

Supplementary data:

Table 1. Identification of various virulence factors in *R. solanacearum*: Rs-09-161, Rs-10-244, GMI1000.

Gene name	Rs-09-161 locus tag*	Accession no.	Rs-10-244 locus tag*	Accession no.	GMI1000 locus tag	Location	Gene description
Exopolysaccharide							
epsA	RALSO161_m00209880	KY661391	RALSO244_m00210550	KY661392	Rsp1020	Megaplasmid	EPS I polysaccharide export outer membrane transmembrane protein
epsB	RALSO161_m00209860	KY661393	RALSO244_m00210530	KY661394	Rsp1018	Megaplasmid	EPS I polysaccharide export transmembrane protein
epsC	RALSO161_m00209850	KY661395	RALSO244_m00210520	KY661396	Rsp1017	Megaplasmid	Udp-n-acetylglucosamine 2-epimerase protein
epsD	-	-	-	-	-	-	Absent in phylotype I strains
epsF	RALSO161_m00209820	KY661399	RALSO244_m00210490	KY661400	Rsp1014	Megaplasmid	EPS I polysaccharide export inner membrane transmembrane protein
epsE	RALSO161_m00209830	KY661397	RALSO244_m00210500	KY661398	Rsp1015	Megaplasmid	EPS I polysaccharide export inner membrane transmembrane protein
epsP	RALSO161_m00209870	KY661401	RALSO244_m00210540	KY661402	Rsp1019	Megaplasmid	Low molecular weight protein-tyrosine- phosphatase
epsR	RALSO161_m00203460	KY661403	RALSO244_m00203750	KY661404	Rsp0338	Megaplasmid	Negative regulator of exopolysaccharide production transcription regulator protein
Cell wall degrading enzymes (CWDE)							
PehA	RALSO161_m00208600	KY661405	RALSO244_m00209360	KY661406	RSp0880	Megaplasmid	Polygalacturonase precursor (pectinase) signal peptide protein
PehB	RALSO161_m00118040	KY661407	RALSO244_m00117610	KY661408	RSc1756	Chromosome	Exo-poly-galacturonase signal peptide protein
PehC	RALSO161_m00208120	KY661409	RALSO244_m00208880	KY661410	RSp0833	Megaplasmid	Polygalacturonase transmembrane protein
Pme	RALSO161_m00201470	KY661411	RALSO244_m00201620	KY661412	RSp0138	Megaplasmid	Putative pectinesterase

Egl	RALSO161_m00201640	KY661413	RALSO244_m00201830	KY661414	RSp0162	Megaplasmid	Endoglucanase precursor (endo-1,4-BETA- glucanase) protein
CbhA	RALSO161_m00205550	KY661415	RALSO244_m00206300	KY661416	Rsp0583	Megaplasmid	exoglucanase A
Chemotaxis							
cheA	RALSO161_m00213570	KY661427	RALSO244_m00214120	KY661428	Rsp1408	Megaplasmid	Chemotaxis sensor histidine kinase transcription regulator protein
cheW	RALSO161_m00213560	KY661417	RALSO244_m00214110	KY661418	Rsp1407	Megaplasmid	chemotaxis protein CheW
Swimming motility							
fliC	RALSO161_m00203910	KY661423	RALSO244_m00204190	KY661424	Rsp0382	Megaplasmid	Flagellin protein
flgM	RALSO161_m00203480	KY661425	RALSO244_m00203770	KY661426	Rsp0340	Megaplasmid	Negative regulator of flagellin synthesis (anti- sigma-28 factor) protein
Twitching motility							
pilA	RALSO161_m00105750	KY661419	RALSO244_m00105800	KY661420	Rsc0558	Chromosome	Type 4 fimbrial pilin signal peptide protein
pilP	RALSO161_m00130530	KY661421	RALSO244_m00129280	KY661422	Rsc2972	Chromosome	Fimbrial type-4 assembly lipoprotein

*Locus tag of Rs-09-161 and Rs-10-244 is the tag provided during assembly and annotation of the genome data.

