

Supplementary files

Identification of allergenic proteins in velvet mesquite (*Prosopis velutina*) pollen: an immunoproteomics approach

José Ángel Huerta-Ocampo ^{a,b,*}, Lino Gerardo Batista-Roche ^b, Martha Beatriz Morales-Amparano ^b, María del Refugio Robles-Burgueño ^b, Gabriela Ramos-Clamont Montfort ^b, Luz Vázquez-Moreno ^b, Fernando Ramírez-Jiménez ^c, Luis M. Terán ^{c,*}.

^a *Consejo Nacional de Ciencia y Tecnología, Mexico City, 03940, Mexico*

^b *Centro de Investigación en Alimentación y Desarrollo, A.C. Hermosillo, Sonora 83304, México*

^c *Instituto Nacional de Enfermedades Respiratorias “Ismael Cosío Villegas”, Ciudad de México 14080, México*

** Corresponding authors: E-mail: jose.huerta@ciad.mx (J.A. Huerta-Ocampo) +52*

6622892400, Ext 513. linteran@iner.gob.mx (L.M. Terán) +52 5554871700, Ext.5259.

Supplementary Table S1. Allergenic proteins identified in velvet mesquite (<i>Prosopis velutina</i>) pollen							
Spot	Protein	Accession number ^a	Mr/pI Exp. ^b	Mr/pI Theor. ^c	PM/SC ^d	Score ^e	Peptide Sequences
1	Thaumatococin-like protein 1b	1624039760	24.8/4.51	25.8/5.05	2/9.9%	32.13	(K)ANINAAACPNDLK(V) + Deamidated N (K)VTGSDGNVIACK(S)
2	Rho GDP-dissociation inhibitor 1-like	1624023092	25.0/4.74	25.2/4.70	2/16.5%	27.99	(R)HASESSVAPTEDDDDDEGTLKLE LGPK(C) (K)VLSLSIISPGR(D)
3	Not identified	-----	-----	-----	-----	-----	-----
4	Polygalacturonase-like	1624065720	44.9/4.80	42.0/5.18	3/10.7%	56.24	(K)AWTDACAATEASK(V) (K)VLVGAGTYNMNAVDLK(G) (R)YNNEQPVSNVNVK(N)
5	Polygalacturonase-like	1624065720	47.8/4.93	42.0/5.18	2/7.3%	41.01	(K)VLVGAGTYNMNAVDLK(G) (R)YNNEQPVSNVNVK(N)
6	Polygalacturonase-like	1624065720	43.9/4.90	42.0/5.18	3/10.7%	63.09	(K)AWTDACAATEASK(V) (K)VLVGAGTYNMNAVDLK(G) (R)YNNEQPVSNVNVK(N)
7	Polygalacturonase-like	1624065720	43.9/4.95	42.0/5.18	2/7.3%	29.11	(K)VLVGAGTYNMNAVDLK(G) (R)YNNEQPVSNVNVK(N)
8	Polygalacturonase-like*	1624023427	44.6/5.03	42.5/5.20	1/3.3%	17.25	(R)YDNEAPVSNVNVK(N)
9	Glyceraldehyde-3-phosphate dehydrogenase 2, cytosolic-like isoform X1	1624102601	34.6/4.91	36.9/8.92	2/4.7%	24.3	(K)IGINGFGR(I) + Deamidated N (K)VLPALNGK(L)
10	Not identified	-----	-----	-----	-----	-----	-----
11	Polygalacturonase-like*	1624023427	47.1/5.19	42.2/5.20	1/3.3%	20.89	(R)YDNEAPVSNVNVK (N)
12	ATP synthase subunit beta, mitochondrial	1624089683	53.6/5.27	60.1/5.90	19/43.6 %	378.49	(K)AHGGFSVFAGVGER(T) (R)DAEGQDVLLFIDNIFR(F) (R)EAPAFVEQATEQQILVTGIK(V) (R)EGNDLYR(E) (R)EMIESGVK(L) (R)FTQANSEVSALLGR(I) (K)GAIGQVCQVIGAVVDVR(F) (K)IGLFGGAGVGK(T) (R)IINVIGEAIK(E) (R)IPSAVGYPQTLATDLGGLQER(I) (K)IVDEFTGK(G) (K)KDPGTGGGK(I) (K)LGDKQSESK(C) (R)LVLEVAQHLGENMVR(T) + Oxidized M (R)TIAMDGTGVVR(G) + Oxidized M (K)TVLIMELINNVAK(A) (R)VGLTGLTVAEHFR(D) (R)VLNTGSPITVPVGR(A) (K)VVDLLAPYQR(G)
13	Carbonic anhydrase, chloroplastic isoform X1	1624114052	47.1/5.34	37.3/8.79	2/7.2%	34.47	(K)EAVNVSLGNLLTYPFVR(E) (K)GGYYDFVK(G)
14	Mitochondrial-processing peptidase subunit alpha-like	1624112156	56.5/5.51	55.2/5.87	6/13.2%	79.45	(K)AVDEVTLKDITSISQK(L) (R)EVEAIGGNVQASASR(E) (K)ITLTPNGVK(V) + Deamidated N (R)KPVESFLK(A) (R)MVASEDIGR(Q) (K)SAILMNLESR(M) + Oxidized M
15	Not identified	-----	-----	-----	-----	-----	-----

