

Effect of endophytic bacterium, *Stenotrophomonas maltophilia* JVB5 on sunflowers

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Table S1. Secretion systems genes

Gene	Locus tag	Product	Pathway
<i>secA</i>	J0661_15525	preprotein translocase subunit (PTS) <i>SecA</i>	
<i>secB</i>	J0661_14910	PTS <i>SecB</i>	
<i>secD</i>	J0661_14335	PTS <i>SecC</i>	
<i>secE</i>	J0661_15895	PTS <i>SecE</i>	
<i>secF</i>	J0661_14340	PTS <i>SecF</i>	
<i>secG</i>	J0661_02610	PTS <i>SecG</i>	
<i>secY</i>	J0661_07275	PTS <i>SecY</i>	
<i>Efh</i>	J0661_02300	signal recognition particle subunit SRP54	
<i>ftsB</i>	J0661_07960	cell division (CD) protein <i>FtsB</i>	
<i>ftsA</i>	J0661_15500	CD protein <i>FtsA</i>	
<i>ftsZ</i>	J0661_15505	CD protein <i>FtsZ</i>	
<i>ftsE</i>	J0661_09830	CD ATP-binding protein <i>FtsE</i>	sec (secretion) system
<i>ftsL</i>	J0661_15450	CD protein <i>FtsL</i>	
<i>ftsW</i>	J0661_15475	putative lipid II flippase <i>FtsW</i>	
<i>ftsQ</i>	J0661_15495	CD protein <i>FtsQ/DivIB</i>	
	J0661_09835		
<i>ftsX</i>	J0661_13780	permease-like CD protein <i>FtsX</i>	
	J0661_19545		
<i>ftsH</i>	J0661_15240	ATP-dependent zinc metalloprotease <i>FtsH</i>	
<i>ftsY</i>	J0661_14735	signal recognition particle-docking protein <i>FtsY</i>	
<i>yajC</i>	J0661_14330	preprotein translocase subunit <i>YajC</i>	
<i>yidA</i>	J0661_09635	sugar-phosphatase	
<i>yidC</i>	J0661_20500	membrane protein insertase <i>YidC</i>	
<i>yidD</i>	J0661_03620	membrane protein insertion efficiency factor <i>YidD</i>	
<i>tatC</i>	J0661_08030	twin-arginine translocase (TAT) subunit <i>TatC</i>	
<i>tatB</i>	J0661_08035	TAT subunit <i>TatB</i>	twin-arginine translocation (<i>Tat</i>) system
<i>tatA</i>	J0661_08040	<i>Sec</i> -independent protein translocase subunit <i>TatA</i>	
<i>tatD</i>	J0661_08185	<i>TatD</i> family hydrolase	
<i>lapB</i>	J0661_13090	lipopolysaccharide assembly protein <i>LapB</i>	adhesin protein transporter
	J0661_05885		
	J0661_14700		
	J0661_16120		
<i>tolC</i>	J0661_19125	<i>TolC</i> family protein/ <i>TolC</i> family outer membrane protein	raxAB-RaxC type I secretion system protein
	J0661_20170		
	J0661_03910		
	J0661_05755		
	J0661_07615		
<i>tolQ</i>	J0661_14095	protein <i>TolQ</i>	
<i>tolR</i>	J0661_14100	protein <i>TolR</i>	
<i>tolA</i>	J0661_14105	cell envelope integrity protein <i>TolA</i>	
<i>tolB</i>	J0661_14110	protein <i>TolB</i>	

