

Genomic Analysis of Endophytic *Bacillus cereus* T4S and Its Plant Growth-promoting Traits

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Table S1. Biochemical, cultural characterization of *B. cereus* T4S.

Characteristics	Result
Gram reaction	+
Shape	rod
Catalase	+
Starch hydrolysis	+
Nitrate	+
Oxidase	+
Citrate	+
Casein hydrolysis	+
Salt tolerance (% <i>v/v</i>) (max)	5.5
Temperature range (°C)	25–45
pH	4–10
Fructose	+
Galactose	+
Sucrose	+
Glucose	+
Xylose	+
Raffinose	+
Mannitol	+
Maltose	+

Key: + = positive reaction.

Table S2. Genes involved in protein secretion systems.

Pathway	Gene	Product	Locus Tag
Sec (secretion) system	<i>secA</i>	preprotein translocase subunit <i>SecA</i>	HWX41_RS21805
	<i>secE/G/Y</i>	preprotein translocase subunit <i>SecE/G/Y</i>	HWX41_RS26260
	<i>secE/G/Y</i>	preprotein translocase subunit <i>SecE/G/Y</i>	HWX41_RS22075
	<i>secE/G/Y</i>	preprotein translocase subunit <i>SecE/G/Y</i>	HWX41_RS26435/HWX41_RS11560
Twin-arginine translocation (Tat) system	<i>yajC</i>	preprotein translocase subunit <i>YajC</i>	HWX41_RS02190
	<i>tatE/tatA</i>	protein translocase protein <i>TatE/TatA</i>	HWX41_RS13235
	<i>tatC</i>	protein translocase protein <i>TatC</i>	HWX41_RS13230
	<i>tatC</i>	twin-arginine translocase subunit <i>TatC</i>	HWX41_RS13230

Table S3. Genes involved in sulfur metabolism.

Pathway	Gene	Product	Locus Tag
Sulfate transport	<i>cysC</i>	adenylyl-sulfate kinase	HWX41_RS16845
	<i>sat</i>	sulfate adenylyltransferase	HWX41_RS16850
	<i>cysT</i>	sulfate transport system permease protein	HWX41_RS18405
	<i>cys</i>	sulfate transport system substrate-binding protein	HWX41_RS18410/HWX41_RS21870
	<i>cysW</i>	sulfate ABC transporter permease subunit <i>CysW</i>	HWX41_RS18400
	<i>cysK</i>	cysteine synthase A	HWX41_RS15030/HWX41_RS26760
	<i>cysS</i>	cysteine--tRNA ligase	HWX41_RS26230
	<i>sulP</i>	sulfate permease	HWX41_RS25435

Table S4. Genes involved in motility, biofilm formation, and chemotaxis.

Pathway	Gene	Product	Locus tag
Chemotaxis	<i>cheV</i>	chemotaxis protein <i>CheV</i>	HWX41_RS15615
	<i>che</i>	chemotaxis protein	HWX41_RS23355
	<i>cheW</i>	purine-binding chemotaxis protein <i>CheW</i>	HWX41_RS15745
	<i>che</i>	methyl-accepting chemotaxis protein	HWX41_RS07060/HWX41_RS2445
Flagella biosynthesis	<i>flgD</i>	flagellar basal body rod modification protein <i>FlgD</i>	HWX41_RS15635
	<i>fliK</i>	flagellar hook-length control protein <i>FliK</i>	HWX41_RS15640
	<i>flhB</i>	flagellar type III secretion system protein <i>FlhB</i>	HWX41_RS15485
	<i>flgB</i>	flagellar basal body rod protein <i>FlgB</i>	HWX41_RS15680
	<i>flhA</i>	flagellar biosynthesis protein <i>FlhA</i>	HWX41_RS15480
	<i>flgE</i>	flagellar hook protein <i>FlgE</i>	HWX41_RS15630
	<i>fliL</i>	flagellar protein export ATPase <i>FliI</i>	HWX41_RS15650
	<i>flgG</i>	flagellar basal-body rod protein	HWX41_RS15470
	<i>flg</i>	flagellar motor switch protein	HWX41_RS15660
	<i>flgG</i>	flagellar biosynthesis protein <i>FlgG</i>	HWX41_RS15685
	<i>flhF</i>	flagellar biosynthesis protein <i>FlhF</i>	HWX41_RS15475
	<i>fliR</i>	flagellar type III secretion system protein <i>FliR</i>	HWX41_RS15490
	<i>fliF</i>	flagellar M-ring protein <i>FliF</i>	HWX41_RS15665
	<i>fliH</i>	flagellar assembly protein H	HWX41_RS15655
	<i>fliQ</i>	flagellar biosynthetic protein <i>FliQ</i>	HWX41_RS15495
	<i>fliS</i>	flagellar protein <i>FliS</i>	HWX41_RS15690
	<i>flp</i>	flagellar type III secretion system pore protein <i>FliP</i>	HWX41_RS15500
	<i>fliN</i>	flagellar motor switch protein <i>FliN</i>	HWX41_RS15510/HWX41_RS15520
	<i>fliC</i>	flagellar basal body rod protein <i>FlgC</i>	HWX41_RS15675/HWX41_RS16785
	<i>fliY</i>	flagellar motor switch phosphatase <i>FliY</i>	HWX41_RS15740
	<i>fliE</i>	flagellar hook-basal body complex protein <i>FliE</i>	HWX41_RS15670