16	UTP--glucose-1-phosphate uridylyltransferase-like	1624020612	52.4/5.74	51.9/5.6	15/34.1 %	273.56	(R)ANPANPAIELGPEFK(K) (R)ANPANPAIELGPEFK(V) (R)DGLTFLDLIVK(Q) (K)DGVKLEVPDGAK(I) (R)FFDNAIGINVPR(S) (K)IATPTDEVVVPYDSLAPSPQDS SEIKK(L) (K)ILNHLVQK(K) (K)LEVDPGAK(I) (K)LLDKLAVLK(L) (R)LVEADALK(M) (R)LVEADALKMEIIPNPK(E) + Oxidized M (R)LVDDYLPPLPSK(G) (K)SAVAELSQISENEK(N) (K)SIPSIVELDNLK(V) (K)VLQLETAAGAAIR(F)
17	Enolase	1624040022	52.4/5.90	48.0/5.83	7/18.4%	121.01	(R)DGGSDYLKG(G) (K)EGLELLK(T) (R)IEELGSDAVYAGASFR(A) (K)IIPALVGK(D) (K)ISGDALKDLYK(S) (K)VNQIGSVTESIEAVR(M) (K)VQIVGDDLLVTNPK(R)
18	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	1624021117	35.3/5.37	40.2/5.77	4/11.1%	65.55	(K)EGMSAEVINLR(S) (R)MAVPQVEDIVR(A) (R)STINASVR(K) (K)VLSPYSSEDAR(G)
19	UDP-arabinopyranose mutase 1	1624085496	36.6/5.55	41.1/5.65	10/27%	157.58	(K)ASCISFK(D) (K)ASNPFVNLR(K) (R)GYPFSLR(E) (K)INALEQHIK(N) (K)TGLPYIYHSK(A) (K)TISVPDGFYELYNR(N) (K)VICDHLGLGVK(T) (K)YIYTIDDDCFVASDPGK(K) (K)YIYTIDDDCFVASDPGK(I) (R)YVDAVLTIPK(G)
20	UDP-arabinopyranose mutase 1	1624085496	36.6/5.75	41.1/5.65	11/28.4 %	187.21	(K)ASCISFK(D) (K)ASNPFVNLR(K) (K)ASNPFVNLRK(E) (R)GYPFSLR(E) (K)INALEQHIK(N) (K)TGLPYIYHSK(A) (K)TISVPDGFYELYNR(N) (K)TISVPDGFYELYNRNDINR(I) (K)VICDHLGLGVK(T) (K)YIYTIDDDCFVASDPGK(K) (R)YVDAVLTIPK(G)
21	Enolase	1624040022	33.1/5.71	48.0/5.83	5/12.3%	87.65	(K)ACNALLK(V) (K)EGLELLK(T) (K)ISGDALKDLYK(S) (K)VNQIGSVTESIEAVR(M) (K)VQIVGDDLLVTNPK(R)
22	Probable fructokinase-5	1624052972	33.6/5.85	35.3/5.79	13/44.3 %	234.55	(K)APGGAPANVACAIK(L) (R)EAGALLSYDPNVR(L) (K)EALTFANACAALCTTQK(G) (K)GAIPALPTASDAQSLISK(S) (K)IFHYGSISLISEPCR(S) (K)LGGNSAFIGK(V) (K)LLIVTDGEK(G) (R)MLADILK(K) (R)MLADILKK(N) (K)NGVNTDGVCFDADAR(T) (R)SAHMAAMK(A) (R)TALAFVTLR(N) (K)VGDDEFGR(M)
23	Enolase	1624040022	36.6/5.90	48.0/5.83	7/17.7%	120.93	(K)ACNALLK(V) (K)EGLELLK(T) (K)ISGDALKDLYK(S) (K)MGVEVYHHLK(A) (K)VNQIGSVTESIEAVR(M) (K)VQIVGDDLLVTNPK(R) (K)VVIGMDVAASEFYK(S)

