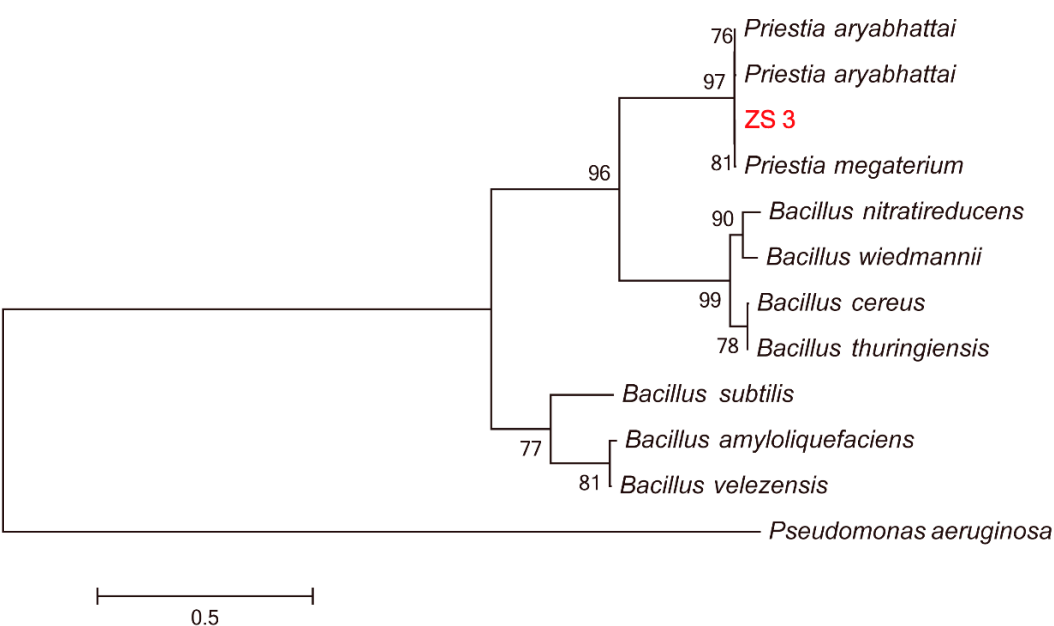
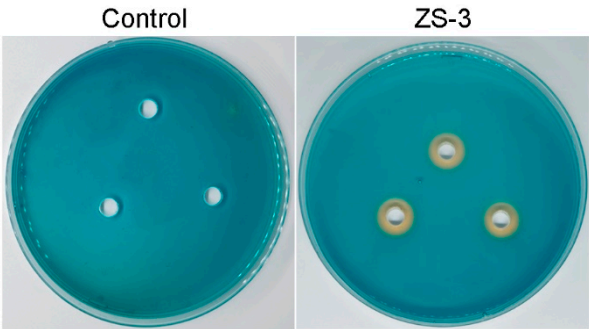


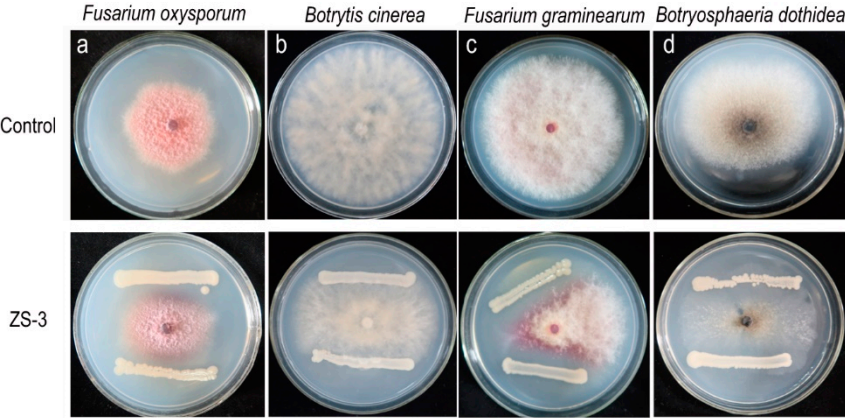
Supplementary Material



**Figure S1** Maximum likelihood (ML) phylogenetic tree generated from analysis of a combined 16s and gyrB sequences dataset. *Pseudomonas aeruginosa* is the outgroup taxa.