Table S2. Genes involved in carbohydrate metabolism

Gene	Locus tag	Product	Pathway
<i>Zwf</i>	J0661_09015	glucose-6-phosphate 1-dehydrogenase	pentose phosphate
<i>Pgl</i>	J0661_09025	6-phosphogluconolactonase	
	J0661_09030		
<i>Gnd</i>	J0661_17345	decarboxylating 6-phosphogluconate dehydrogenase	
-	J0661_20950	transaldolase	
<i>Tkt</i>	J0661_17945	transketolase	EMP Glycolysis
-	J0661_01950	phosphoglucumutase, alpha-D-glucose phosphate-specific	
-	J0661_02170	glucokinase	
-	J0661_07230		
-	J0661_09020		
<i>Gpi</i>	J0661_15020	glucose-6-phosphate isomerase	EMP Glycolysis
-	J0661_04475	1-phosphofructokinase	
-	J0661_13185	fructose-bisphosphate aldolase class I	
<i>Gap</i>	J0661_15085	type I glyceraldehyde-3-phosphate dehydrogenase	
-	J0661_17950	phosphoglycerate kinase	
<i>GpmA</i>	J0661_03795	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	glucose and glucose-1-phosphate degradation
<i>Eno</i>	J0661_02505	enolase	
<i>Pyk</i>	J0661_13190	pyruvate kinase	
<i>glk</i>	J0661_07230	glucokinase	
	J0661_09020		
	J0661_02170		
<i>Agp</i>	J0661_11895	bifunctional glucose-1-phosphatase/inositol phosphatase	glucose and glucose-1-phosphate degradation
<i>Gale</i>	J0661_12795	UDP-glucose 4-epimerase <i>GalE</i>	
<i>YidA</i>	J0661_09635	sugar-phosphatase	
<i>Pgm</i>	J0661_01950	phosphoglucumutase, alpha-D-glucose phosphate-specific	
<i>GalU</i>	J0661_13105	<i>GalU</i> - UTP--glucose-1-phosphate uridylyltransferase	
<i>FruK</i>	J0661_04475	1-phosphofructokinase	fructose degradation
<i>RfbD</i>	J0661_01590	dTDP-4-dehydrorhamnose reductase	ribose degradation
<i>RbsK</i>	J0661_08800	Ribokinase	
<i>ManA</i>	J0661_01580	mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	mannose degradation
<i>RfbC</i>	J0661_01595	dTDP-4-dehydrorhamnose 3,5-epimerase	
<i>RfbA</i>	J0661_01600	glucose-1-phosphate thymidyltransferase <i>RfbA</i>	
<i>RfbB</i>	J0661_01605	dTDP-glucose 4,6-dehydratase	
<i>NudK</i>	J0661_08460	UDP-glucose/GDP-mannose dehydrogenase family protein	GDP-mannose degradation
<i>TreZ</i>	J0661_21545	malto-oligosyltrehalose trehalohydrolase	trehalose degradation
-	J0661_21550	4-alpha-glucanotransferase	
<i>TreY</i>	J0661_21555	malto-oligosyltrehalose synthase	
<i>OtsA</i>	J0661_02630	alpha-trehalose-phosphate synthase	
<i>OtsB</i>	J0661_02620	trehalose-phosphatase	
<i>NagA</i>	J0661_06410	<i>N</i> -acetylglucosamine-6-phosphate deacetylase	D-erythrulose/ D-threitol degradation
	J0661_07210		
<i>PfkA</i>	J0661_00770	6-phosphofructokinase	<i>nagZ</i>
<i>NagZ</i>	J0661_13380	beta- <i>N</i> -acetylhexosaminidase	

Table S2 to be continued

Gene	Locus tag	Product	Pathway
<i>MmsB</i>	J0661_09035	bifunctional 4-hydroxy-2-oxoglutarate	myo-inositol degradation
	J0661_13460	3-hydroxyisobutyrate dehydrogenase	
<i>Eda</i>	J0661_09425	2-dehydro-3-deoxy-phosphogluconate aldolase	KDPG degradation
<i>DkgA</i>	J0661_10035	2,5-diketo-D-gluconate reductase B	5-KG to 2-keto-L-gulonic acid
	J0661_15865		
<i>PdxH</i>	J0661_13020	pyridoxamine 5-phosphate oxidase	D-threonate degradation
<i>PdxY</i>	J0661_18395	pyridoxal kinase	
<i>PdxA</i>	J0661_08665	4-hydroxythreonine-4-phosphate dehydrogenase <i>PdxA</i>	
<i>LldP</i>	J0661_21315	L-lactate permease	L-lactate degradation
<i>LldR</i>	J0661_21320	transcriptional regulator <i>LldR</i>	
<i>LldD</i>	J0661_21325	FMN-dependent L-lactate dehydrogenase <i>LldD</i>	
<i>Dld</i>	J0661_21330	D-lactate dehydrogenase	D-lactate degradation
<i>GlgA</i>	J0661_21535	glycogen synthase <i>GlgA</i>	glycogen degradation
<i>GlgX</i>	J0661_21565	glycogen debranching protein <i>GlgX</i>	

