Potato skin proteome is enriched with plant defence components. *Gilli Barel and Idit Ginzber*

Supplementary Data

Supplementary Figure S1. Representative images of 2-DE (pH interval of 4-7) of skin proteomes at four time points during tuber development (see Figure 1): 5 weeks post-sprout emergence (5W), when the skin is composed of only a few layers and suberization of the outer layers is just beginning; 8 weeks post-sprout emergence (8W), a period of active skin development; 5 days post-foliage removal to induce skin set (5dA); and 2 weeks after foliage removal (2WA), with mature skin that has almost set. The proteomes are similar. Some of the spots that are common for all proteomes are encircled with a dashed line for better identification of neighboring spots and to demonstrate the high similarity in the proteomes during skin development. A few spots exhibit high intensity on the 8W gel (light blue, green and purple circles). Dark blue line encircles POP_A polypeptides, dark green line encircles a group of patatin proteins.

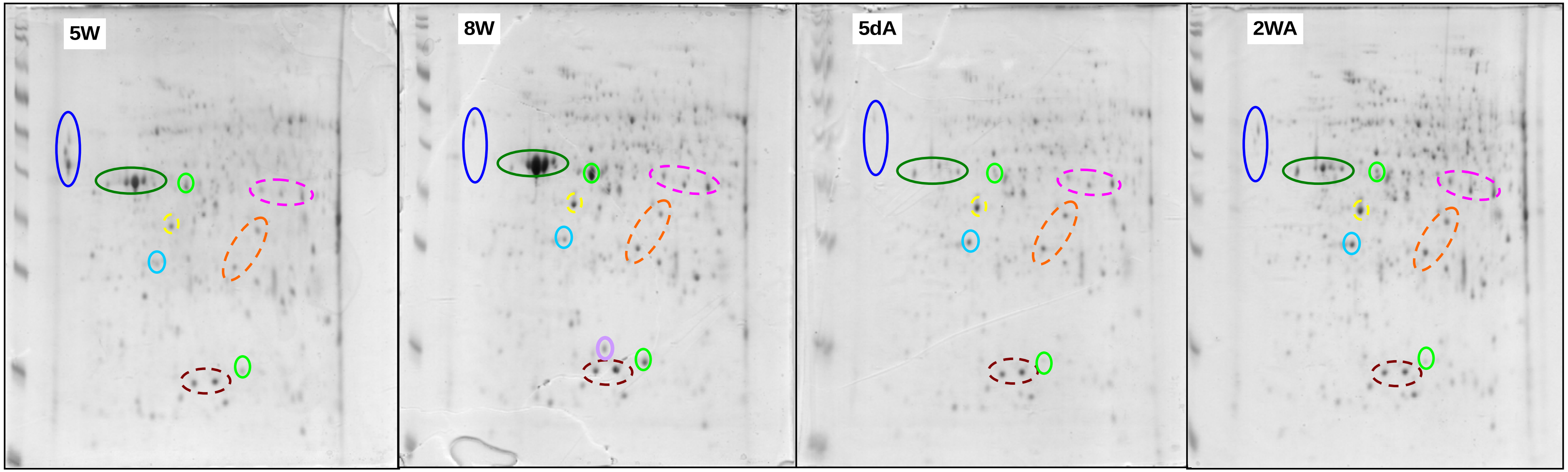

Table S1. *Comparison of results obtained from TIGR potato EST database as of February 2007 and NCBI non-redundant protein database as of September 2006*