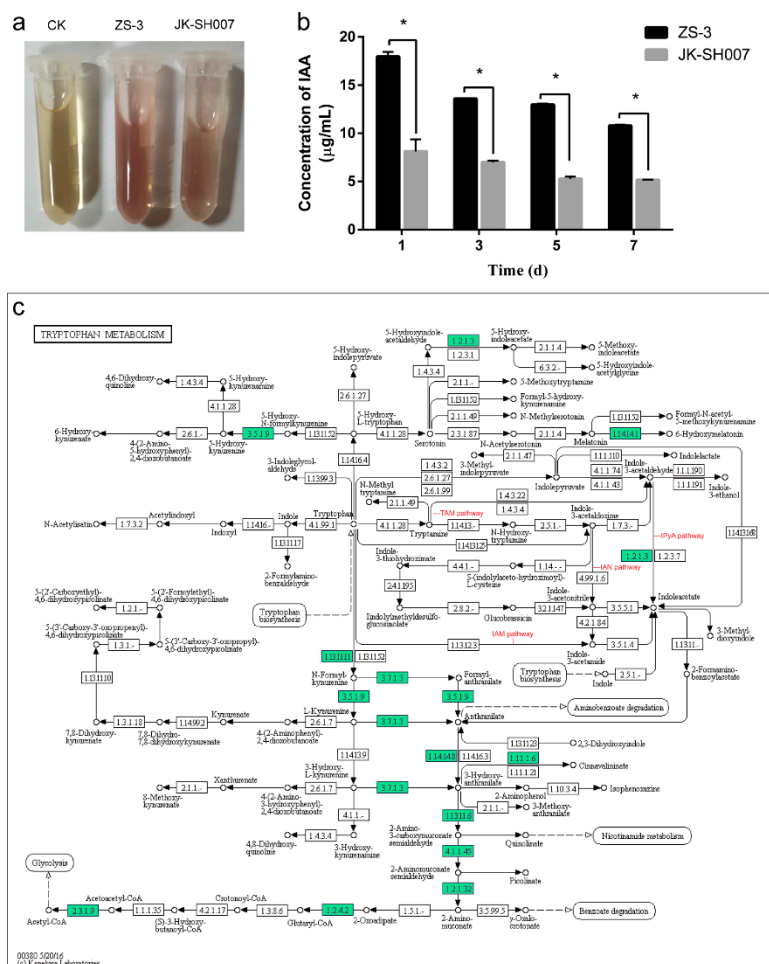


**Figure S2** The ability of *P. megaterium* ZS-3 to secrete siderophores was detected in CAS medium.



**Figure S3** Effect of antagonistic cultures of *P. megaterium* ZS-3 with the following

pathogens: a. *F. oxysporum*; b. *B. cinerea*; c. *F. graminearum*; d. *Botryosphaeria dothidea*. The control group was a single inoculated treatment with the pathogen and the others were antagonistic cultures of ZS-3 with the pathogen.



**Figure S4** Analysis of the IAA secretion and KEGG synthesis pathways. Colour development reaction (a) and quantitative analysis (b) of Salkowski's reagent mixed with ZS-3 and JK-SH007 cell supernatants. CK is TSB medium without bacteria inoculation. Putative "KEGG pathway" of trp metabolism and IAA biosynthetic pathways in the *P. megaterium* ZS-3. The numbers in the boxes represent the EC numbers of key enzymes in the metabolic pathway, and the green boxes indicate the presence of genes corresponding to the relevant enzymes in the genome. Values represent the means of three biological experiments, each in three technical replicates. Error bars represent SE. Asterisks on the bars indicate significant differences between the treatments analysed according to the t test ( $P < 0.05$ ).

