

FigureS1 (a)Electrophoretic analysis of polymerase chain reaction(PCR)-amplified DNA from *R. solanacearum* strains RsM and RsH using primer pairs(Nmult21F/Nmult21RR and 759/760)(Fegan and Prior, 2005). LanesM. DNA Marker DL2000; line 1.a representative phylotype I in *R. solanacearum* strain RsM ; line2. a representative phylotype I in *R. solanacearum* strain RsH I; line3. *R. solanacearum*-specific band in RsM; line4. *R. solanacearum*-specific band in RsH, the arrow represent the Phylotype I specific band (166bp); (b) PCR products of different phylotypes.

NW Score	Identities	Gaps	Str
1332	666/666(100%)	0/666(0%)	Plu:
Query 1	ACCGACACCAAGCCCTGAAGACGGCCGCCACCACTCGATCTCGCCGTTGTGGCTCACC	60	
Sbjct 1	ACCGACACCAAGCCCTGAAGACGGCCGCCACCACTCGATCTCGCCGTTGTGGCTCACC	60	
Query 61	GTCGCCAAGGACAGCGCGGCGTTACGGTGAGCGGCACGCGACGGTGCGCTATGGCGCC	120	
Sbjct 61	GTCGCCAAGGACAGCGCGGCGTTACGGTGAGCGGCACGCGACGGTGCGCTATGGCGCC	120	
Query 121	GGCAGCGCGTGGGTGGCGAAGAGCATGTCCGGCACAGGCCAGTGACCGCGCCCTTCTTC	180	
Sbjct 121	GGCAGCGCGTGGGTGGCGAAGAGCATGTCCGGCACAGGCCAGTGACCGCGCCCTTCTTC	180	
Query 181	GGCAAGGATCCGGCGCGCGGTGTCGCCAAGGTGTGCCAAGTGCGCAGGGCACGGGCACC	240	
Sbjct 181	GGCAAGGATCCGGCGCGCGGTGTCGCCAAGGTGTGCCAAGTGCGCAGGGCACGGGCACC	240	
Query 241	CTGCTGTGGCGCGGCTCAGCCTGGCCGGCGCCGAGTTCGGGGAGGGCAGCCTGCCGGC	300	
Sbjct 241	CTGCTGTGGCGCGGCTCAGCCTGGCCGGCGCCGAGTTCGGGGAGGGCAGCCTGCCGGC	300	
Query 301	ACCTACGGGAGCAACTACATCTATCCGTCCGCCGACAGCGGACCTACTACAAGAACAAG	360	
Sbjct 301	ACCTACGGGAGCAACTACATCTATCCGTCCGCCGACAGCGGACCTACTACAAGAACAAG	360	
Query 361	GGCATGAACCTGGTGGCGCTGCCGTTCCGCTGGGAGCGGCTGCAGCCACGCTCAACCAG	420	
Sbjct 361	GGCATGAACCTGGTGGCGCTGCCGTTCCGCTGGGAGCGGCTGCAGCCACGCTCAACCAG	420	
Query 421	GGGCTCGACGCAACGAGCTGTGCGGCTGACCGGGTTCGTCAACGCCGTGACGGCGGCC	480	
Sbjct 421	GGGCTCGACGCAACGAGCTGTGCGGCTGACCGGGTTCGTCAACGCCGTGACGGCGGCC	480	
Query 481	GGCCAGACGGTGTGCTCGATCCGCACAACCTACGCGGCTACTACGGCAACGTGATCGGC	540	
Sbjct 481	GGCCAGACGGTGTGCTCGATCCGCACAACCTACGCGGCTACTACGGCAACGTGATCGGC	540	
Query 541	TCGAGCGCGGTGCCCCAACAGCGCGTACGCCGATTCTGGCGGCGGTGGCCACCCAGTTC	600	
Sbjct 541	TCGAGCGCGGTGCCCCAACAGCGCGTACGCCGATTCTGGCGGCGGTGGCCACCCAGTTC	600	
Query 601	AAGGGCAATGCCCGGCTCATCTTCGGGCTGATGAACGAGCCCAATTCGATGCCGACCGAG	660	
Sbjct 601	AAGGGCAATGCCCGGCTCATCTTCGGGCTGATGAACGAGCCCAATTCGATGCCGACCGAG	660	
Query 661	CAGTGG 666		
Sbjct 661	CAGTGG 666		

Figure S2 Comparison of *egl* gene between and *R. solanacearum* strains RsM(upper sequence) and

RsH(lower sequence).