24	Triosephosphate isomerase, cytosolic	1624021851	26.3/6.07	27.2/5.88	4/16.2%	80.16	(R)IYGGSVN G ANCK(E) + Deamidated N (K)VATPAQAQEVHAE L R(K) (K)VATPAQAQEVHAE L RK(W) (K)VIACVGETLEQR(E)
25	S-adenosylmethionine synthase 1-like	1624121540	47.8/6.50	43.0/6.08	3/11.7%	47.09	(R)FVIGGPHGDAGLTGR(K) (K)SVVASGLAR(R) (K)VLVNIEQQSPDIAQGVHGLTK(K)
26	S-adenosylmethionine synthase 1-like	1624121540	47.1/6.65	43.0/6.08	4/12.5%	75.79	(R)FVIGGPHGDAGLTGR(K) (R)GIGFVSADVGLDADNCK(V) (K)SVVASGLAR(R) (K)VACETCTK(T)
27	Polygalacturonase-like	1624065841	50.0/6.97	38.4/6.32	5/15.3%	83.14	(R)FDNVDIK(Y) (K)IQISDVTFR(N) (K)STNVNVINSR(I) (K)TPILIDQEYCPSK(K) (K)VDGTIQGIINPSTLK(Q)
28	Polygalacturonase-like	1624065851	45.7/6.98	43.6/6.72	5/14.5%	73.17	(K)FVEETPIDKFTVK(N) (K)GLPN G DITQALTK(A) + Deamidated N (K)ISDVTFK(N) (K)VLDIASYK(G) (K)VSAPEDSPNTDGIHVGR(S)
29	GDSL esterase/lipase Atlg29670-like	1624029014	40.6/6.82	37.9/6.07	7/16.7%	101.4	(K)AAFLFNANLR(S) (R)GVNYASGAAGIR(N) (K)HLGSDISLR(L) (K)IDPSLGFK(V) (R)LQLTNHR(T) (K)SSEKVEQLLNK(C) (K)VEQLLNK(C)
30	Fructose-bisphosphate aldolase 6, cytosolic-like isoform X2	1624108864	36.6/6.98	38.8/6.69	13/38.5 %	242.47	(R)ALQQSTIK(A) (K)ANSEATLGTYK(G) (K)CADVTER(V) (K)EGGVLP G IK(V) (K)GILAADESTGTIGK(R) (K)GILAADESTGTIGKR(L) (K)IGPNEPSPLAIHENAYGLAR(Y) (R)LASINVENVESNR(R) (K)TASGKPFVDVLK(E) (R)VAPEVIAEHTVR(A) (R)VLAACYK(A) (K)YQDELIANAAYIGTPGK(G) (K)YYEAGAR(F)
31	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	1624127796	34.0/6.98	36.5/7.81	12/43.9 %	183.42	(R)AASFNIIPSSTGA A K(A) (K)AGISLSN N FK(L) (K)DAPM F VVGVNEK(E) + Oxidized M (K)EASEGSLK(G) (K)GASYDEIK(A) (K)GVLGYTEDDVVSTDFVGD C R(S) (K)IGINGFGR(I) + Deamidated N (K)SDINIVSNASCTTNCLAPLAK(V) (K)TLVFGDKPVSVFGTK(N) (K)VIISAPSK(D) (K)VLP S LNGK(L) + Deamidated N (R)VPTVDVSVVDLTVR(L)
32	Glucan endo-1,3-beta-glucosidase, basic isoform-like	1624040970	30.1/6.98	38.9/8.81	5/18.6	92.67	(R)AVQNVYQAIR(A) (R)GYQNLFDALLDSVHAALDSTK(I) (R)LYDPNQAALEALR(N) (R)TYLDNLIR(H) (K)YIAVGNEVNPVGR(N)
33	Proteasome subunit alpha type-4-like	1624127659	28.4/6.73	27.5/6.75	6/26.4	109.34	(K)AAAIGANNQAAQSILK(Q) (K)DGVVLVGEK(K) (K)HGVTPPPTDTA(-) (K)LLQTSTSTEK(M) (R)TTIFSP E GR(L) (K)YQVCSPETLTK(L)
34	Glutelin type-D 1-like	1624065233	32.7/6.59	38.4/6.33	5/14.3%	85.23	(K)AGNLFIVPR(F) (K)ALSPTVLQAGFNVD S K(L) (K)LEQLFR(S) (K)TLVGSQSGK(G) (R)TSDAIFPPPK(-)