Table S3. Predicted genes involved in carbohydrate metabolism

Gene	Locus tag	Function/Product	Pathway
<i>nagZ</i>	J0661_13380	beta- <i>N</i> -acetylhexosaminidase	<i>N</i> -Acetylglucosamine-specific II component
<i>nagA</i>	J0661_06410	<i>N</i> -acetylglucosamine-6-phosphate deacetylase	
	J0661_07210		
	J0661_04480	PTS fructose transporter subunit EIIBC	fructose specific (FS) II component
<i>fruB</i>	J0661_21150	PTS system, FS IIA	

Table S4. Predicted genes involved in organic acids metabolism

Gene	Locus tag	Function/Product	Pathway
<i>acnA</i>	J0661_19775	aconitate hydratase	
<i>acnB</i>	J0661_19790	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	
<i>sdhC</i>	J0661_12340	succinate dehydrogenase (SD), cytochrome b556 subunit	
<i>sucB</i>	J0661_12230	dihydrolipoyllysine-residue succinyltransferase	
<i>acnD</i>	J0661_11035	Fe/S-dependent 2-methylisocitrate dehydratase <i>AcnD</i>	
<i>sucD</i>	J0661_02700	succinate--CoA ligase subunit alpha	
<i>sucA</i>	J0661_12235	2-oxoglutarate dehydrogenase E1 component	
	J0661_09775		
<i>Icd</i>	J0661_08320	isocitrate dehydrogenase [NADP]	
	J0661_09775		TCA cycle
<i>pdhA</i>	J0661_17590	pyruvate dehydrogenase (acetyl-transferring) E1 component subunit alpha	
<i>sucC</i>	J0661_02705	ADP-forming succinate--CoA ligase subunit beta	
<i>acnA</i>	J0661_19775	aconitate hydratase	
<i>sdhD</i>	J0661_12345	SD hydrophobic membrane anchor protein	
	J0661_12350	SD flavoprotein	
	J0661_12355	SD iron-sulfur subunit	
	J0661_12360	SD assembly factor 2	
<i>acnB</i>	J0661_19790	aconitate hydratase 2	
<i>acnD</i>	J0661_11035	Fe/S-dependent 2-methylisocitrate dehydratase <i>AcnD</i>	
<i>fdhE</i>	J0661_00530	formate dehydrogenase (FD) accessory protein <i>FdhE</i>	
<i>fdnG</i>	J0661_00515	FD-N subunit alpha	
<i>fdxH</i>	J0661_00520	FD subunit beta	formate degradation
	J0661_00525	FD subunit gamma	
<i>fdhD</i>	J0661_10100	FD accessory sulfurtransferase <i>FdhD</i>	
<i>Acs</i>	J0661_04655	Acetyl-coenzyme A synthetase/acetate--CoA ligase	acetate degradation
<i>mdcH</i>	J0661_09275	malonate decarboxylase (MD) subunit epsilon	
<i>mdcG</i>	J0661_15265	MD subunit	
<i>mdcE</i>	J0661_15270	gamma biotin-independent MD subunit	malonate degradation I (biotin-independent)
	J0661_15275	beta MD acyl carrier protein	
	J0661_15280		
<i>mdcA</i>	J0661_15285	MD subunit alpha	