**Table S1- Genes involved in osmotic stress tolerance.**

Gene ID	Gene	Annotation	EC numbers	Pathway
GE004605	<i>rocD-</i>	Ornithine--oxo-acid transaminase	EC:2.6.1.1 3	Arginine and proline metabolism
GE000066 GE002967	<i>proA</i>	Glutamate-5-semialdehyde dehydrogenase	EC: 1.2.1.41	Proline biosynthesis
GE000065 GE002968	<i>proB</i>	Glutamate 5-kinase	EC: 2.7.2.11	
GE002969 GE003249 GE000862	<i>proC</i>	Pyrroline-5-carboxylate reductase	EC:1.5.1.2	
GE000222 GE000297 GE000298 GE001454	<i>proDH</i>	Proline dehydrogenase	EC: 1.5.5.2	
GE003159	<i>gltB</i>	Glutamate synthase [NADPH] small chain	EC:1.4.1.1 3	Glutamate biosynthesis
GE003158	<i>gltD</i>	Glutamate synthase [NADPH] large chain	EC: 1.4.1.13	
GE001177	<i>glnA</i>	Glutamine synthetase	EC:6.3.1.2	Glutamine biosynthesis
GE003736	<i>opuAC</i>	Glycine betaine/proline transport system substrate-binding protein	--	Glycine betaine/proline transport and biosynthesis
GE003737	<i>proW</i>	Glycine betaine/proline transport system permease protein	--	
GE003738	<i>opuAA</i>	Glycine betaine/proline transport system ATP-binding protein	EC:7.6.2.9	
GE003739		Glycine betaine catabolism A	--	
GE003927 GE003928	<i>opuD</i>	Glycine betaine transporter OpuD	--	
GE000200 GE002996 GE004398	<i>betB</i>	Betaine-aldehyde dehydrogenase	EC:1.2.1.8	
GE000199	<i>gbsB</i>	Choline dehydrogenase	EC:1.1.1.1	Trehalose biosynthesis
GE001261	<i>ptbA</i>	PTS glucose transporter subunit IIA	EC:2.7.1.-	
GE004306	<i>treC</i>	Trehalose-6-phosphate hydrolase	EC:3.2.1.9 3	
GE001851 GE001950 GE002623 GE004211 GE004788	<i>gltP</i>	Proton glutamate symport protein	--	Glutamate transport
GE003524 GE004532		Na(+)/H(+) antiporter NhaS5		Sodium and chloride transporters
GE004011	<i>NhaC</i>	Na(+)/H(+) antiporter NhaC		
GE004063	<i>natB</i>	Sodium transport system permease protein	--	
GE004064	<i>natA</i>	Sodium transport system ATP-binding protein	EC:7.2.2.4	
GE000370	<i>mnhA</i>	Multicomponent Na+:H+ antiporter subunit A	--	
GE000369	<i>mnhB</i>	Multicomponent Na+:H+ antiporter subunit B	--	
GE000368	<i>mnhC</i>	Multicomponent Na+:H+ antiporter subunit C	--	
GE000367	<i>mnhD</i>	Multicomponent Na+:H+ antiporter subunit D	--	
GE000366	<i>mnhE</i>	Multicomponent Na+:H+ antiporter subunit E	--	
GE000365	<i>mnhF</i>	Multicomponent Na+:H+ antiporter subunit F	--	
GE000364	<i>mnhG</i>	Multicomponent Na+:H+ antiporter subunit G	--	
GE005122	<i>yfbS</i>	Ca-activated chloride channel homolog	--	
GE002415	<i>nhaK</i>	Sodium, potassium, lithium and rubidium/H(+) antiporter	--	
GE001374 GE003450	<i>ktrB</i>	Ktr system potassium uptake protein B	--	Low-affinity potassium transport system
GE001373 GE003940	<i>ktrC</i>	Ktr system potassium uptake protein C	--	
GE004044	<i>ktrD</i>	Ktr system potassium uptake protein D	--	
GE000117 GE003785 GE004546 GE004761	<i>clsAB</i>	Cardiolipin synthase A/B	EC:2.7.8.-	Cardiolipin biosynthesis
GE001334 GE003236 GE004417	<i>ltaS</i>	Lipoteichoic acid synthase	EC:2.7.8.2 0	Lipoteichoic acid biosynthesis

GE003788	<i>des</i>	Fatty acid desaturase	--	Fatty acid membrane modifications
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**Table S2-** Genes involved in heavy metal transport and resistance.