	<i>motA</i>	flagellar motor stator protein <i>MotA</i> /Chemotaxis protein <i>MotA</i>	HWX41_RS01775
	<i>flgK</i>	flagellar hook-associated protein <i>FlgK</i>	HWX41_RS15705
	<i>fliM</i>	flagellar motor switch protein <i>FliM</i>	HWX41_RS15515
	<i>motB</i>	flagellar motor protein <i>MotB</i> /Chemotaxis protein <i>MotB</i>	HWX41_RS01780/HWX41_RS04225
	ND	flagellar hook-associated protein 2 / protein 3	HWX41_RS15695
	ND	flagellin	HWX41_RS15700
	ND	flagellin	HWX41_RS15530
			HWX41_RS15535
Pilus and fimbriae biosynthesis	ND	isopeptide-forming domain-containing fimbrial protein	HWX41_RS27290
Biofilm formation	<i>efp</i>	elongation factor P	HWX41_RS03245
	<i>hfq</i>	RNA chaperone <i>Hfq</i>	HWX41_RS05840/HWX41_RS15770
	<i>crp</i>	<i>Crp/Fnr</i> family transcriptional regulator	HWX41_RS16660

Key: ND—not determined.

Table S5. Genes involved in attachment to plant surfaces.

Pathway	Gene	Product	Locus tag
LPS, Lipid A biosynthesis and modifications	<i>murF</i>	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	HWX41_RS25735
	<i>murA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	HWX41_RS21065/HWX41_RS21305
	<i>murB</i>	UDP-N-acetylmuramate dehydrogenase	HWX41_RS04775
	<i>murC</i>	UDP-N-acetylmuramate--L-alanine ligase	HWX41_RS00935
	<i>murE</i>	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase	HWX41_RS04750
	<i>murD</i>	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase	HWX41_RS04760
	<i>murG</i>	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	HWX41_RS04770
	<i>galE</i>	UDP-glucose 4-epimerase <i>GalE</i>	HWX41_RS21410
	<i>wecB</i>	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	HWX41_RS21750
	ND	UDP-N-acetylmuramate dehydrogenase	HWX41_RS22310
	ND	UDP-glucosyltransferase	HWX41_RS11130
	ND	UDP-galactose-lipid carrier transferase	HWX41_RS15090
	ND	UDP-glucose/GDP-mannose dehydrogenase family protein	HWX41_RS25510
	<i>glmU</i>	bifunctional UDP-N-acetylglucosamine diphosphorylase	HWX41_RS26655
	<i>glmU</i>	glucosamine-1-phosphate N-acetyltransferase <i>GlmU</i>	HWX41_RS26655
	<i>uppP</i>	bacitracin resistance undecaprenyl-diphosphatase, undecaprenyl-diphosphate phosphatase <i>UppP</i>	HWX41_RS17035
			HWX41_RS27450
LPS, O-antigen biosynthesis	<i>rfbD</i>	dTDP-4-dehydrorhamnose reductase	HWX41_RS17900
	<i>rfbB</i>	dTDP-glucose 4,6-dehydratase	HWX41_RS17905
	<i>rfbC</i>	dTDP-4-dehydrorhamnose 3,5-epimerase	HWX41_RS17910

Key: ND— not determined.

