

Additional file 6. RT-PCR analysis of the transcripts of some genes encoding CWP identified through proteomics.

A. Quantitative analysis

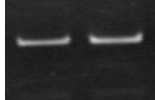
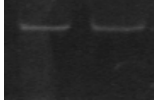
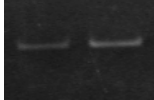
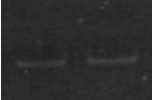
Results of Q (quantitative)-PCR are expressed in number of Cts (cycle thresholds). *At1g49240* encoding an actin was used as a control. Results of transcriptomics are expressed as \log_2 of signal intensity measured on CATMA arrays. Results of proteomics are indicated as follows: + means that the protein was identified; - means that the protein was not identified; nd means that the protein is not a cell wall protein. Note that the results of Q-PCR are consistent with CATMA results. The higher the level of transcripts measured on CATMA arrays, the lower the number of Cts measured by Q-PCR.

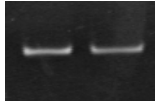
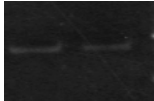
gene accession number	functional annotation	Q-PCR		transcriptomics (CATMA)		proteomics
		5-days Ct	11 days Ct	5-days \log_2	11 days \log_2	
At1g49240	actin 8	21.89	21.69	13.42	13.29	nd
At5g11420	expressed protein (DUF642)	23.68	23.61	12.14	12.05	+
At1g28290	AtAGP31	22.91	22.18	11.98	11.89	+
At3g16850	GH28 (polygalacturonase)	23.60	23.46	8.39	8.18	+
At1g05850	GH9	21.62	21.78	13.22	12.68	-
At1g66180	Asp protease	23.37	23.62	11.80	11.06	-
At3g07130	Purple acid phosphatase (AtPAP15)	27.00	27.07	6.43	6.47	+
At1g10550	GH16 (AtXTH33)	28.38	28.79	6.47	6.47	+

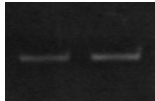
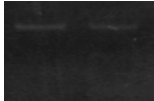
Semi-quantitative analysis

B. Genes with high or moderate level of transcripts in CATMA analysis and for which the proteins were identified by proteomics (+). *At1g49240* encoding an actin was used as a control. **C.** Genes with high level of transcripts in CATMA analysis but for which the proteins were not identified by proteomics (-); or with low level of transcripts in CATMA analysis for which the proteins were identified by proteomics (+). **D.** Genes with transcript level under background in CATMA analysis (lower than 6.83) and for which the proteins were identified by proteomics (+). PCR was run for 26 cycles for genes having high levels of transcripts in CATMA analysis (**B** and **C**), or for 30 cycles for genes having level of transcripts lower than background in CATMA analysis (**D**).

Sequences of primers are provided in Additional file 6. Note that PCR amplifications result in a single band at the expected size.

B	days	At1g49240		At5g11420		At1g28290		At3g16850	
		5	11	5	11	5	11	5	11
	PCR: 26 cycles								
	CATMA	13.42	13.29	12.14	12.05	11.98	11.89	8.39	8.18
	proteomics	nd	nd	+	+	+	+	+	+

C	days	At1g05850		At1g66180	
		5	11	5	11
	PCR: 26 cycles				
	CATMA	13.22	12.68	11.80	11.06
	proteomics	-	-	-	-

D	days	At3g07130		At1g10550	
		5	11	5	11
	PCR: 30 cycles				
	CATMA	6.43	6.47	6.47	6.47
	proteomics	+	+	+	+