Gene ID	Gene	Annotation	EC numbers	Pathway
GE000408	<i>znuA</i>	Zinc transport system substrate-binding protein	--	Zinc transport
GE000750		Zinc transport system ATP-binding protein	EC:7.2.2.-	
GE000751		Zinc transport system permease protein	--	
GE003468		Zinc transporter, ZIP family	--	
GE003705				
GE004018				
GE004866	<i>zitB</i>	Cobalt-zinc-cadmium efflux system protein	--	Cobalt-zinc-cadmium transport
GE001208	<i>cutC</i>	Copper homeostasis protein cutC	--	Copper resistance transport
GE004500				
GE002267	<i>copD</i>	Copper resistance protein D	--	
GE002266	<i>copC</i>	Copper resistance protein C	--	
GE003352	--	Copper-exporting P-type ATPase	--	
GE003353	<i>copZ</i>	Copper chaperone CopZ	--	Arsenite transport and reduction
GE003342	<i>arsB</i>	Arsenical pump membrane protein	--	
GE003529				
GE004204				
GE000303	<i>arsC</i>	Arsenate reductase (glutaredoxin)	EC:1.20.4.1	
GE003530		Arsenate reductase (thioredoxin)	EC:1.20.4.4	
GE002245	<i>chrA</i>	Chromate transporter	--	Chromate reduction and transport
GE002246				
GE002110	<i>cadA</i>	Cadmium-transporting ATPase	--	Cadmium transport
GE004869				
GE002111	<i>cadC</i>	Cadmium resistance transcriptional regulatory protein CadC	--	
GE004866	<i>czcD</i>	Cadmium, cobalt and zinc/H(+)-K(+) antiporter	--	Manganese transport
GE002726	<i>mntH</i>	Manganese transport protein	--	
GE000140	<i>mntP</i>	Putative manganese efflux pump MntP	--	
GE004533	<i>mgtE</i>	Magnesium transporter MgtE	--	Magnesium trasnport
GE002360	<i>corA</i>	Magnesium transporter	--	
GE003322				
GE004110				
GE004533				
GE004906				
GE000384	<i>mgtC</i>	Putative Mg <sup>2+</sup> transporter-C (MgtC) family protein	--	
GE001320				
GE004699	<i>crcB</i>	Fluoride exporter	--	Fluoride transport
GE004700				

**Table S3-** Genes involved in phytohormone production/modulation.

Gene ID	Gene	Annotation	EC numbers	Pathway
GE003925	<i>speA</i>	Arginine decarboxylase	--	<b>Putrescine biosynthesis</b>
GE000113 GE002997	<i>speB</i>	Agmatinase	EC:3.5.3.11	
GE000524	<i>speH</i>	S-adenosylmethionine decarboxylase	EC:4.1.1.50	<b>Spermidine biosynthesis</b>
GE000112 GE004482	<i>speE</i>	Spermidine synthase	EC:2.5.1.16	
GE004397	<i>pat</i>	Putrescine aminotransferase	EC:2.6.1.82	<b>Putrescine degradation</b>
GE003640	<i>speG</i>	Spermidine/Spermine N (1)-acetyltransferase		<b>Acetyl spermidine formation</b>
GE005012	<i>potD</i>	Spermidine/putrescine transport system substrate-binding protein	--	<b>Polyamine transport</b>
GE005013	<i>potC</i>	Spermidine/putrescine transport system permease protein	--	
GE005014	<i>potB</i>	Spermidine/putrescine transport system permease protein	--	
GE005015	<i>potA</i>	Spermidine/putrescine transport system ATP-binding protein	EC:7.6.2.11	
GE004395 GE004784	<i>puuP</i>	Putrescine importer	--	
GE000956	<i>trpB</i>	Tryptophan synthase beta chain	EC:4.2.1.20	<b>Tryptophan biosynthetic</b>
GE000957	<i>trpA</i>	Tryptophan synthase alpha chain	EC:4.2.1.20	
GE001688	<i>kynA</i>	Tryptophan 2,3-dioxygenase	EC:1.13.11.1	<b>Tryptophan metabolism</b>
GE001883 GE002878 GE003111 GE003378 GE003717	-	Aldehyde dehydrogenase (NAD+)	EC:1.2.1.3	<b>IAA biosynthesis</b>
GE002787	<i>gadB</i>	Glutamate decarboxylase	EC:4.1.1.15	<b>GABA biosynthesis and transport</b>
GE001201 GE003827	<i>gabD</i>	Succinate-semialdehyde dehydrogenase	EC:1.2.1.16 1.2.1.79 1.2.1.20	
GE002879 GE004199 GE004319	<i>gabT</i>	4-aminobutyrate aminotransferase	EC:2.6.1.19	
GE001456 GE004499	<i>gabP</i>	GABA permease	--	