Table S6. Genes involved in the protection against oxidative and nitrosative stress.

Pathway	Gene	Product	Locus tag
Degradation of superoxide anion radicals	<i>sodA</i>	superoxide dismutase	HWX41_RS20530/HWX41_RS02855
	<i>sodA</i>	superoxide dismutase family protein	HWX41_RS23120
	<i>sodA</i>	superoxide dismutase	HWX41_RS16575
Degradation of hydrogen peroxide	<i>katB</i>	catalase	HWX41_RS18175
	ND	manganese catalase family protein	HWX41_RS19840
	<i>kat</i>	catalase	HWX41_RS07625/HWX41_RS09520
Degradation of hydrogen peroxide and organic hydroperoxides	<i>tpx</i>	Thiol peroxidase	HWX41_RS01185
	<i>bcp</i>	thioredoxin-dependent thiol peroxidase	HWX41_RS25065
	<i>osmC</i>	<i>OsmC</i> family protein (peroxiredoxin osmc)	HWX41_RS23535
	<i>ahpC</i>	Peroxiredoxin	HWX41_RS24440
	<i>ahpF</i>	Alkyl hydroperoxide reductase subunit F	HWX41_RS24435
	ND	alkylphosphonate utilization protein	HWX41_RS25420
	ND	organic hydroperoxide resistance protein	HWX41_RS01930
Detoxification of peroxidized compounds	<i>bsaA</i>	glutathione peroxidase	HWX41_RS13745
	<i>grx</i>	glutaredoxin family protein	HWX41_RS22030/HWX41_RS04375
	<i>grx</i>	glutaredoxin family protein	HWX41_RS19015
NOS resistance	ND	nitric oxide synthase oxygenase	HWX41_RS20535
Hydroxylamine reduction	<i>hcp</i>	hydroxylamine reductase	HWX41_RS06975
ROS resistance	ND	PQQ-dependent sugar dehydrogenase	HWX41_RS11455

Key: ND—not determined.

Table S7. Genes involved in carbohydrate metabolism.

Pathway	Gene	Product	Locus tag
Pentose phosphate	<i>tkt</i>	transketolase	HWX41_RS05950
EMP	<i>glcK</i>	glucokinase	HWX41_RS02915
Glycolysis	<i>glcU</i>	glucose uptake protein <i>GlcU</i>	HWX41_RS00785
	<i>ND</i>	glucose-6-phosphate isomerase	HWX41_RS23165
	<i>ND</i>	glucose 1-dehydrogenase	HWX41_RS19280/HWX41_RS00790
	<i>ND</i>	glucose-6-phosphate dehydrogenase	HWX41_RS08270/HWX41_RS27525
	<i>pfkA</i>	6-phosphofructokinase	HWX41_RS01390
	<i>pfkB</i>	1-phosphofructokinase	HWX41_RS05815
	<i>ND</i>	fructose-bisphosphate aldolase	HWX41_RS21060
	<i>ND</i>	glyceraldehyde-3-phosphate dehydrogenase	HWX41_RS01470
	<i>gap</i>	type I glyceraldehyde-3-phosphate dehydrogenase	HWX41_RS22040
	<i>gapN</i>	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	HWX41_RS19640
	<i>ND</i>	phosphoglycerate kinase	HWX41_RS22045
	<i>gpmL</i>	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	HWX41_RS22055
	<i>mtnW</i>	2,3-diketo-5-methylthiopentyl-1-phosphate enolase	HWX41_RS04125
	<i>mtnA</i>	S-methyl-5-thioribose-1-phosphate isomerase	HWX41_RS04145
	<i>pdhA</i>	pyruvate dehydrogenase E1 component subunit alpha	HWX41_RS04455
	<i>pdhB</i>	pyruvate dehydrogenase complex E1 component subunit beta	HWX41_RS04460
	<i>pdhC</i>	pyruvate dehydrogenase complex dihydrolipoyllysine-residue acetyltransferase	HWX41_RS04465
	<i>pyc</i>	pyruvate carboxylase	HWX41_RS04585
	<i>ND</i>	pyruvate kinase	HWX41_RS08535
Maltose transport	<i>malC</i>	maltosaccharide ABC transporter permease <i>MalC</i>	HWX41_RS04255
	<i>malD</i>	maltosaccharide ABC transporter permease <i>MalD</i>	HWX41_RS04260
	<i>malR</i>	maltose operon transcriptional repressor <i>MalR</i>	HWX41_RS04265
Glucose and glucose-1-phosphate degradation	<i>gntK</i>	gluconokinase	HWX41_RS08285

