

Supplementary tables

Fire blight host-pathogen interaction: proteome profiles of *Erwinia amylovora* infecting apple rootstocks

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Supplementary table S2.

Primers used in this study

Gene name	Forward Primer	Reverse Primer
<i>Primers for reference genes LMG2024</i>		
<i>proC</i>	GCCGGCCTATGTGTTTATGT	GATTGCGCTGCAAACCTGATA
<i>rpoS</i>		
<i>Primers for reference genes PFB5</i>		
<i>rpsL</i>	AACCCGCACTGCGTAAAGT	GGATCAGGATCACGGAGTGT
<i>gyrA</i>	CGAGCACGTTTCATAGCGTAA	TATGCAATGTCGGTCATCGT
<i>Primers for genes related to stress</i>		
<i>clpB</i>	GCTTTACGCTGCATGTTTCA	GCTGCTGGATAGCTCGTTTTC
<i>katA</i>	GCCAGTGATGAGCATTCTT	TGCGTTCACGGTTGAAATTA
<i>htpG</i>	GGAAGGCCAGGAGAAGATT	GAACCTCGATGCCTTTCTTG
<i>pspA</i>	AACAAAAGCTGACCGACCTG	CTTCCAGCTCGCTGATTTT
<i>sodA</i>	CAGTTTGGCGATCAGCTCTT	CACACCAAACCCATCAAGC
<i>cspA</i>	AAGTTTTCGGCTTCATCTCC	TGACCTTCTTCCAGCGTCTT
<i>dps</i>	CGATATGCGCAAAGCTATCA	TGGACTCGATGAACCACAGA
<i>dnaK</i>	GTTAGTCCTGGCCATCGGTA	AGGGATTCAACTGCATCTGG
<i>sspA</i>	ATTGACCTCAACCCATACCG	GGAAAACGTTTCGTCCAGGTA
<i>ibpA</i>	GGATAACCCCGTTATTTCC	CGCTTTACCGTTCATCCATT
<i>Primers for genes related to the F₀F₁-ATP synthase</i>		
<i>atpA</i>	ACCGATTTGTAACCGGTCTG	GCTATCGACAACGACGGTTT
<i>atpD</i>	TATGCCTTCTGCGGTAGGTT	AGGTGATTGAACCGTTTTG
<i>atpF</i>	TGGGTGACGATCTTGTTACG	CTCAGGTCATCATCGAGCAG

Supplementary table S3.

Proteins identified as higher abundant *in vitro* for both strains

Spot number	Description	Gene name	LMG2024		PFB5	
			Anova P-value	Fold change	Anova P-value	Fold change
16	phosphoribosylformylglycineamide synthetase	<i>purL</i>	6,50E-04	8,5	0,002	4,6
44	aconitate hydratase 2	<i>acnB</i>	0,007	4,6	0,001	2,1
45	aconitate hydratase 2	<i>acnB</i>	0,006	3,8	0,011	2,3
	preprotein translocase subunit SecA	<i>secA</i>				
73	5-methyltetrahydropteroyltriglutamate/homocysteine S-methyltransferase	<i>metE</i>	7,95E-04	13,3	2,48E-04	6,8
75	5-methyltetrahydropteroyltriglutamate/homocysteine S-methyltransferase	<i>metE</i>	0,002	4,8	0,007	3,1
78	5-methyltetrahydropteroyltriglutamate/homocysteine S-methyltransferase	<i>metE</i>	4,92E-04	15,9	8,60E-05	9,5
110	phosphate acetyltransferase	<i>pta</i>	2,28E-04	3,2	0,014	2
124	dipeptidyl carboxypeptidase II	<i>dcp</i>	8,37E-06	2,4	0,003	4,1
149	transketolase	<i>tktA1</i>	4,04E-06	3,2	0,004	2,7
150	transketolase	<i>tktA1</i>	1,11E-05	11,7	3,65E-04	7
151	transketolase	<i>tktA1</i>	1,21E-06	16,6	2,92E-04	6
166	Zn-dependent oligopeptidase	<i>prlC</i>	0,002	2,9	0,003	2,3
174	succinate dehydrogenase flavoprotein subunit	<i>sdhA</i>	0,006	2,3	5,94E-04	2,5
175	protease maturation protein	<i>ybaU</i>	0,002	2,4	0,007	2,5
274	beta-galactosidase/beta-glucuronidase	<i>lacZ1</i>	0,012	2	0,011	2
	inosine-5'-monophosphate dehydrogenase	<i>guaB</i>				
301	argininosuccinate lyase	<i>argH</i>	5,34E-05	4,8	0,005	2,2
	glutamyl-tRNA synthetase	<i>gltX</i>				
341	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase	<i>murF</i>	1,99E-05	11,6	0,007	3,6
	serine hydroxymethyltransferase	<i>glyA</i>				
345	serine hydroxymethyltransferase	<i>glyA</i>	1,31E-04	7,6	0,005	3,3
372	harpin elicitor	<i>hrpN</i>	0,005	4,8	0,003	10,2