Table S4- Genes involved in vocproduction/degradation.

Gene ID	Gene	Annotation	EC numbers	Pathway
GE004474	<i>aldC</i>	Alpha-acetolactate decarboxylase		<b>Acetoin biosynthesis</b>
GE000582	<i>alsS</i>	Acetolactate synthase		
GE000583				
GE003566				
GE004310				
GE004473				<b>Acetoin catabolism</b>
GE000469	<i>acuA</i>	Acetoin utilization protein AcuC	--	
GE000470	<i>acuB</i>	Acetoin utilization protein AcuB	--	
	<i>acuC</i>		EC:2.3.1.	
GE000471		Acetoin utilization protein AcuA	-	
GE003389	<i>acoA</i>	Acetoin:2,6-dichlorophenolindophenol oxidoreductase subunit alpha	--	
GE003388	<i>acoB</i>	Acetoin:2,6-dichlorophenolindophenol oxidoreductase subunit beta	--	
GE003387	<i>acoC</i>	Dihydrolipoyllysine-residue acetyltransferase component of acetoin cleaving system	--	
GE000835	<i>acoL</i>	Dihydrolipoyl dehydrogenase	EC:1.8.1.4	
GE003386				
GE003930				
GE003385	<i>acoR</i>	Acetoin dehydrogenase operon transcriptional activator AcoR	--	<b>Butanediol degradation</b>
GE003384	<i>bdhA</i>	(R,R)-butanediol dehydrogenase	EC:1.1.1.4 1.1.1.- 1.1.1.303	
GE001552	<i>dhaT</i>	1,3-propanediol dehydrogenase	--	<b>1,3-propanediol catabolism</b>
GE002594				<b>Dimethyl sulfone degradation</b>
GE003682	<i>dmoA</i>	Dimethyl-sulfide monooxygenase	--	
GE004390				
GE001930	<i>sfnG</i>	FMNH(2)-dependent dimethylsulfone monooxygenase	--	