	<i>glgC</i>	glucose-1-phosphate adenylyltransferase	HWX41_RS00075
	<i>glgB</i>	1,4-alpha-glucan branching protein <i>GlgB</i>	HWX41_RS00070
	<i>glgD</i>	glucose-1-phosphate adenylyltransferase subunit <i>GlgD</i>	HWX41_RS00080
	<i>glgA</i>	glycogen synthase <i>GlgA</i>	HWX41_RS00085
	<i>glgP</i>	glycogen phosphorylase	HWX41_RS00090
	<i>glcU</i>	glucose uptake protein <i>GlcU</i>	HWX41_RS00785
	<i>galU</i>	UTP--glucose-1-phosphate uridylyltransferase	HWX41_RS23065/HWX41_RS2550
			5
Glucose transport	<i>pstG</i>	PTS glucose transporter subunit IIAABC	HWX41_RS04055
	<i>pstH</i>	phosphocarrier protein HPr	HWX41_RS04060
Fructose degradation	<i>pfkA</i>	6-phosphofructokinase	HWX41_RS01390
	<i>pfkB</i>	1-phosphofructokinase	HWX41_RS05815
	<i>fsa</i>	fructose-6-phosphate aldolase	HWX41_RS23420
Ribose degradation	<i>rbsK</i>	ribokinase	HWX41_RS23445
	<i>doeC</i>	deoxyribose-phosphate aldolase	HWX41_RS14830
	<i>rpiA</i>	ribose 5-phosphate isomerase A	HWX41_RS10690
	<i>rpiB</i>	ribose 5-phosphate isomerase B	HWX41_RS21150
	<i>rbsD</i>	D-ribose pyranase	HWX41_RS23440
Ribose transport	<i>rbsB</i>	ribose ABC transporter substrate-binding protein <i>RbsB</i>	HWX41_RS23425
	<i>rbsC</i>	ribose ABC transporter permease	HWX41_RS23430
	<i>rbsA</i>	ribose ABC transporter ATP-binding protein <i>RbsA</i>	HWX41_RS23435
	<i>rbsR</i>	ribose operon transcriptional repressor <i>RbsR</i>	HWX41_RS23450
Hexose metabolism	<i>ND</i>	aldose 1-epimerase family protein	HWX41_RS15905
GDP-mannose degradation	<i>ppaX</i>	GDP-mannose pyrophosphatase <i>PpaX</i>	HWX41_RS21930
	<i>deoB</i>	phosphopentomutase	HWX41_RS03865
Trehalose degradation	<i>treC</i>	alpha, alpha-trehalase	HWX41_RS23595
	<i>treC</i>	alpha,alpha-trehalase	HWX41_RS0424
D-galactosamine and N-acetyl-D-galactosamine degradation	<i>nagA</i>	N-acetylglucosamine-6-phosphate deacetylase	HWX41_RS04030
	<i>nagA</i>	N-acetylglucosamine-6-phosphate deacetylase	HWX41_RS04030
	<i>nagB</i>	glucosamine-6-phosphate deaminase	HWX41_RS04035
	<i>pfkA</i>	6-phosphofructokinase	HWX41_RS01390
Myo-inositol degradation	<i>ND</i>	inositol-1-monophosphatase protein family	HWX41_RS04530
	<i>iolE</i>	myo-inosose-2 dehydratase	HWX41_RS07140
	<i>iolG</i>	inositol 2-dehydrogenase	HWX41_RS07120