35	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	1624127796	28.9/6.54	36.5/7.81	11/37.3 %	182.95	(R)AASFNIIPSTGA(A) (K)AGISLSNNFVK(L) (K)DAPMFVVGVEK(E) (K)EASEGSLK(G) (K)GASYDEIK(A) (K)GVLGYTEDDVVSTDFVGDCR(S) (K)KVIISAPSK(D) (K)SDINIVSNASCTTNCLAPLAK(V) (K)VIISAPSK(D) (K)VLPSSLnGK(L) + Deamidated N (R)VPTVDVSVVDLTVR(L)
36	Glutelin type-D 1-like	1624065233	33.1/6.37	38.4/6.33	7/20.5%	121.26	(K)AGNLFIVPR(F) (K)ALSPVLQAGFNVDK(L) (R)AQVVGPDGKR(V) (K)LALEKNGFALPR(Y) + Deamidated (K)LEQLFR(S) (K)TLVGSQSGK(G) (R)TSDAIFPPPK(-)
37	Malate dehydrogenase, mitochondrial	1624051156	36.1/6.30	36.3/8.81	10/30.7 %	188.26	(K)ALEGSDVVIIPAGVPR(K) (K)ANLGDDDIK(A) (R)DDLFINAGIVK(S) (R)LFQVTTLDVVR(A) (K)QGLESLLPELK(A) (K)RLFGVTTLDVVR(A) (K)RTQDGGTEVVEAK(A) (R)SEVAGYQGEELGK(A) (R)TQDGGTEVVEAK(A) (K)VAVLGAAGGIGQPLSLMK(L)
38	Triosephosphate isomerase, cytosolic	1624021851	26.5/6.34	27.2/5.88	9/51.9%	168.05	(R)EAGSTM A VVAEQTK(A) + Oxidized M (K)FFVGGNWK(C) (R)IIYGGSVNGANCK(E) + Deamidated N (K)IVTTLNEAQVPGEDVVEVVSP PFVFLSLVK(S) (R)QLFNEANEFVADK(V) (K)VATPAQAQEVHAELR(K) (K)VAYALSQGLK(V) (K)VIACVGETLEQR(E) (K)WIHSNVSAEVASSVR(I)
39	Superoxide dismutase [Mn], mitochondrial-like	1624128322	22.0/6.64	26.5/7.20	4/18.8%	62.58	(K)ALEQLHDAMEK(G) (K)HHQTYITNYNK(A) (R)LVVETTANQDPLVTG(G) (K)YASEVYEK(E)
40	Profilin	1624112235	16.1/4.63	14.4/4.78	3/25.5%	51.28	(K)DFEEPGYLAPK(G) (R)LG DYLVQGL(-) (K)YMQVIGEPGAVIR(G) + Oxidized M
41	Nucleoside diphosphate kinase 1	1624076552	14.5/6.98	16.4/6.85	6/39.8%	109.08	(R)GDY AIDIGR(N) (R)GLVGEISR(F) (K)IIGATNPAQSEPGTIR(G) (K)LISVDRPFAEK(H) (R)NVIHGSDSVESAR(K) (R)NVIHGSDSVESARK(E)
	Pathogenesis-related protein 1-like	1624126639	14.5/6.98	18.1/9.05	2/17.2%	30.44	(R)LVHSGDGGK(Y) (R)SQVGVPNIAWDETVAFAFAR(N)

Spot numbers according to Fig. 1. ^a Accession numbers according to the *Prosopis alba* subset of the nrNCBI protein database. ^b Experimental molecular mass (kDa)/isoelectric point. ^c Theoretical molecular mass (kDa)/isoelectric point. ^d Number of peptides matched/protein sequence coverage. ^e Spectrum Mill Protein Score (Scores ≥ 24 and at least two peptides were necessary for confident protein identification).