385	carboxypeptidase G2	<i>EAMY_3587</i>	5,52E-04	2,3	0,012	2,3
	acetate kinase	<i>ackA</i>				
	protein TolB	<i>tolB</i>				
	morphinone reductase	<i>nemA3</i>				
	bifunctional acetylornithine delta-aminotransferase/N-succinyldiaminopimelate aminotransferase	<i>aat3</i>				
388	acetate kinase	<i>ackA</i>	3,46E-04	3,9	0,001	2,9
	bifunctional acetylornithine delta-aminotransferase/N-succinyldiaminopimelate aminotransferase	<i>aat3</i>				
419	phospho-2-dehydro-3-deoxyheptonate aldolase	<i>aroF</i>	0,001	7	0,013	2,8
505	N-acetyl-gamma-glutamyl-phosphate reductase	<i>argC</i>	2,88E-05	10,9	2,05E-04	4,6
	5,10-methylenetetrahydrofolate reductase	<i>metF</i>				
532	iron ABC transporter substrate-binding protein	<i>sitA</i>	2,63E-05	11,1	1,20E-040	6,6
546	flagellin, filament structural protein FliC	<i>fliC1</i>	5,05E-05	10,1	0,007	2,5
	2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase	<i>dapD</i>				
612	putative ABC transport system, periplasmic component	<i>EAIL5_0767</i>	9,80E-05	3,6	0,013	2,5
619	glutaredoxin-2	<i>grxB</i>	1,16E-06	4,6	0,012	2,6
	hypothetical protein EAMY_1021	<i>EAMY_1021</i>				

Supplementary table S4.