Table 2. Comparison of the general features of the *R. solanacearum* strain Rs-09-161 and Rs-10-244 with GMI1000.

Features	Rs-09-161	Rs-10-244	GMI1000
Genome size (MB)	5.645	5.659	5.81
Chromosome	3.68	3.66	3.72
Megaplasmid	1.95	1.99	2.09
Per cent GC	66.82	66.98	66.97
Number of protein coding genes	5185	5171	5129
Average length of protein coding genes (bp)	974.85	969.3	989

Table 3. Sequence similarity of virulence genes of Rs-09-161 and Rs-10-244 with representative phylotype strains.

	epsA		epsB		epsC		epsE		epsF		epsP		epsR
	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244	Rs-09-161
Rs-09-161													
Rs-10-244	0.995357		0.997778		0.99734		0.996186		0.996818		1		0.999
GMI1000_(P-I)	0.999071	0.996286	0.996444	0.997778	0.998227	0.99734	0.996949	0.996186	0.998409	0.995227	0.997717	0.997717	1
CFBP2957_(P-IIA)	0.907149	0.907149	0.923111	0.922222	0.935284	0.93617	0.888635	0.89016	0.894193	0.894193	0.906393	0.906393	0.885
Po82_(P-IIB)	0.899721	0.899721	0.928	0.927111	0.934397	0.935284	0.887872	0.890923	0.889419	0.890215	0.917808	0.917808	0.887
CMR15_(P-III)	0.955432	0.954503	0.975556	0.974222	0.967199	0.966312	0.976354	0.978642	0.956245	0.957836	0.984018	0.984018	0.965
Psi07_(P-IV)	0.931291	0.930362	0.936889	0.935556	0.960993	0.960106	0.919908	0.922197	0.90533	0.904535	0.945205	0.945205	0.918

	pglA		PehB		PehC		Pme		egl		CbhA	
	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244
Rs-09-161												
Rs-10-244	0.987835		0.991214		0.993615		0.997		0.991		0.997018	
GMI1000_(P-I)	0.993512	0.991079	0.992248	0.992765	0.994106	0.998527	0.992	0.994	0.99	0.995	0.992248	0.991652
CFBP2957_(P-IIA)	0.912409	0.914842	0.90491	0.90491	0.961198	0.963163	0.898	0.897	0.93	0.933	absent	absent
Po82_(P-IIB)	0.898621	0.901054	0.902326	0.901292	0.924853	0.928291	0.909	0.907	0.928	0.929	absent	absent
CMR15_(P-III)	0.946472	0.949716	0.967442	0.967959	0.971022	0.972495	0.952	0.952	0.95	0.953	0.880143	0.878354
Psi07_(P-IV)	0.911	0.91	0.886	0.884	0.928	0.931	0.893	0.892	0.946	0.949	0.951699	0.949911

	CheA		CheW		fliC		flgM		pilA		pilP	
	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244	Rs-09-161	Rs-10-244
Rs-09-161												
Rs-10-244	0.997		0.997967		1		0.996885		0.895277		0.996337	
GMI1000_(P-I)	0.998	0.998	0.995935	0.997967	0.998783	0.998783	1	0.996885	0.913758	0.926078	0.996337	1
CFBP2957_(P-	0.945	0.945	0.96748	0.969512	0.980535	0.980535	0.906542	0.909657	0.882957	0.936345	0.941392	0.945055

IIA)												
Po82_(P-IIB)	0.948	0.948	0.97561	0.977642	0.956204	0.956204	0.900312	0.903427	0.817248	0.794661	0.935897	0.93956
CMR15_(P-III)	0.975	0.976	0.989837	0.99187	0.995134	0.995134	0.953271	0.956386	0.73922	0.724846	0.981685	0.985348
Psi07_(P-IV)	0.947	0.948	0.965447	0.96748	0.952555	0.952555	0.950156	0.953271	0.747433	0.74538	0.961538	0.965201