>	tssC-1	76.8	T6SS-1 component	unaffected pathogenicity	Fire blight	Chr2:1914899-1916407+
<i>Raphanus sativus</i>	XC_2203	72.3	Nucleotide diphosphate kinase	reduced virulence	Black rot disease	Chr3:2235768-2236193-
<i>Solanum lycopersicum</i>	fabG1	80.2	3-ketoacyl-acyl carrier protein reductase	lethal	Bacterial wilt	Chr3:1259785-1260534+
Animals						
<i>Anas platyrhynchos</i>	cheA	74.4	Chemotaxis protein	unaffected pathogenicity	Meningitis	Chr3:228533-230806+
	cheW	71.8	Chemotaxis protein	unaffected pathogenicity	Meningitis	Chr3:230858-231373+
<i>Caenorhabditis elegans</i>	oqxB	71	Multidrug efflux pump	reduced virulence	Pneumonia	Chr2:2491195-2494407-
	cstA	70.6	Peptide-utilizing carbon starvation protein	reduced virulence	Salmonellosis	Chr2:3432824-3434902-
	paaE	98.1	phenylacetic acid catabolism	reduced virulence	Cystic fibrosis-like conditions	Chr3:338946-340034-
	paaD	95.2	phenylacetic acid catabolism	reduced virulence	Cystic fibrosis-like conditions	Chr3:340040-340600-
	paaC	94	phenylacetic acid catabolism	reduced virulence	Cystic fibrosis-like conditions	Chr3:340624-341427-
	paaB	98.9	phenylacetic acid catabolism	reduced virulence	Cystic fibrosis-like conditions	Chr3:341438-341722-
	paaA	98.2	phenylacetic acid catabolism	reduced virulence	Cystic fibrosis-like conditions	Chr3:341760-342758-
<i>Galleria mellonella</i>	atsR	90.4	global virulence regulator	increased virulence (hypervirulence)	Cystic fibrosis-like conditions	Chr2:394965-396725-

	BceD	98	Protein tyrosine phosphatases	reduced virulence	Cystic fibrosis-like conditions	Chr2:1011100-1011543+
	BCAM1331	88.2	Tyrosine kinases	reduced virulence	Cystic fibrosis-like conditions	Chr2:1629150-1631366+

Table S2 Continued

Host species	Gene Name	Identity	Gene Function	Mutant Phenotype	Disease Name	Chromosome Location
	flmQ	87.9	flagellin glycosyltransferase	reduced virulence	Cystic fibrosis-like conditions	Chr3:208838-211177-
	BCAL2200	95	Protein tyrosine phosphatases	reduced virulence	Cystic fibrosis-like conditions	Chr3:2614977-2615459-
	ntnC	93.1	activator protein	unaffected pathogenicity	Cystic fibrosis-like conditions	Chr3:2682121-2683638-
	BCAL0960	94	O-oligosaccharyltransferase	reduced virulence	Cystic fibrosis	Chr3:3225197-3226951-
<i>Homo sapiens</i>	BceF	96.8	Tyrosine Kinase	reduced virulence	Cystic fibrosis	Chr2:1012766-1014991+
<i>Locusta migratoria</i>	MakatG1	70.5	Catalase-peroxidase	unaffected pathogenicity	No data found	Chr3:799462-801648+
<i>Mus musculus</i>	pchB	70.3	Isochorismate pyruvate lyase	unaffected pathogenicity	Infections	Chr2:2805929-2806234+
	VK055_195273.1		Betaine aldehyde dehydrogenase	unaffected pathogenicity	Pneumonia	Chr2:2916874-2918343+
	wcbS	92.5	Capsule	reduced virulence	Melioidosis	Chr3:893383-894300+
	wcbT	89.3	Capsule	reduced virulence	Melioidosis	Chr3:894365-895693+
	IsfA	80.2	1-Cys peroxiredoxin with thioldependent peroxidase activity	reduced virulence	Opportunistic infections	Chr3:920428-921066+
	Hfq	88.3	RNA Chaperone	reduced virulence	Pertussis	Chr3:2226753-2227004-
	clpP	74	ATP-dependent Clp protease proteolytic subunit	reduced virulence	Nosocomial infections	Chr3:2355346-2355972-
	BPSL2105	92	Putative phage-shock protein A (PspA) homologue	reduced virulence	Melioidosis	Chr3:2385713-2386393+