Proteins identified as higher abundant *in planta* for both strains

Spot number	Description	Gene name	LMG2024		PFBS	
			Anova P-value	Fold change	Anova P-value	Fold change
219	oligopeptide ABC transporter substrate-binding protein OppA	<i>oppA1</i>	4,62E-04	6,7	0,009	3
220	acetolactate synthase large subunit	<i>alsS</i>	0,001	3,4	0,006	2,8
	catalase	<i>katA</i>				
258	ABC transporter substrate-binding protein	<i>dppA3</i>	0,001	7,9	0,013	2,9
313	6-phosphogluconate dehydrogenase	<i>metK</i>	0,01	2	0,014	3,3
425	DNA-directed RNA polymerase subunit alpha	<i>eno</i>	0,004	3,2	0,007	4,7
	hypothetical protein EAMY_2128	<i>gnd</i>				
	phosphoglycerate kinase	<i>rpoA</i>				
457	transaldolase A	<i>ycdO</i>	6,59E-04	3,1	8,13E-04	3,7
	glyceraldehyde-3-phosphate dehydrogenase	<i>pgk</i>				
458	oxidoreductase	<i>mocA</i>	7,46E-04	3,5	6,13E-04	3,1
	glyceraldehyde 3-phosphate dehydrogenase A	<i>gapA</i>				
461	oxidoreductase	<i>mocA</i>	3,96E-04	2,4	0,008	2,1
	D-arabinose 5-phosphate isomerase	<i>yrbH</i>				
	glyceraldehyde 3-phosphate dehydrogenase A	<i>gapA</i>				
462	FOF1 ATP synthase subunit beta	<i>atpD</i>	2,07E-04	4,1	0,002	5,3
464	ABC transporter substrate-binding protein	<i>dppA3</i>	2,79E-05	5,5	7,40E-05	4,3
549	septum site-determining protein minD	<i>minD</i>	0,001	2,5	0,004	2,2
	FeS assembly ATPase SufC	<i>sufC</i>				
	enolase	<i>eno</i>				
570	septum site-determining protein minD	<i>minD</i>	0,001	3,6	1,91E-04	3,5
	elongation factor EF-P	<i>yeiP</i>				
	FOF1 ATP synthase subunit beta	<i>atpD</i>				
572	sorbitol-6-phosphate dehydrogenase	<i>srlD</i>	0,002	2,3	0,005	3,7
579	sorbitol-6-phosphate dehydrogenase	<i>srlD</i>	3,06E-05	8,2	3,35E-06	4
616	NAD(P)H-flavin reductase	<i>ubiB</i>	1,57E-06	22,5	4,90E-04	6,3
	hypothetical protein EAMY_1021	<i>EAMY_1021</i>				
	phage shock protein A	<i>pspA</i>				

631	dethiobiotin synthetase	<i>ynfK</i>	0,003	3	0,008	2,7
647	hypothetical protein EAM_0402	<i>EAM_0402</i>	0,003	2	0,004	2,6
655	hypothetical protein EAM_0402	<i>EAM_0402</i>	9,22E-05	3,1	0,003	3,3
	carbonate dehydratase	<i>cynT</i>				
657	3-oxoacyl-ACP reductase	<i>fabG</i>	1,64E-05	4,4	0,01	2,3
	superoxide dismutase, manganese	<i>sodA</i>				
668	alkyl hydroperoxide reductase subunit C	<i>ahpC</i>	1,70E-04	5,3	0,002	4,7
688	peptide deformylase	<i>def</i>	0,015	3,6	0,002	2,5
694	ribosome recycling factor	<i>frr</i>	0,003	2,2	0,006	2,5
	hypothetical protein EAMY_0970	<i>yajQ</i>				
719	hypothetical protein EAMY_1435	<i>yceI</i>	0,007	5	0,007	3,6
724	shikimate kinase I	<i>aroK</i>	9,93E-05	6	3,45E-04	5,5
	ATP synthase subunit B protein	<i>atpF</i>				
	DNA protection during starvation protein	<i>dps</i>				
730	DNA protection during starvation protein	<i>dps</i>	0,003	4,1	0,002	4,3
733	putative type VI secretion system, effector protein hcp	<i>EAIL5_3094</i>	0,008	2,7	0,006	2,5
	DNA protection during starvation protein	<i>dps</i>				
753	bacterioferritin comigratory protein	<i>bcp</i>	0,001	13,2	0,008	8,5
756	50S ribosomal protein L9	<i>rplI</i>	0,009	3,2	0,011	2,4
767	DNA-binding protein H-NS	<i>hns</i>	0,007	3,7	0,001	4,1
	30S ribosomal protein S6	<i>rpsF</i>				
768	DNA protection during starvation protein	<i>dps</i>	7,45E-04	3,1	5,29E-04	3,2
	global DNA-binding transcriptional dual regulator H-NS	<i>hns</i>				
	30S ribosomal protein S6	<i>rpsF</i>				
774	30S ribosomal protein S6	<i>rpsF</i>	0,002	4,7	0,011	2,7
775	30S ribosomal protein S6	<i>rpsF</i>	0,01	3	0,003	2,9
	hypothetical protein EAMY_1829	<i>EAMY_1829</i>				