**Table S5 - Genes involved in nitrogen, sulfur, and phosphorus metabolism.**

Gene ID	Gene	Annotation	EC numbers	Pathway
GE000658	<i>pstS</i>	Phosphate transport system substrate-binding protein	--	<b>Phosphate transport</b>
GE000659	<i>pstC</i>	Phosphate transport system permease protein	--	
GE000660	<i>pstA</i>	Phosphate transport system permease protein	--	
GE000763	<i>pstB</i>	Phosphate transport system ATP-binding protein	EC:7.3.2.1	
GE003766	<i>phoA</i>	Alkaline phosphatase	EC:3.1.3.1	<b>Phosphate assimilation</b>
GE004055				
GE000211	<i>phoD</i>	Alkaline phosphatase D	EC:3.1.3.1	
GE000057	<i>phoR</i>	Alkaline phosphatase synthesis sensor protein	--	
GE000517	<i>phoP</i>	Alkaline phosphatase synthesis transcriptional regulatory protein	--	
GE002287	<i>ureC</i>	Urease subunit alpha	EC:3.5.1.5	<b>Urea degradation and transport</b>
GE002286	<i>ureB</i>	Urease subunit beta	EC:3.5.1.5	
GE002285	<i>ureA</i>	Urease subunit gamma	EC:3.5.1.5	
GE002293	<i>ureH</i>	Urease accessory protein UreH	--	
GE002291	<i>ureD</i>	Urease accessory protein UreD	--	
GE002290	<i>ureG</i>	Urease accessory protein UreG	--	
GE002289	<i>ureF</i>	Urease accessory protein UreF	--	
GE002288	<i>ureE</i>	Urease accessory protein UreE	--	
GE000380	--	Adenylyl-sulfate kinase		<b>Sulfur metabolic and transport</b>
GE000377	<i>cysH</i>	Phosphoadenylyl-sulfate reductase	EC:1.8.4.8 1.8.4.10	
GE000378	<i>cysP</i>	Sulfate permease		
GE000379	<i>sat</i>	Sulfate adenylyltransferase	EC:2.7.7.4	
GE000380		Adenylylsulfate kinase	EC:2.7.1.25	
GE000566		Sulfonate transport system ATP-binding protein	EC:3.6.3.-	
GE000567		Sulfonate transport system substrate-binding protein		
GE000568		Sulfonate transport system permease protein		
GE002152	<i>cysJ</i>	Sulfite reductase (NADPH) flavoprotein alpha-component	EC:1.8.1.2	
GE002153	<i>cysI</i>	Sulfite reductase (NADPH) hemoprotein beta-component	EC:1.8.1.2	
GE003131	<i>cysA</i>	Sulfate/thiosulfate import ATP-binding protein CysA	EC:7.3.2.3	
GE003132	<i>cysW</i>	Sulfate transport system permease protein CysW	--	
GE003133	<i>cysT</i>	Sulfate transport system permease protein CysT	--	
GE003134	--	Sulfate/thiosulfate transport system substrate-binding protein	--	
GE003291	--	Thiosulfate/3-mercaptopyruvate sulfurtransferase	EC:2.8.1.1 2.8.1.2	
GE000570				
GE004388	--	Alkanesulfonate monooxygenase	EC:1.14.14.5	
GE000569	--	FMN reductase (NADPH)	EC:1.14.14.5	
GE004123	<i>nirB</i>	Nitrite reductase (NADH) large subunit	EC:1.7.1.15	<b>Dissimilatory nitrate reduction</b>
GE004485				
GE004122	<i>nirD</i>	Nitrite reductase (NADH) small subunit	EC:1.7.1.15	<b>Nitrate/nitrite transporter</b>
GE004484	<i>nasA</i>	Assimilatory nitrate reductase catalytic subunit	EC:1.7.99.-	
GE004483	--	MFS transporter, NNP family, nitrate/nitrite transporter	--	<b>Ammonia transport</b>
GE004120	<i>nirC</i>	Nitrite transporter	--	
GE002618	<i>amt</i>	Ammonium transporter, Amt family		
GE002330				
GE004609				

**Table S6-** Genes involved in the production of antagonistic traits.

Gene ID	Gene	Annotation	EC numbers	Pathway
GE004479 GE005004	<i>murF</i>	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	EC:6.3.2.10	Phosphonate biosynthesis
GE004478	<i>aepX</i>	Phosphoenolpyruvate phosphomutase	--	
GE004477	<i>aepY</i>	Phosphonopyruvate decarboxylase	--	
GE002042	<i>phnX</i>	Phosphonoacetaldehyde hydrolase	--	
GE002043	<i>phnW</i>	2-aminoethylphosphonate--pyruvate transaminase	--	
GE002841	-	MBL fold metallo-hydrolase	--	Phosphonate and phosphinate metabolism
GE001239	-	N-acetyltransferase	--	
GE001300				
GE001310				
GE002709	-	L-amino acid N-acyltransferase MnaT	--	Alkylresorcinol, alkylpyrones biosynthesis
GE001893	-	LysR family transcriptional regulator	--	
GE001201	-	Glutarate-semialdehyde dehydrogenase	--	
GE003827		Succinate-semialdehyde dehydrogenase [NADP(+)]	--	
GE003825	-	Type III polyketide synthase, Putative chalcone synthase	--	
GE003824	-	Isoprenylcysteine carboxyl methyltransferase	--	
GE000624	-	GTPase	--	