	<i>iolD</i>	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione acylhydrolase (decyclizing)	HWX41_RS07135
	<i>iolC</i>	5-dehydro-2-deoxygluconokinase	HWX41_RS07125
	<i>ND</i>	5-deoxy-glucuronate isomerase	HWX41_RS07155
	<i>ND</i>	methylmalonate-semialdehyde dehydrogenase (CoA acylating)	HWX41_RS12755
D-gluconate degradation	<i>gntK</i>	gluconokinase	HWX41_RS19365/HWX41_RS0828 5
D-gluconate transformation to 2-keto D-gluconate (2- KG)	<i>gntP</i>	gluconate permease <i>GntP</i>	HWX41_RS19360
	<i>gntR</i>	gluconate operon transcriptional repressor <i>GntR</i>	HWX41_RS19370
2KG to 6-phospho-D- gluconate	<i>dhbA</i>	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	HWX41_RS12675
	<i>dhbC</i>	isochorismate synthase <i>DhbC</i>	HWX41_RS12670
L-lactate degradation	<i>ND</i>	L-lactate dehydrogenase	HWX41_RS22670
	<i>ND</i>	L-lactate dehydrogenase	HWX41_RS00065
	<i>ND</i>	L-lactate dehydrogenase	HWX41_RS14695
L-lyxose, 2,3-diketo-L- gulonate, L-ascorbate degradation	<i>ND</i>	L-ribulose-5-phosphate 4-epimerase	HWX41_RS05030
D-tagatose degradation	<i>nagA</i>	N-acetylglucosamine-6-phosphate deacetylase	HWX41_RS04030
Degradation of Beta-Glucosides (e.g. cellobiose, salicin, arbutin, esculin)	<i>celF</i>	6-phospho-beta-glucosidase	HWX41_RS21710
Cellobiose transport	<i>celB</i>	PTS cellobiose transporter subunit IIC	HWX41_RS21665/HWX41_RS2170 0
	<i>celF</i>	6-phospho-beta-glucosidase	HWX41_RS21710
Degradation of unknown glucosides	<i>ND</i>	glycosyl hydrolase	HWX41_RS15345/HWX41_RS2046 5
	<i>ND</i>	glycoside hydrolase/lysozyme	HWX41_RS05625
	<i>ND</i>	glycoside hydrolase/lysozyme	HWX41_RS06965
	<i>ND</i>	glycoside hydrolase/lysozyme	HWX41_RS09710
	<i>ND</i>	glycoside hydrolase/lysozyme	HWX41_RS14465

Chitin degradation	<i>ND</i>	chitobiase/beta-hexosaminidase C-terminal domain-containing protein	HWX41_RS18500
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Key: ND—not determined.

Table S8. Genes involved in carbohydrate transport.

Pathway	Gene	Product	Locus tag
Maltose/maltodextrin and multiple sugars transport	<i>malR</i>	maltose operon transcriptional repressor <i>MalR</i>	HWX41_RS04265
Trehalose-specific EIIBC component	<i>treP</i> ¹	PTS system, trehalose-specific EIIBC component	HWX41_RS23600
	<i>treC</i>	alpha,alpha-phosphotrehalase	HWX41_RS23595
	<i>treR</i>	trehalose operon repressor	HWX41_RS23605
	<i>bcr</i>	<i>Bcr/CflA</i> family efflux MFS transporter	HWX41_RS26020
	ND	DHA2 family efflux MFS transporterpermease subunit	
	ND	DHA2 family efflux MFS transporter permease subunit	HWX41_RS01545/HWX41_RS04310 HWX41_RS09945/ HWX41_RS12645
	ND	DHA2 family efflux MFS transporter permease subunit	HWX41_RS12645/HWX41_RS15080
	ND	peptide MFS transporter	HWX41_RS23330
	ND	OFA family MFS transporter	HWX41_RS12690
Sugar acids transport	<i>lldP</i>	L-lactate permease	HWX41_RS21585/HWX41_RS17765

Key: ND—not determined.