Table S5. Predicted genes involved in amino acid metabolism and transport

Gene	Locus tag	Product	Pathway
<i>map</i>	J0661_00880	type I methionyl aminopeptidase	methionine degradation
	J0661_03895		
<i>alr</i>	J0661_20820	alanine racemase	D-alanine degradation
<i>speA</i>	J0661_11230	biosynthetic arginine decarboxylase, partial	L-arginine degradation
<i>cysK</i>	J0661_13170	cysteine synthase A	L-cysteine degradation
<i>gluB</i>	J0661_11115	glutamate synthase (NADPH/NADH) large chain	L-glutamine degradation
<i>hutH</i>	J0661_06820	histidine ammonia-lyase	L-histidine degradation
<i>hutC</i>	J0661_06805	histidine utilization repressor	
<i>hutG</i>	J0661_06825	N-formylglutamate deformylase	
<i>epmB</i>	J0661_03660	<i>EpmB</i>	L-lysine degradation
<i>putA</i>	J0661_17255	<i>PutA</i>	L-proline degradation
<i>hpdD</i>	J0661_17620	4-hydroxyphenylpyruvate dioxygenase	L-tyrosine degradation
<i>mmsB</i>	J0661_13460	3-hydroxyisobutyrate dehydrogenase	L-valine degradation
<i>gcvP</i>	J0661_10905	aminomethyl-transferring glycine dehydrogenase	glycine cleavage
<i>gcvH</i>	J0661_08310	glycine cleavage system (GCS) protein <i>GcvH</i>	
<i>gcvT</i>	J0661_08315	GCS aminomethyltransferase <i>GcvT</i>	
<i>lpdA</i>	J0661_11610	dihydrolipoyl dehydrogenase	
	J0661_12225		

Table S6. Predicted genes involved in nitrogen fixation and metabolism

Gene	Locus tag	Product	Pathway
<i>nifS</i>	J0661_17475	cysteine desulfurase	nitrogen fixation
<i>nifF</i>	J0661_20290	flavodoxin	
<i>amt</i>	J0661_06970	ammonium transporter	ammonia transport
<i>atzF</i>	J0661_03650	allophanate hydrolase	urea degradation and transport

Table S7. Predicted genes involved in sulfur metabolism

Gene	Locus tag	Product	Pathway
<i>cysQ</i>	J0661_13670	bisphosphate nucleotidase <i>CysQ</i>	sulfate transport
<i>cysK</i>	J0661_13170	cysteine synthase A	

Table S8. Predicted genes involved in motility and chemotaxis

Gene	Locus tag	Function/Product	Pathway
<i>cheA</i>	J0661_14170 J0661_14205 J0661_05200 J0661_06075	chemotaxis protein (kinase) <i>CheA</i>	Chemotaxis
<i>cheW</i>	J0661_06095 J0661_12650 J0661_14155 J0661_14185	chemotaxis protein <i>CheW</i> - purine-binding	
<i>cheR</i>	J0661_12935 J0661_19810	protein-glutamate O-methyltransferase <i>CheR</i> / chemotaxis protein <i>CheR</i>	
<i>cheB</i>	J0661_12940	chemotaxis family protein-glutamate methylesterase/glutaminase	
<i>cheY</i>	J0661_14215	chemotaxis response regulator <i>CheY</i>	
-	J0661_19800	chemotaxis response regulator protein-glutamate methylesterase	
<i>cheD</i>	J0661_19805	chemoreceptor glutamine deamidase <i>CheD</i>	
<i>cheZ</i>	J0661_14210	chemotaxis protein <i>CheZ</i> /protein phosphatase <i>CheZ</i>	
<i>cheV</i>	J0661_10725	chemotaxis protein <i>CheV</i>	
<i>motA</i>	J0661_20850	flagellar motor stator protein <i>MotA</i>	
<i>motB</i>	J0661_20855	flagellar motor protein <i>MotB</i>	Flagella biosynthesis
<i>mcp</i>	J0661_06080	chemotaxis protein (methyl-accepting)	
<i>flgA</i>	J0661_19330	flagellar basal body (FBB) protein	
<i>flgM</i>	J0661_19335 J0661_19340	flagellar biosynthesis (FB) <i>FlgN</i>	
<i>flgB</i>	J0661_10730	FBB rod protein <i>FlgB</i>	
<i>flhF</i>	J0661_14230	FB <i>FlhF</i>	
<i>flhA</i>	J0661_14235	FB protein <i>FlhA</i>	
<i>flhB</i>	J0661_14240	FB protein <i>FlhB</i>	
<i>flgD</i>	J0661_10740	flagellar hook assembly protein <i>FlgD</i>	
<i>flgC</i>	J0661_10735	FBB rod protein <i>FlgC</i>	
<i>flgF</i>	J0661_10750	FBB rod protein <i>FlgF</i>	
<i>flgH</i>	J0661_10760	FBB L-ring protein <i>FlgH</i>	
-	J0661_10765	FBB P-ring protein <i>FlgI</i>	
<i>flgG</i>	J0661_10755	FBB rod protein <i>FlgG</i>	
<i>flhA</i>	J0661_14235	FB protein <i>FlhA</i>	
<i>flgE</i>	J0661_10745	flagellar hook protein <i>FlgE</i>	
<i>flhB</i>	J0661_14240	FB protein <i>FlhB</i>	
<i>flhF</i>	J0661_14230	FB protein <i>FlhF</i>	
<i>fliR</i>	J0661_14255 J0661_14260	FB protein <i>FliR</i> FB protein <i>FliQ</i>	
<i>flip</i>	J0661_14265	<i>FliP</i>	
<i>fliO</i>	J0661_14270	FB protein <i>FliO</i>	
<i>fliN</i>	J0661_14275	<i>FliN</i>	
<i>fliM</i>	J0661_14280 J0661_14285	<i>FliM</i> FBB-associated <i>FliL</i> family protein	
	J0661_14290	<i>FliK</i>	
<i>fliJ</i>	J0661_14295 J0661_14300	<i>FliJ</i> <i>FliI/YscN</i> family ATPase	