**Table S7-** Genes involved in iron transport and siderophore production.

Gene ID	Gene	Annotation	EC numbers	Pathway
GE002693	<i>fbpB</i>	Iron(III) transport system permease protein	--	Iron(III) transport
GE001268	<i>fbpC</i>	Fe(3+) ions import ATP-binding protein FbpC	--	
GE004363	<i>feoA</i>	Ferrous iron transport protein A	--	Iron(II) transport
GE001714 GE004364 GE001713	<i>feoB</i>	Ferrous iron transport protein B	--	
GE000291 GE002064 GE002802 GE003268 GE003753 GE004386	<i>fhuD</i>	Iron complex transport system substrate-binding protein	--	Iron complex transport
GE000292 GE000293 GE002061 GE002062 GE002313 GE003754 GE003755 GE004384 GE004385	<i>fhuB</i>	Iron complex transport system permease protein	--	
GE000294 GE002063 GE002314 GE003078	<i>fhuC</i>	Iron complex transport system ATP-binding protein	EC:7.2.2.-	
GE001213 GE004878	<i>rhbD</i>	Lysine 6-monooxygenase	--	
GE001211	<i>rhbC</i>	Siderophore biosynthesis protein RhbC	--	
GE001213 GE004878	<i>rhbE</i>	Siderophore biosynthesis protein RhbE	--	
GE001215	<i>rhbF</i>	Siderophore biosynthesis protein RhbF	--	
GE000292	<i>yfiZ</i>	Probable siderophore transport system permease protein YfhZ	--	Siderophore transport
GE000293	<i>yfhA</i>	Probable siderophore transport system permease protein YfhA	--	
GE000291	<i>yfiY</i>	Probable siderophore-binding lipoprotein YfiY	--	



**Table S8- Genes involved in chemotaxis and motility.**

Gene ID	Gene	Annotation	EC numbers	Pathway
GE001106 GE003735	<i>CheA</i>	Two-component system, chemotaxis family, sensor kinase CheA	EC:2.7.13.3	Chemotaxis
GE001107	<i>CheW</i>	Purine-binding chemotaxis protein CheW	--	
GE001108	<i>CheD</i>	Chemotaxis protein CheD	EC:3.5.1.44	
GE000949 GE003734	<i>CheR</i>	Chemotaxis protein methyltransferase CheR	EC:2.1.1.80	
GE001105 GE002970	<i>CheB</i>	Two-component system, chemotaxis family, CheB/CheR fusion protein	EC:2.1.1.80 3.1.1.61	
GE001096	<i>CheY</i>	Two-component system, chemotaxis family, chemotaxis protein CheY	--	
GE003963	<i>CheV</i>	Two-component system, chemotaxis family, chemotaxis protein CheV	--	
GE000467 GE003218	<i>MotA</i>	Chemotaxis protein MotA	--	
GE000468 GE003217	<i>MotB</i>	Chemotaxis protein MotB	--	
GE002775 GE004721	<i>Mcp</i>	Methyl-accepting chemotaxis protein	EC:4.1.1.15	
GE001385	<i>HemAT</i>	Heme-based aerotactic transducer	-	
GE001102	<i>FlhA</i>	Flagellar biosynthesis protein FlhA	--	Flagellar assembly
GE001109	<i>FliA</i>	RNA polymerase sigma factor for flagellar operon FliA	--	
GE001080	<i>FlgB</i>	Flagellar basal-body rod protein FlgB	--	
GE001101	<i>FlhB</i>	Flagellar biosynthetic protein FlhB	--	
GE001081	<i>FlgC</i>	Flagellar basal-body rod protein FlgC	--	
GE004169	<i>FliC</i>	Flagellin		
GE001090	<i>FlgD</i>	Flagellar basal-body rod modification protein FlgD	--	
GE001092	<i>FliB</i>	Flagellar protein FliB; Swarming motility protein SwrD	--	
GE001082	<i>FliE</i>	Flagellar hook-basal body complex protein FliE	--	
GE001091	<i>FlgE</i>	Flagellar hook protein FlgE	--	
GE001083	<i>FliF</i>	Flagellar M-ring protein FliF	--	
GE001103	<i>FlhF</i>	Flagellar biosynthesis protein FlhF		
GE000165 GE000166	<i>FlgG</i>	Flagellar basal-body rod protein FlgG	--	
GE000186	<i>FliS</i>	Flagellar protein FliS		
GE001084	<i>FliG</i>	Flagellar motor switch protein FliG		
GE001104	<i>FlhG</i>	Flagellar biosynthesis protein FlhG		
GE001085	<i>FliH</i>	Flagellar assembly protein FliH		
GE001087	<i>FliJ</i>	Flagellar FliJ protein		
GE000194	<i>FlgK</i>	Flagellar hook-associated protein 1 FlgK		
GE000195	<i>FlgL</i>	Flagellar hook-associated protein 3 FlgL		
GE001093	<i>FliL</i>	Flagellar FliL protein		
GE001094	<i>FliM</i>	Flagellar motor switch protein FliM		
GE001095	<i>FliN/FliY</i>	Flagellar motor switch protein FliN/FliY		
GE001097	<i>FliO/FliZ</i>	Flagellar protein FliO/FliZ		
GE001098	<i>FliP</i>	Flagellar biosynthetic protein FliP		
GE001099	<i>FliQ</i>	Flagellar biosynthetic protein FliQ		
GE001100	<i>FliR</i>	Flagellar biosynthetic protein FliR		
GE000205	<i>FliS</i>	Flagellar protein FliS		
GE000206	<i>FliT</i>	Flagellar protein FliT		
GE000196	<i>FliW</i>	Flagellar assembly factor FliW		
GE000204	<i>FliD</i>	Flagellar hook-associated protein 2		
GE001086	<i>FliS</i>	Flagellum-specific ATP synthase	EC:7.4.2.8	
GE001089	<i>FliK</i>	Flagellar hook-length control protein FliK		