Functional categories	Potato TA[a]	Match peptides[b]	Cover (%)[c]	Swiss-Prot Identification		Match peptides[b]	Cover (%)[c]
				Accession number	Organism		
Cell proliferation							
Actin (ACT)	TA24741	10	21	AAW63030	*Isatis tinctoria*	9	29
Adenosine kinase isoform 2S (ADK)	TA25950	1	8	ABB72823	*S. tuberosum*	2	10
P23 tumor protein-like (P23/TCTP)	TA24105	2	10	ABB29923	*S. tuberosum*	2	15
Proteasome α -7 subunit	TA26206	6	20	ABB86280	*S. tuberosum*	6	28
Proteasome β - 2A subunit	TA32826	8	30	CAC43325	*Nicotina tabacum*	3	19
Translation initiation factor 5A-3, eukaryotic (eIF-5A3)	TA23158	6	30	ABA81854	*S. tuberosum*	7	51
Tubulin α -chain	TA24049	11	32	CAD13178	*N. tabacum*	11	38
WD-40 repeat protein	TA26204	7	16	UID			
Signal transduction – cell wall							
Remorin (REM)	DN921712	4	16	P93788	*S. tuberosum*	4	21
General metabolism							
UDP-glucose:protein transglucosylase (uptg2)	TA24497	9	21	CAC84517	*S. tuberosum*	9	32
Disulfide-isomerase protein (PDI)	TA25269	5	17	ABB02620	*S. tuberosum*	5	23
Oxidative respiratory chain							
APFI (Hypothetical protein F8G22.2)	TA26786	4	12	UID			
ATP synthase, mitochondrial, putative	TA28240	1	6	AAT40531	*S. demissum*	10	62
NADH-ubiquinone oxidoreductase 18 kDa subunit, mitochondrial precursor	TA29219	2	6	UID			
NADH-:FMN oxidoreductase - like protein	TA30877	5	22	AAO12869	*Vitis vinifera*	4	31
One-carbon (C_1) metabolism							
Dihydrolipoamide dehydrogenase (LPD)	TA28007	5	21	AAN23154	*Lycopersicum esculentum*	8	21
Glutamate-ammonia ligase (GS1)	TA25277	5	21	AAB61597	*Hevea brasiliensis*	3,4	18,19
Serine hydroxymethyltransferase 4 (SHMT4)	TA24707	10	28	NP193129	*Aarabidopsis thaliana*	3	9
Methionine synthase (MS)	TA24454	11-16	19-30	AAF74983	*S. tuberosum*	17,11	38,22
Carbohydrates metabolism							
Triose phosphate isomerase, (TPI) cytosolic	TA25726	3	16	CAD13178	*N. tabacum*	11	38

Fructokinase-like (FK)	TA24175	2	7	ABB29938	*S. tuberosum*	3	14
Abiotic and biotic stress							
Plasma membrane polypeptide (DREPP)	TA26238	9	25	UID			
Oxidative stress							
Aldo/keto reductase (AKR)	TA27942	2	7	NP564762	*A. thaliana*	2	11
Ascorbate peroxidase 1 (APX1), cytosolic	TA24251	12	35	AAY21068	*Capsicum annuum*	10	46
Catalase isozyme 2 (CAT2)	TA23780	17	35	CAA85470	*S. tuberosum*	18	46
Catechol oxidase B, chloroplast precursor	TA25457	6	10	AAC69365	*Diospyros kaki*	5	13
Copper-zinc superoxide dismutase (CuZn-SOD)	TA24916	1	5	UID			
Polyphenol oxidase (PPO)	TA24911	7	11	CAA78300	*S. lycopersicum*	2	4
Polyphenol oxidase (PPO), precursor	TA25456	8	14	UID			
Polyphenol oxidase, precursor (PPO)	CV429604	1	5	AAC69365	*D. kaki*	6	17
Plant defense							
Alpha-galactosidase, putative	TA35770	2	12	UID			
Cysteine protease 1 (CYP1)	CK256743	3	8	CAB53515	*S. tuberosum*	4	8
Elicitor-inducible protein EIG-J7	TA32425	3	12	AAR83862	*C. annuum*	2	15
Elicitor-inducible protein EIG-J7	TA36879	2	8	XP467841	*japonica cultivar-group*	1	5
Elicitor-inducible protein EIG-J7	TA39811	4	15	UID			
Endochitinase 2 precursor	TA24214	4	18	AAP32201	*S. dulcamara*	3	19
Endochitinase 2 precursor	CN213814	2	11	AAP32201	*S. dulcamara*	2,2	11,11
Kunitz-type proteinase inhibitor group B5	CV502293	3	12	CAA31852	*S. tuberosum*	1	6
Major latex protein-like, protein 28 (MLP)	TA35293	2	12	UID			
Patatin	TA23294	3-9	10-27	AAZ75962	*S. tuberosum*	8,3,9, 10,10,7	25,11,25, 30,30,23
Patatin	CN515681	2	11	ABC55700	*S. tuberosum*	1	4
Patatin putative homolog	TA35081	5	14	BAD38550	*Oryza sativa*	1	7
Patatin protein 07	TA23344	3-11	9-26	ABC55694, ABC55690,UID	*S. tuberosum*	11,10	30,30
Pathogenesis-related protein 10 (PR-10)	CN213132	10	38	BAD95797	*L. esculentum*	2	12
Pathogenesis-related protein 10 (PR-10)	TA22962	3	13	BAD95797	*L. esculentum*	1	8