Table S9. Genes involved in the metabolism of organic acids

Pathway	Gene	Product	Locus Tag
TCA cycle	<i>aceA</i>	isocitrate lyase	HWX41_RS18305
	<i>prpB</i>	methylosuccinate lyase	HWX41_RS12770
	<i>aceB</i>	malate synthase A	HWX41_RS18310
	<i>icd</i>	NADP-dependent isocitrate dehydrogenase	HWX41_RS01420
	<i>odhA</i>	2-oxoglutarate dehydrogenase E1 component	HWX41_RS17695
	<i>odhB</i>	2-oxoglutarate dehydrogenase complex	HWX41_RS17700
		dihydrolipoyllysine-residue succinyltransferase	
	<i>gabT</i>	4-aminobutyrate--2-oxoglutarate transaminase	HWX41_RS19330/HWX41_RS24350
		adenylosuccinate synthase	HWX41_RS20390
	<i>purB</i>	adenylosuccinate lyase	HWX41_RS24180
	<i>argG</i>	argininosuccinate synthase	HWX41_RS01225/HWX41_RS06510
	<i>argH</i>	argininosuccinate lyase	HWX41_RS01230
	<i>sdhC</i>	succinate dehydrogenase cytochrome B558	HWX41_RS01750
	<i>sdhA</i>	succinate dehydrogenase flavoprotein subunit	HWX41_RS01755
	<i>ND</i>	succinate CoA transferase	HWX41_RS07255
	<i>sdhB</i>	succinate dehydrogenase iron-sulfur subunit	HWX41_RS01760
	<i>fumA</i>	fumarate hydratase class I	HWX41_RS24845
	<i>fumC</i>	fumarate hydratase class II	HWX41_RS15315
	<i>mdh</i>	malate dehydrogenase	HWX41_RS01425
	<i>citZ</i>	citrate synthase	HWX41_RS01415
	<i>mmgD</i>	citrate synthase	HWX41_RS12780
	<i>mend</i>	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-carboxylic-acid synthase	HWX41_RS00135
	<i>menH</i>	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase	HWX41_RS00140
	<i>menB</i>	1,4-dihydroxy-2-naphthoyl-CoA synthase	HWX41_RS00145
	<i>menC</i>	o-succinylbenzoate synthase	HWX41_RS00155
Glyoxylate bypass TCA	<i>acnA</i>	aconitate hydratase	HWX41_RS06265
	<i>aceA</i>	isocitrate lyase	HWX41_RS18305
	<i>aceB</i>	malate synthase	HWX41_RS18310
Formate degradation	<i>fdhD</i>	formate dehydrogenase accessory sulfurtransferase <i>FdhD</i>	HWX41_RS15580/HWX41_RS23795
	<i>fdhF</i>	formate dehydrogenase subunit alpha	HWX41_RS15595/HWX41_RS23790

Key: ND—not determined.

Table S10. Genes involved in amino acid metabolism and transport

Pathway	Gene	Product	Locus Tag
Methionine degradation	<i>metK</i>	methionine adenosyltransferase	HWX41_RS00560
D-alanine degradation	<i>alr</i>	alanine racemase	HWX41_RS13960/HWX41_RS25705
	<i>ald</i>	alanine dehydrogenase	HWX41_RS07920
	<i>ald</i>	alanine dehydrogenase	HWX41_RS01270
	<i>ald</i>	alanine dehydrogenase	HWX41_RS13960
	<i>ald</i>	alanine dehydrogenase	HWX41_RS23775
	<i>ald</i>	alanine dehydrogenase	HWX41_RS25230
L-arginine degradation	<i>speA</i>	arginine decarboxylase	HWX41_RS04510
	<i>lysA</i>	diaminopimelate decarboxylase	HWX41_RS16865
L-aspartate degradation/conversion	<i>aspB</i>	aspartate aminotransferase <i>AspB</i>	HWX41_RS16185
	<i>aspA</i>	Aspartate ammonia-lyase	HWX41_RS15170/HWX41_RS23690
	<i>panD</i>	Aspartate 1-decarboxylase	HWX41_RS16205
	<i>nadB</i>	L-aspartate oxidase	HWX41_RS02115
	<i>pryB</i>	aspartate carbamoyltransferase	HWX41_RS04875
	<i>dapG</i>	Aspartate kinase	HWX41_RS05435/HWX41_RS15135
	<i>aspS</i>	aspartate--tRNA(Asn) ligase	HWX41_RS13465
L-cysteine degradation	<i>cysK</i>	cysteine synthase A	HWX41_RS26760/HWX41_RS15035
	<i>ND</i>	cysteine hydrolase	HWX41_RS26930
	<i>ND</i>	cysteine hydrolase	HWX41_RS02940
	<i>ND</i>	cysteine hydrolase	HWX41_RS09875
Cysteine transformation	<i>sufS</i>	cysteine desulfurase	HWX41_RS01140/HWX41_RS22740
	<i>iscS</i>	<i>IscS</i> subfamily cysteine desulfurase	HWX41_RS02110/HWX41_RS02290
D-cysteine degradation	<i>ND</i>	D-cysteine desulfhydrase	HWX41_RS08870
L-glutamate degradation	<i>gudB</i>	NAD-specific glutamate dehydrogenase	HWX41_RS16465
	<i>pruA</i>	L-glutamate gamma-semialdehyde dehydrogenase	HWX41_RS24270
L-glutamine degradation	<i>ND</i>	glutamate synthase	HWX41_RS25035