Table S8 to be continued

Gene	Locus tag	Function/Product	Pathway
	J0661_14305	<i>FliH</i>	
<i>fliG</i>	J0661_14310	<i>FliG</i>	
<i>fliF</i>	J0661_14315	<i>FliF</i>	
<i>fliE</i>	J0661_14320	complex protein <i>FliE</i>	Flagella biosynthesis
<i>fliS</i>	J0661_13550	<i>FliS</i>	
<i>fliD</i>	J0661_13555	<i>FliD</i> , partial	
<i>pilG</i>	J0661_06065	twitching motility response regulator <i>PilG</i>	
<i>pilB</i>	J0661_03600	type IVa pilus assembly ATPase <i>PilB</i>	
<i>pilW</i>	J0661_04690	type IV <i>PilW</i>	
<i>cpaB</i>	J0661_03155	<i>Flp</i> pilus assembly protein <i>CpaB</i>	
-	J0661_03185	<i>Flp</i> pilus assembly protein <i>TadD</i>	
-	J0661_04860	fimbria/pilus periplasmic chaperone	
	J0661_04865	type 1 fimbrial protein (FP)	
	J0661_04870	FP	
	J0661_04875	FP	
	J0661_04880	FP	
	J0661_10665	<i>Tfp</i> pilus assembly protein (AP) <i>FimT/FimU</i>	
<i>pilV</i>	J0661_10670	type IV pilus modification protein <i>PilV</i>	
	J0661_10675	<i>PilW</i> family protein	
	J0661_10680	protein <i>PilX</i>	
	J0661_10685	pilus AP <i>PilV</i>	
	J0661_10690	type IV pilin protein	
	J0661_17910	<i>PilT/PilU</i>	
	J0661_17920	motility protein <i>PilT</i>	
<i>pilH</i>	J0661_10980	twitching motility response regulator <i>PilH</i>	
<i>pilG</i>	J0661_06065	twitching motility response regulator <i>PilG</i>	Pilus and fimbriae biosynthesis
	J0661_18930	type IV <i>PilQ</i> family protein	
<i>pilO</i>	J0661_18940	type 4a protein <i>PilO</i>	
	J0661_18945	<i>PilN</i> domain-containing protein	
	J0661_18950	PA protein <i>PilM</i>	
	J0661_18990		
	J0661_03165		
	J0661_04845	FP	
	J0661_04870		
	J0661_04880		
	J0661_18780		
<i>fimV</i>	J0661_15685	FP <i>FimV</i>	
	J0661_04860	fimbria/pilus periplasmic chaperone	
	J0661_04865	type 1 FP	
	J0661_18795		
	J0661_00895		
	J0661_04875		
	J0661_05100	fimbrial biogenesis outer membrane usher protein	
	J0661_18790		
	J0661_10665	<i>Tfp</i> PA protein <i>FimT/FimU</i>	