Pathogenesis-related protein 10 (PR-10)	TA22953	4	22	AAU00066	*S. virginianum*	2	14
Synthesis of plant defense compounds							
Arginase 1	TA28681	6	19	UID			
Hyoscyamine 6-beta-hydroxylase-like protein (H6H)	BQ506105	2	11	BAC23050	*S. tuberosum*	2	9
2- oxoglutarate-dependent dioxygenase (SPP2)	TA24517	3	9	AAC95363	*S. chacoense*	4	15
2- oxoglutarate-Fe(II) oxygenase	TA29527	3	9	UID			
Phenylcoumaran benzylic ether reductase (PCBER)	TA28775	2	8	UID			
Suberization/lignification							
ACP-17kD beta-hydroxyacyl-acyl carrier protein	TA29588	6	17	NP193129	*A. thaliana*	3	9
Caffeoyl-CoA O-methyltransferase -5 (CCoAOMT-5)	TA33337	6	26	AAM64800	*A. thaliana*	1	4
Caffeoyl-CoA O-methyltransferase- 6 (CCoAOMT-6)	TA30542	7	29	BAC23054	*S. tuberosum*	2	12
Caffeoyl-CoA O-methyltransferase -3 (CCoAOMT-3)	TA30485	4	14	UID			
Peroxidase (POD 18)	TA25873	10-11	27-28	UID			
peroxidase PER9-6 secretory (POD 20)	TA23216	12	22	AAK52084	*N. tabacum*	9	22
Peroxidase 136, class III, precursor (POD 9)	TA39454	10	34	UID			
Peroxidase putative (POD 5)	CV504265	3	12	UID			
Peroxidase, suberization-associated anionic peroxidas (POP_A)	TA25019	5	15	CAA33852	*L. esculentum*	3	11
Reference protein							
Nascent polypeptide-associated complex NAC; UBA-like	TA25576	4	20	AAB18266	*N. tabacum*	2	68

a - Potato Transcript Assemblies; b – number of peptides identified; c- sequence coverage in between (%)

* - Calculated using the most similar protein; † - spot that contains more than one protein; UID- unidentified

Table S2. *List of skin proteins from differential spots that contained two proteins*

Functional categories	Potato TA [a]	Match peptides [b]	Cover (%)[c]	MW(kDa)/pI	
				Experimental	Theoretical
Cell proliferation					
Adenosine kinase isoform 2S (ADK)	TA25950	1	8	38.1/4.96	37.55/5.2*
WD-40 repeat protein	TA26204	7	16	38/4.8	37.7/5.4
General metabolism					
Oxidative respiratory chain					
ATP synthase, mitochondrial, putative	TA28240	1	6	19/4.93	21/5.4
One-carbon (C_1) metabolism					
Dihydrolipoamide dehydrogenase (LPD)	TA28007	5	21	53.7/6.6	33.2/9.3
Carbohydrates metabolism					
Fructokinase-like (FK)	TA24175	2	7	31.2/5.3	35/5.6
Abiotic and biotic stress					
Oxidative stress					
Aldo/keto reductase (AKR)	TA27942	2	7	36.9/5.8	37.7/6.1
Copper-zinc superoxide dismutase (CuZn-SOD)	TA24916	1	5	16/6.48	15.3/5.47
Polyphenol oxidase (PPO), precursor	TA25456	8	14	53.7/6.6	66/6.4
Polyphenol oxidase, precursor (PPO)	CV429604	1	5	57.3/6.07	66.2/6.3*
Plant defense					
Alpha-galactosidase, putative	TA35770	2	12	41/6	48.4/4.7*
Elicitor-inducible protein EIG-J7	TA36879	2	8	16/6.48	20/6.88
Major latex protein-like, protein 28 (MLP)	TA35293	2	12	16.9/5.33	17.2/4.91
Patatin	CN515681	2	11	39.7/5.55	42.6/5.3*
Pathogenesis-related protein 10 (PR-10)	TA22953	4	22	16.9/5.33	17.4/5.2
Synthesis of plant defense compounds					
Arginase 1	TA28681	6	19	37.5/4.8	37.01/5.66
Hyoscyamine 6-beta-hydroxylase-like protein (H6H)	BQ506105	2	11	39.5/5.75	37.9/5.54*
2- oxoglutarate-Fe(II) oxygenase	TA29527	3	9	39.7/5.55	40.9/6.1*

a - Potato Transcript Assemblies; b – number of peptides identified; c- sequence coverage in between (%)

* - Calculated using the most similar protein