	<i>racE</i>	glutamate racemase	HWX41_RS01860/HWX41_RS1964 5
L-histidine degradation	<i>hutH</i>	histidine ammonia-lyase	HWX41_RS06090
	<i>hutU</i>	urocanate hydratase	HWX41_RS06095
	<i>hutI</i>	Imidazolonepropionase	HWX41_RS06100
	<i>hutG</i>	Formiminoglutamase	HWX41_RS06105
	<i>hutP</i>	hut operon transcriptional regulator <i>HutP</i>	HWX41_RS06085
	<i>resE</i>	sensor histidine kinase <i>ResE</i>	HWX41_RS16530
	<i>resC</i>	cytochrome c biogenesis protein <i>ResC</i>	HWX41_RS16540
	<i>resB</i>	cytochrome c biogenesis protein <i>ResB</i>	HWX41_RS16545
	<i>resA</i>	thiol-disulfide oxidoreductase <i>ResA</i>	HWX41_RS16550
	<i>dcuS</i>	two-component system sensor histidine kinase <i>DcuS</i>	HWX41_RS23850
L-proline degradation	<i>ND</i>	proline dehydrogenase	HWX41_RS22610
	<i>proS</i>	proline--tRNA ligase	HWX41_RS24700
L-tyrosine degradation	<i>hppD</i>	4-hydroxyphenylpyruvate dioxygenase	HWX41_RS25765
	<i>xerS</i>	tyrosine recombinase <i>XerS</i>	HWX41_RS25285
Glycine cleavage	<i>thiO</i>	glycine oxidase <i>ThiO</i>	HWX41_RS20150
	<i>gcvH</i>	glycine cleavage system protein <i>GcvH</i>	HWX41_RS22695
	<i>gcvT</i>	glycine cleavage system aminomethyltransferase <i>GcvT</i>	HWX41_RS03090
	<i>gcvPA</i>	aminomethyl-transferring glycine dehydrogenase subunit 1	HWX41_RS03095
	<i>gcvPB</i>	aminomethyl-transferring glycine dehydrogenase subunit 2	HWX41_RS03100
Branched-chain amino acid transport	<i>asn</i>	asparagine synthase (glutamine-hydrolyzing) branched-chain amino acid transport system II carrier protein	HWX41_RS13200
	<i>brnQ</i>	branched-chain amino acid transport system II carrier protein	HWX41_RS01645
	<i>brnQ</i>	branched-chain amino acid transport system II carrier protein	HWX41_RS14100
	<i>brnQ</i>	branched-chain amino acid transport system II carrier protein	HWX41_RS14750
	<i>brnQ</i>	branched-chain amino acid transport system II carrier protein	HWX41_RS16755
	<i>brnQ</i>	branched-chain amino acid transport system II carrier protein	HWX41_RS19845
	<i>brnQ</i>	branched-chain amino acid transport system II carrier protein	HWX41_RS23325
	<i>brnQ</i>	branched-chain amino acid transport system II carrier protein	HWX41_RS14100

branched-chain amino acid transport system II
carrier protein
branched-chain amino acid transport system II
carrier protein

dat

D-amino-acid transaminase

HWX41_RS13175

Key: ND—not determine.

Table S11. Genes involved in opine and GABA transport and metabolism.