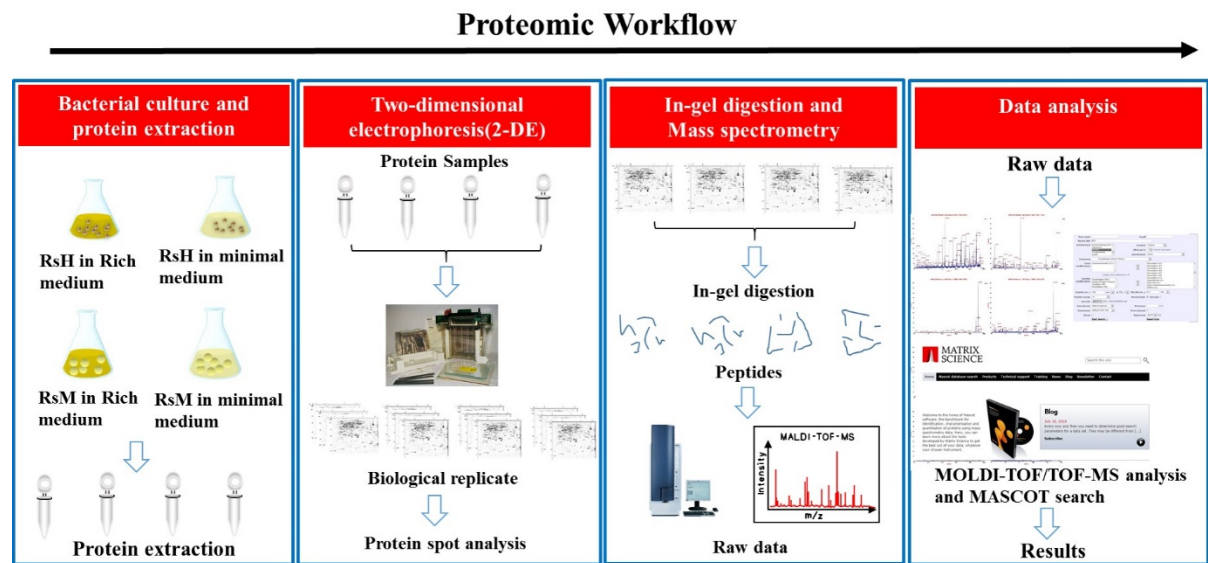


Figure S3 Experimental system of proteomic workflow.

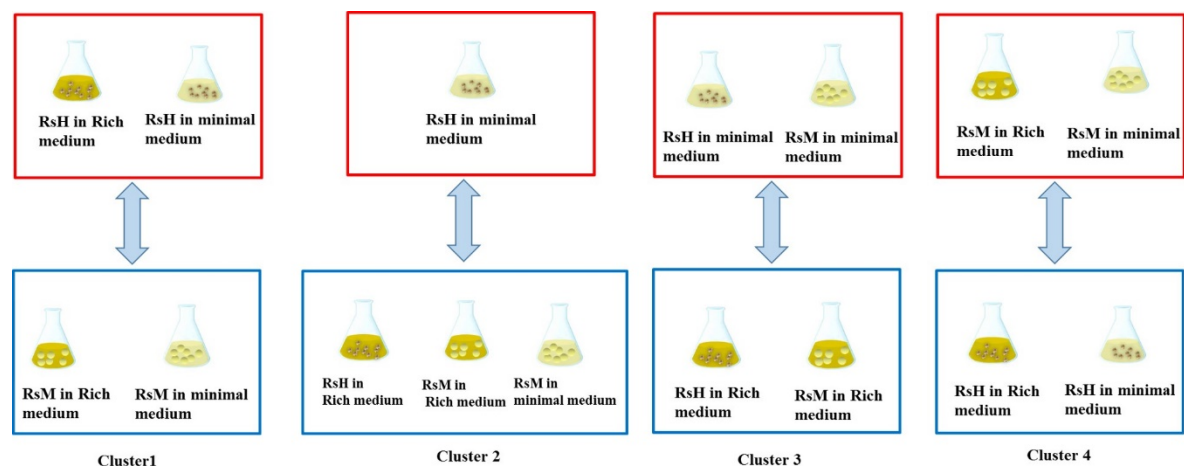


Figure S4 a brief layout of the comparison based on the protein abundance in different samples. Red box represent the protein abundance increased compared with those in blue box samples.