

Potato (*Solanum tuberosum* L.) tuber ageing induces changes in the proteome and antioxidants associated with the sprouting pattern. Pierre Delaplace, Marie-Laure Fauconnier, Kjell Sergeant, Jean-François Dierick, Mouhssin Oufir, Froukje van der Wal, Antoine H.P. America, Jenny Renaut, Jean-François Hausman, and Patrick du Jardin.

Supplementary data

Fig. S1. Changes in the lipid oxidation context during ageing. The carotenoid content (A) was measured spectrophotometrically according to Morris *et al.* (2004) after acetone extraction. The LOX activity assay was based on the measurement of the absorbance of conjugated dienes produced by the enzyme according to the method originally developed by Surrey (1964). The presented data are means of three independent replicates \pm SD. Means sharing the same letter were not statistically distinct using the Newman and Keuls test.

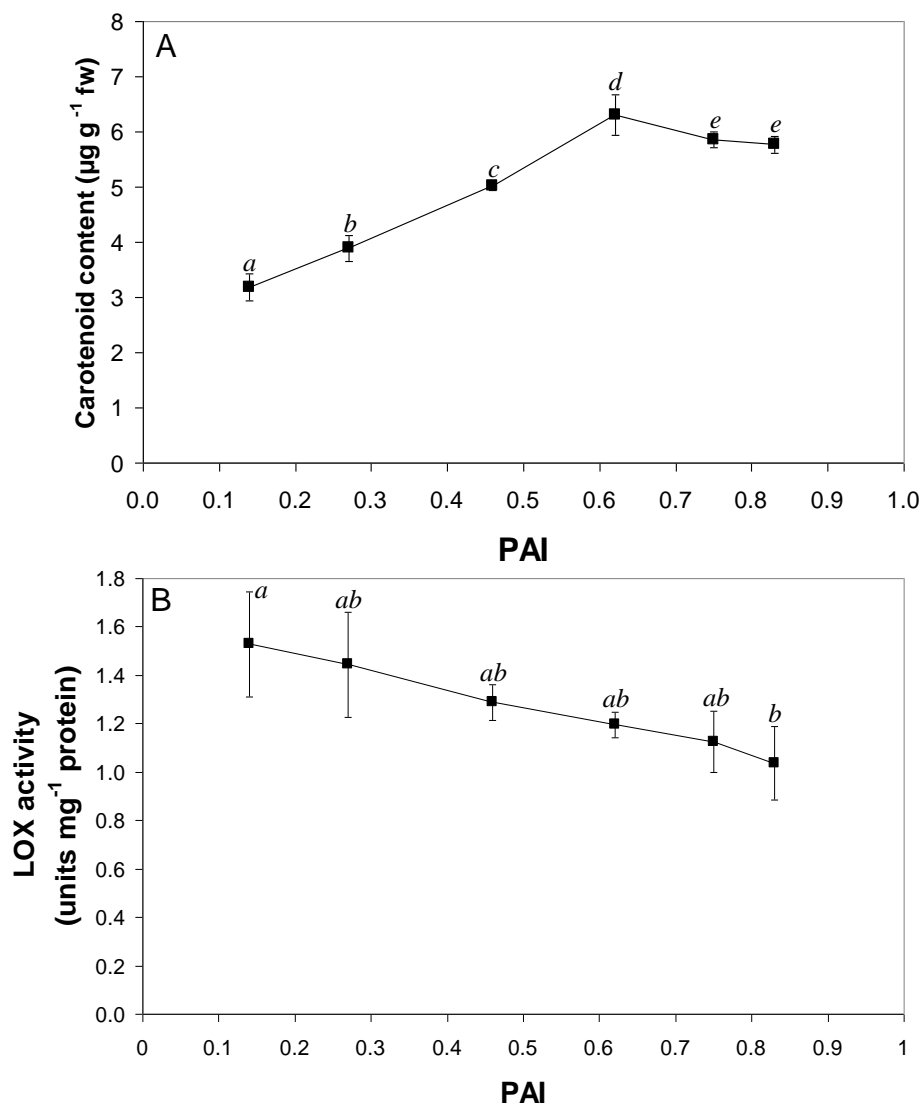


Table S1. MS/MS identifications of up-regulated proteins during potato ageing*.