Pathway	Gene	Product	Locus Tag
Myo-inositol, Rhizopine metabolism	<i>iolE</i>	myo-inosose-2 dehydratase	HWX41_RS07140
	<i>iolG</i>	myo-inositol 2-dehydrogenase	HWX41_RS07120
	<i>iolD</i>	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione acylhydrolase (decyclizing)	HWX41_RS07135
	<i>iolC</i>	5-dehydro-2-deoxygluconokinase	HWX41_RS07125
	<i>ND</i>	5-deoxy-glucuronate isomerase	HWX41_RS07155
Putrescine and spermidine production and transport	<i>speB</i>	agmatinase	HWX41_RS07085/HWX41_RS20910
	<i>speE</i>	spermidine synthase	HWX41_RS20905
	<i>ND</i>	glutathionylspermidine synthase family protein	HWX41_RS10015/HWX41_RS16005
	<i>potD</i>	spermidine/putrescine ABC transporter substrate-binding protein <i>PotD</i>	HWX41_RS17570
	<i>potC</i>	spermidine/putrescine ABC transporter permease <i>PotC</i>	HWX41_RS17575
	<i>potB</i>	spermidine/putrescine ABC transporter permease <i>PotB</i>	HWX41_RS17580
	<i>potA</i>	spermidine/putrescine ABC transporter ATP-binding protein <i>PotA</i>	HWX41_RS17585
GABA biosynthesis	<i>ND</i>	gamma-glutamyl-gamma-aminobutyrate hydrolase family protein	HWX41_RS17805/HWX41_RS07225

Key: ND—not determined.

Table S12. Genes involved in lignin degradation and degradation against toxic peroxides.

Pathway	Gene	Product	Locus Tag
Lignin degradation	ND	multicopper oxidase domain-containing protein	HWX41_RS14790
Degradation of toxic peroxides	ND	Superoxide dismutase	HWX41_RS16575
	<i>sodA</i>	Superoxide dismutase	HWX41_RS20530/HWX41_RS02855
	<i>sodA</i>	superoxide dismutase family protein	HWX41_RS23120
	<i>ahpC</i>	Peroxiredoxin	HWX41_RS24440
	<i>katB</i>	Catalase	HWX41_RS07625/HWX41_RS09520
	<i>katB</i>	Catalase	HWX41_RS18175
	<i>bcp</i>	thioredoxin-dependent thiol peroxidase	HWX41_RS25065
	<i>tpx</i>	thiol peroxidase	HWX41_RS01185
	<i>ahpC</i>	Peroxiredoxin	HWX41_RS24440
Metabolism of alcohols and aldehydes	ND	organic hydroperoxide resistance protein	HWX41_RS01930
	<i>adhP</i>	alcohol dehydrogenase <i>AdhP</i>	HWX41_RS13135
	<i>adhP</i>	alcohol dehydrogenase <i>AdhP</i>	HWX41_RS13135
	ND	zinc-binding alcohol dehydrogenase family protein	HWX41_RS06915
	ND	iron-containing alcohol dehydrogenase	HWX41_RS05805/HWX41_RS13340
	<i>adhE</i>	bifunctional acetaldehyde-CoA/alcoholdehydrogenase	HWX41_RS02425

Key: ND—not determine.

Table S13. Genes involved in biological control.

Pathway	Gene	Product	Locus Tag
Volatile degradation	<i>acoA</i>	acetoin:2,6-dichlorophenolindophenol oxidoreductase subunit alpha	HWX41_RS10755
	<i>acoB</i>	acetoin:2,6-dichlorophenolindophenol oxidoreductase subunit beta	HWX41_RS10760
2,3-Butanediol	<i>ilvA</i>	threonine ammonia-lyase <i>ilvA</i>	HWX41_RS14970
	<i>ilvD</i>	dihydroxy-acid dehydratase	HWX41_RS14975
	<i>ilvC</i>	ketol-acid reductoisomerase	HWX41_RS16965
	<i>ilvN</i>	acetolactate synthase small subunit	HWX41_RS16970
	<i>ilvB</i>	acetolactate synthase large subunit	HWX41_RS16975
	<i>ilvE</i>	branched-chain-amino-acid transaminase	HWX41_RS16980
Isoprene	<i>ispG</i>	4-hydroxy-3-methylbut-2-enyl-diphosphate synthase	HWX41_RS02835
Colonization	<i>minD</i>	septum site-determining protein <i>MinD</i>	HWX41_RS02025

Table S14. Physical and chemical analysis of the soil samples.

Parameter	Result Output
Manganese (mg/kg)	43.57
Phosphorus (mg/kg)	74.93
Organic carbon (%)	1.19
Total nitrogen (%)	0.10
pH (H ₂ O)	7.40
Magnesium (mg/kg)	642.00
Organic matter (%)	3.20
Potassium (mg/kg)	399.00
Iron (mg/kg)	2.00
Clay (%)	22.20
Sand (%)	68.30
Silt (%)	7.92