**Table S9.** Effect of strain ZS-3 on aboveground and underground biomass of *C. camphora*

Group	Aboveground		Underground	
	Fresh weight (g)	Dry weight (g)	Fresh weight (g)	Dry weight (g)
S-CK	8.37±0.78b	3.57±0.19c	5.03±0.26b	2.70±0.39b
S-ZS-3	15.69±1.52a	7.34±0.89a	11.2±2.54a	5.73±1.33a
N-CK	9.27±0.67b	3.92±0.45c	5.26±0.64b	3.25±0.24b
N-ZS-3	13.67±1.44a	5.52±0.63b	9.27±0.78a	5.28±0.51a

Note: Results are the mean ± standard deviation from 15 independent experiments. Different lowercase letters above the bars represent significant differences based on one-way ANOVA ( $P < 0.05$ ). The four treatment groups were as follows: (1) S-CK: saline soil inoculated with ddH<sub>2</sub>O; (2) S-ZS-3: saline soil inoculated with ZS-3; (3) N-CK: neutral soil inoculated with ddH<sub>2</sub>O; and (4) N-ZS-3 neutral soil inoculated with ZS-3.

**Table S10.** Effect of strain ZS-3 on root development of *C. camphora*

Group	Total root length/cm	Root surface area/cm <sup>2</sup>	Root volume/cm <sup>3</sup>	Root tip number/individual	Bifurcation Number/individual
S-CK	113.09±12.56 c	173.29±18.28 c	19.60±1.31c	2851.67±123b	4182.33±127.97d
S-ZS-3	185.92±10.92 a	379.41±31.08 a	37.80±2.99a	3398±210.23a	12398.67±1164.30a
N-CK	141.20±10.38 b	148.29±10.33 c	23.53±3.98c	2878±349.69b	6123±290.10c
N-ZS-3	157.55±9.677 b	280.68±22.64 b	28.95±2.09b	3126±306.99a b	9226±912.69b

Note: Results are the mean ± standard deviation from 15 independent experiments. Different lowercase letters above the bars represent significant differences based on one-way ANOVA ( $P < 0.05$ ). The four treatment groups were as follows: (1) S-CK: saline soil inoculated with ddH<sub>2</sub>O; (2) S-ZS-3: saline soil inoculated with ZS-3; (3) N-CK: neutral soil inoculated with ddH<sub>2</sub>O; and (4) N-ZS-3 neutral soil inoculated with ZS-3.