Spot	Protein	Organism Gi Accession	Pept	experim. Mr	calc. Mr	Mass Δ	Sequences	E value	Pept. score
26	Phosphoglycerate mutase	<i>Solanum tuberosum</i> L. Gi 4582924	2	1546,7427	1546,6939	0,0488	K.ALEYEDFKDFDR.V	0,028	46
				1427,8027	1427,7521	0,0506	R.DAILSHKFDQVR.V	0,5	33
21	Enolase	<i>Solanum lycopersicum</i> L. Gi 19281	5	1803,9327	1803,9366	-0,0039	R.AAVPSGASTGIYEALRL.D	0,0038	54
				2003,0927	2003,0951	-0,0024	K.LVLPVPAFNVINGGSHAGNK.L	3,90E-07	92
				1859,8327	1859,8173	0,0154	K.SYDLNFKKEESNDGSQK.I	0,0075	50
				1910,9727	1910,9633	0,0094	K.LAMQEFMILPVGAANFK.E	1,50E-05	81
				1895,9527	1895,9489	0,0038	R.GNPTVEVDVHVSNGVFAR.A	1,10E-05	79
23	α -glucane phosphorylase (precursor)	<i>Solanum tuberosum</i> L. Gi 217999	3	1334,8127	1334,7710	0,0417	R.QLLNIFGIVYR.Y	0,001	58
				2524,1427	2524,1141	0,0286	R.SGAFGSYNYDDLIGSLEGNEGFR.A	3,30E-10	122
				1924,9917	1924,9682	0,0235	K.FVPDERFEEVKEFVR.S	0,0076	54
25	Tubulin (β -2 chain)	<i>Lupinus albus</i> L. Gi 8928412	1	1138,6864	1138,6862	0,0002	K.LAVNLIPFPR.L	5	26
1	Class I small Heat Shock Protein 1A	<i>Nicotiana tabacum</i> L. Gi 37704399	6	914,5510	914,5185	0,0325	R.ILQISGER.S	0,13	42
				993,5229	993,4879	0,0350	R.ETSVFANAR.I	0,68	37
				1042,5427	1042,5083	0,0344	R.ETSVFAYAR.I	0,89	34
				1001,6027	1001,5658	0,0370	R.FRLPENVK.M	3,4	25
				2974,5027	2974,5188	-0,0161	R.SNIVDPLSLHIGDPFEGFPIANPPSSVR.E	8,50E-05	66
				1575,8627	1575,8442	0,0185	K.FRLPENVKMGEIK.A	0,42	36
20	DREPP4	<i>Nicotiana tabacum</i> L. Gi 7801133	4	1446,8127	1446,7969	0,0158	K.VLEIYEAHAVEIK.S	3,4	27
				2497,2727	2497,2739	-0,0012	K.AVSEASSNFGPSYVSGPILFVLEK.V	2,1	25
				1620,8727	1620,8762	-0,0035	K.FLDELVKIEFPGSK.A	0,012	49
				3186,5827	3185,6091	0,9736	K.VSTFIVVTEDKKGEPPAAAADDVHATATSVK.E	4,40E+02	19
15	Catalase	<i>Solanum tuberosum</i> L. Gi 40950550	3	1083,5727	1083,5349	0,0378	R.IFAYADTQR.H	77	14
				1608,9327	1608,8875	0,0452	K.TWPEDLLPLIPVGR.L	0,027	45
				1556,8327	1556,8020	0,0307	R.IGPNYMQLPVNAPK.C	0,077	41
5	Glyoxalase I	<i>Oryza sativa</i> L. Gi 4126809	5	1542,8227	1542,8253	-0,0025	K.SAEVNVLTQELGGK.I	0,055	43
				2424,2527	2424,2688	-0,0161	K.GGSTVIAFVKDPDGYLFEILQR.E	0,016	27
				1480,8327	1480,8361	-0,0034	K.ITRQPGSIPGLNTK.I	16	18
				1110,5927	1110,6033	-0,0106	R.QPGSIPGLNTK.I	3,30E+02	7
				913,4707	913,4909	-0,0202	R.SIKFYEK.A	5,7	25
11	20S proteasome subunit	<i>Glycine max</i> (L.) Merr. Gi 7839485	3	2263,2827	2263,2827	0,0001	R.LFQVEYAIKLGSTAIGIK.T	0,092	38
				1327,8127	1327,7823	0,0305	K.TKEGVVLAWEKR.I	22	30
				1726,8127	1726,7910	0,0217	R.TEYDRGVNTFSPEGR.L	5,3	25
16	5-Lipoxygenase (breakdown product)	<i>Solanum tuberosum</i> L. Gi 2789652	3	1658,9327	1658,9395	-0,0068	R.LYEGGIKLPQGPLFK.A	0,13	52
				1911,0727	1911,0829	-0,0102	R.IPLILSLDIYVPRDER.F	8,4	19
				1510,9127	1510,9123	0,0005	R.IPLILSLDIYVPR.D	3,3	21

*Each identification mentions the protein name, its Gi accession number as well as the organism, the number of fragmented peptides matching a database entry, the experimental and calculated relative molecular weights, the difference between both MW values, the peptide sequences, the E values and the peptide scores.