Table S8 to be continued

Gene	Locus tag	Function/Product	Pathway
-	J0661_03145	prepilin peptidase	type IVa pilus homolog protein
-	J0661_03580		
-	J0661_17270	protein transport protein <i>HofB</i>	
<i>pilC</i>	J0661_10685	PA protein <i>PilC</i>	
-	J0661_03150	PA protein	
<i>cpaB</i>	J0661_03155	<i>Flp</i> PA protein <i>CpaB</i>	
<i>tadD</i>	J0661_03185	<i>Flp</i> pilus assembly protein <i>TadD</i>	

Table S9. Genes involved in attachment to plant surfaces

Gene	Locus tag	Product	Pathway
<i>lpxA</i>	J0661_17880	<i>LpxA</i>	LPS, Lipid A biosynthesis and modifications
<i>lpxB</i>	J0661_18455	<i>LpxB</i>	
<i>lpxD</i>	J0661_17890	<i>LpxD</i>	
<i>lpxH</i>	J0661_03440	<i>LpxH</i>	
<i>waaA</i>	J0661_16130	<i>WaaA</i>	
<i>eptA</i>	J0661_08085	<i>EptA</i>	
<i>kdsA</i>	J0661_07940	<i>KdsA</i>	
<i>kdsB</i>	J0661_13730	<i>KdsB</i>	LPS, core biosynthesis
<i>waaA</i>	J0661_16130	<i>WaaA</i>	
<i>wecB</i>	J0661_18800	<i>WecB</i>	LPS, O-antigen biosynthesis
<i>rfbD</i>	J0661_01590	<i>RfbD</i>	
<i>rfbC</i>	J0661_01595	<i>RfbC</i>	
<i>rfbA</i>	J0661_01600	<i>RfbA</i>	
<i>rfbB</i>	J0661_01605	dTDP-glucose 4,6-dehydratase	

Table S10. Genes involved in quorum-sensing mechanisms

Gene	Locus tag	Product	Pathway
<i>cycA</i>	J0661_15400	D-serine/D-alanine/glycine transporter	N-Acyl-homoserine-lactone production

Table S11. Genes involved in the protection against oxidative and nitrosative stress

Gene	Locus tag	Product	Pathway/function
<i>sod2</i>	J0661_11640	superoxide dismutase family protein	degradation of superoxide anion radicals
<i>sod1</i>	J0661_11645	superoxide dismutase family protein	
<i>katE</i>	J0661_04990	catalase	degradation of hydrogen peroxide
	J0661_10925		
<i>katG</i>	J0661_18670	catalase-peroxidase	degradation of hydrogen peroxide and organic hydroperoxides
<i>ahpC</i>	J0661_20970	peroxiredoxin	
<i>ahpF</i>	J0661_20965	alkyl hydroperoxide reductase subunit F	

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Table S12. Predicted genes involved in the degradation of lignin

Gene	Locus tag	Function/Product	Pathway
<i>katE</i>	J0661_04990	catalase	degradation of toxic peroxides
	J0661_10925		
<i>katG</i>	J0661_18670	catalase-peroxidase	
	J0661_18670		
<i>ahpC</i>	J0661_20970	peroxiredoxin	
<i>ahpF</i>	J0661_20965	alkyl hydroperoxide reductase subunit F	
<i>aldH</i>	J0661_06320	aldehyde dehydrogenase	metabolism of alcohols and aldehydes
-	J0661_06405	zinc-type alcohol dehydrogenase-like protein	

Table S13. Genes involved in osmotic stress tolerance

Gene	Locus tag	Product	Pathway
<i>betA</i>	J0661_19755	choline dehydrogenase	glycine betaine biosynthesis
<i>betT</i>	J0661_06100	choline BCCT transporter <i>BetT</i>	
	J0661_20740		
<i>betL</i>	J0661_19765	transcriptional regulator <i>BetI</i>	
<i>betB</i>	J0661_19760	betaine-aldehyde dehydrogenase	proline biosynthesis
-	J0661_03005	gamma-glutamyl phosphate reductase	