Table S1. MS/MS identifications of up-regulated proteins during potato ageing (continued)*.

Spot	Protein	Organism Gi Accession	Pept	Experim. Mr	Calc. Mr	Mass Δ	Sequences	E value	Pept. score
2	Patatin precursor	<i>Solanum tuberosum</i> L. Gij73426671	3	1704,9025	1704,8967	0,0058	-.TLGEMVTVLSIDGGGIK.G	3,50E-009	120
				1756,9445	1756,9359	0,0086	R.VHQALTEVAISSFDIK.T	9,50E-009	115
				3641,7100	3641,8035	-0,0934	R.LADYFDVIGGTSTGGLLTAMITTPNENRPFAAAK.D	4,7	27
3	Patatin (A3 group)	<i>Solanum tuberosum</i> L. Gij84316375	2	1046,6096	1046,6124	-0,0028	K.TNKPVIFTK.S	3,8	29
				1756,9298	1756,9359	-0,0061	R.VHQALTEVAISSFDIK.T	2,90E-008	111
4	Patatin 04	<i>Solanum tuberosum</i> L. Gij84316397	1	1756,9422	1756,9359	0,0063	R.VHQALTEVAISSFDIK.T	2,70E-008	111
6	Patatin precursor	<i>Solanum tuberosum</i> L. Gij73426671	3	1704,9135	1704,8967	0,0168	-.TLGEMVTVLSIDGGGIK.G	1	35
				1756,9480	1756,9359	0,0121	R.VHQALTEVAISSFDIK.T	0,02	52
				1867,1079	1867,0818	0,0261	K.GIIPGIILEFLEGQLQK.M	0,0036	57
7	Patatin precursor	<i>Solanum tuberosum</i> L. Gij73426675	1	1756,9345	1756,9359	-0,0014	R.VHQALTEVAISSFDIK.T	0,00021	72
8	Patatin precursor	<i>Solanum tuberosum</i> L. Gij129640	2	1498,7930	1498,7820	0,0108	K.IFEPSPGFHLVEPK.Y	3,1	28
				1756,9430	1756,9359	0,0068	R.VHQALTEVAISSFDIK.T	0,00034	67
9	Patatin precursor	<i>Solanum tuberosum</i> L. Gij73426683	1	1875,9011	1875,8962	0,0049	K.SVSEDNHETYEVALKR.F	0,00059	68
10	Patatin 07	<i>Solanum tuberosum</i> L. Gij84316403	3	1463,6743	1463,6892	-0,0149	K.DNPETYEEALKR.F	92	15
				1875,8630	1875,8962	-0,0335	K.SVSEDNHETYEVALKR.F	2,8	28
				1288,683	1288,6663	0,0164	R.LAQEDPAFASIK.S	0,0051	56
12	Patatin precursor	<i>Solanum tuberosum</i> L. Gij73426683	2	1498,7801	1498,7820	-0,0018	K.IFEPSPGFHLVEPK.Y	1,80E+002	12
				1756,9350	1756,9359	-0,0009	R.VHQALTEVAISSFDIK.T	1,9	32
13	Patatin precursor	<i>Solanum tuberosum</i> L. Gij73426683	2	1704,9192	1704,8967	0,0225	-.TLGEMVTVLSIDGGGIK.G	2,2	32
				1756,9458	1756,9359	0,0099	R.VHQALTEVAISSFDIK.T	0,00069	67
14	Patatin precursor	<i>Solanum tuberosum</i> L. Gij73426683	2	1498,7857	1498,7820	0,0038	K.IFEPSPGFHLVEPK.Y	1,6	33
				1756,9358	1756,9359	-0,0001	R.VHQALTEVAISSFDIK.T	0,00024	71
17	Patatin precursor	<i>Solanum tuberosum</i> L. Gij73426671	3	1756,9331	1756,9359	-0,0028	R.VHQALTEVAISSFDIK.T	1,2E+002	14
				1204,6150	1204,5724	0,0426	R.AEEDPAFASIR.S	1,1E+002	15
				1360,7130	1360,6735	0,0392	R.RAEEDPAFASIR.S	22	20
18	Patatin precursor	<i>Solanum tuberosum</i> L. Gij73426683	2	1046,5801	1046,6124	-0,0323	K.TNKPVIFTK.S	1,50E+002	14
				1288,6227	1288,6663	-0,0436	R.LAQEDPAFASIK.S	3	30
19	Patatin precursor T5	<i>Solanum tuberosum</i> L. Gij129644	4	1166,5800	1166,6005	-0,0208	K.YLMQVLQEKL.L	0,083	45
				1834,9650	1834,9676	-0,0029	K.QMLLLSLGTGTNSEFDK.T	0,0085	53
				1360,6630	1360,6735	-0,0108	R.RAEEDPAFASIR.S	0,0023	58
				1756,9430	1756,9359	0,0068	R.VHQALTEVAISSFDIK.T	0,00018	71

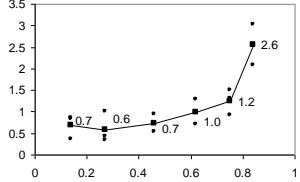
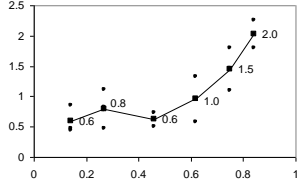
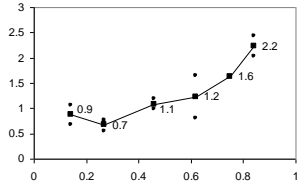
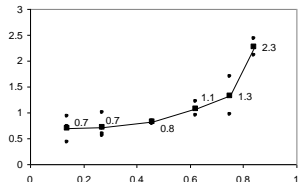
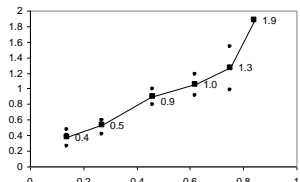
Table S2. MS/MS identifications of down-regulated proteins during potato ageing*.

Spot	Protein	Organism Gi Accession	Pept	experim. Mr	calc. Mr	Mass Δ	Sequences	E value	Pept. score
22	Actin	<i>Gossypium hirsutum</i> L. Gi 32186906	3	1773,8974	1773,8897	0,0078	K.NYELPDGQVITIGAER.F	0,42	39
				1882,9412	1882,9312	0,0100	K.LAYVALDYEQELETAR.S	0,0041	59
				2492,2305	2492,2394	-0,0089	R.SSSSIEKNYELPDGQVITIGAER.F	1E+002	15
29	Elongation factor	<i>Oryza sativa</i> L. Gi 115456914	2	1345,7667	1345,7717	-0,0050	R.VIYASQLTAKPR.L	2,5E+002	11
				1741,9002	1741,9038	-0,0036	K.AYLPVVESFGFSGTLR.A	9,3	26
27	Protein disulfide isomerase	<i>Ipomoea batatas</i> (L.) Lam. Gi 47933777	3	1037,6247	1037,5981	0,0266	R.GGPVVKPTLR.L	46	16
				1904,0727	1904,0367	0,0361	K.SQPIPEVNDEPVKVVVR.D	0,0019	55
				1556,8227	1556,7946	0,0281	K.LRGEVDFAHTVDAK.H	9,3	21
28	Protein disulfide isomerase	<i>Ipomoea batatas</i> (L.) Lam. Gi 47933777	3	1548,8527	1548,8147	0,0380	R.TKEAIIIEFIESNR.D	3,7	24
				1904,0727	1904,0367	0,0361	K.SQPIPEVNDEPVKVVVR.D	0,51	31
				1556,8227	1556,7946	0,0281	K.LRGEVDFAHTVDAK.H	9,9	20
24	26S Proteasome regulatory subunit 7	<i>Prunus persica</i> (L.) Batsch Gi 3172331	3	1406,6127	1406,6062	0,0066	R.FDDGVGGDNEVQR.T	5,9	23
				1388,7327	1388,7299	0,0028	R.KVEFGLPDLESR.T	1,00E+02	11
				1738,8427	1738,8348	0,0079	K.ACIVFFDEVDAIGGAR.F	14	19
30	Lipoxygenase I	<i>Solanum tuberosum</i> L. Gi 585417	3	1658,9352	1658,9395	-0,0043	R.LYEGGIKLPQGPLFK.A	0,44	33
				1261,6427	1261,6455	-0,0028	K.NTHINEFFLK.S	0,00011	72
				2074,0527	2074,0694	-0,0167	K.VSFQLISSVQGDPTNGLQGK.H	0,017	46
31	Lipoxygenase	<i>Solanum tuberosum</i> L. Gi 1495816	3	1658,9527	1658,9395	0,0132	R.LYEGGIKLPQGPLFK.A	0,00033	64
				2134,1127	2134,1098	0,0029	R.IFFANQPYPSETPELLR.K	0,0011	58
				1911,1027	1911,0829	0,0198	R.IPLILSLDIYVPRDR.F	0,016	46

*Each identification mentions the protein name, its Gi accession number as well as the organism, the number of fragmented peptides matching a database entry, the experimental and calculated relative molecular weights, the difference between both MW values, the peptide sequences, the E values and the peptide scores.

Table S3. Up-regulated protein abundance kinetics during ageing: partim patatin breakdown products.

The p values corresponding to ANOVA using PAI as fixed factor are presented as well as the ratios between extreme abundance values. Critical PAI values corresponding to the major changes are also presented in the table. Standard abundances as a function of PAI are displayed in the graphics.

Spot #	Protein	Organism Gi Accession	Physiological function	p ANOVA	Abundance ratio	Critical PAI	Expression kinetics
2	Patatin precursor	<i>Solanum tuberosum</i> L. Gi 73426671	Patatin breakdown products, amino acid source for protein synthesis	0.018	4.34	0.6	
3	Patatin (A3 group)	<i>Solanum tuberosum</i> L. Gi 84316375	Patatin breakdown products, amino acid source for protein synthesis	0.014	3.43	0.6	
4	Patatin 04	<i>Solanum tuberosum</i> L. Gi 84316397	Patatin breakdown products, amino acid source for protein synthesis	0.026	3.28	0.4	
6	Patatin precursor	<i>Solanum tuberosum</i> L. Gi 73426671	Patatin breakdown products, amino acid source for protein synthesis	0.0037	3.25	0.6	
7	Patatin precursor	<i>Solanum tuberosum</i> L. Gi 73426675	Patatin breakdown products, amino acid source for protein synthesis	4.4E-005	4.94	- (steady progression)	

Spot #	Protein	Organism Gi Accession	Physiological function	p ANOVA	Abundance ratio	Critical PAI	Expression kinetics
8	Patatin precursor	<i>Solanum tuberosum</i> L. Gi 129640	Patatin breakdown products, amino acid source for protein synthesis	0.00023	3.17	0.6	
9	Patatin precursor	<i>Solanum tuberosum</i> L. Gi 73426683	Patatin breakdown products, amino acid source for protein synthesis	0.0047	3.62	0.6	
10	Patatin 07	<i>Solanum tuberosum</i> L. Gi 84316403	Patatin breakdown products, amino acid source for protein synthesis	0.011	2.74	0.6	
12	Patatin precursor	<i>Solanum tuberosum</i> L. Gi 73426683	Patatin breakdown products, amino acid source for protein synthesis	0.0094	3.75	0.6	
13	Patatin precursor	<i>Solanum tuberosum</i> L. Gi 73426683	Patatin breakdown products, amino acid source for protein synthesis	0.00058	4.31	0.6	

Spot #	Protein	Organism Gi Accession	Physiological function	p ANOVA	Abundance ratio	Critical PAI	Expression kinetics
14	Patatin precursor	<i>Solanum tuberosum</i> L. Gi 73426683	Patatin breakdown products, amino acid source for protein synthesis	0.00013	4.88	0.6	
17	Patatin precursor	<i>Solanum tuberosum</i> L. Gi 73426671	Patatin breakdown products, amino acid source for protein synthesis	0.048	2.09	0.4	
18	Patatin precursor	<i>Solanum tuberosum</i> L. Gi 73426683	Patatin breakdown products, amino acid source for protein synthesis	0.0081	3.30	0.4	
19	Patatin precursor T5	<i>Solanum tuberosum</i> L. Gi 129644	Patatin breakdown products, amino acid source for protein synthesis	0.034	2.55	- (steady progression)	