SUPPLEMENTAL DATA

Table S1.

1

2 3 4 5 Identification of recombinant protein obtained in E. coli (54% sequence coverage) and native

6 protein purified from ESPs (51% sequence coverage) by MALDI-TOF/TOF analysis. The

7 peptides were obtained using trypsin and the mass spectra search was performed by MASCOT

8 software. The following parameters were stated: missed-cleavage, one; peptide tolerance, 50 ppm;

9 fragment mass tolerance, 0.3 Da; fixed modification, carbamidomethylation of cysteine; and

10 variable modification, methionine oxidation.

Calc. Mass	Error (ppm)	Peptides	Ion Score	Score ¹
Recombina		768		
828.440	37	YPFFVR*	70	
948.4938	35	WPDVYLR*	62	
1217.679	31	LRWPDVYLR*	45	
1222.5919	28	MLCGGSLLTDR	78	
1472.7792	29	HVLTVSHCVVGHK*	86	
1717.8789	28	GVVQVGMLIGATNSDEK*	38	
1844.9187	31	YPFFVRLEMVMNNGK		
1987.0641	27	GVVQVGMLIGATNSDEKLR*	70	
2180.8689	28	TSYFCDFFAQATGNAFSCS*	65	
2629.2788	34	IVCTVGPHGTHGAGAGESGGPLVAQDGK*	92	
2915.4421	36	HYDDINNVAVIELSSPVDFTATAQPAK*	66	
3386.6394	31	IATDNDKIVCTVGPHGTHGAGAGESGGPLVAQDGK*	79	
Native Sc-SP-1				708
874.4741	7	ILRDDSR*	52	
888.3669	6	FDYCQR*	67	
922.4854	8	TLHNPQGR*	68	
948.4938	5	WPDVYLR*	65	
1217.679	7	LRWPDVYLR*	72	
1717.8789	16	GVVQVGMLIGATNSDEK		
1987.0542	7	HVLTVSHCVVGHKLGESK		
2003.0591	12	GVVQVGMLIGATNSDEKLR*	73	
2629.2788	12	IVCTVGPHGTHGAGAGESGGPLVAQDGK*	95	
2915.4421	10	HYDDINNVAVIELSSPVDFTATAQPAK*	81	
3386.6394	7	IATDNDKIVCTVGPHGTHGAGAGESGGPLVAQDGK*	110	

11 * peptides that were obtained the MS/MS sequences; 1, scores obtained with Mowse algorithm

12 (scores >100 are significant with p<0.05); ppm –parts per million.

13

14 **FIGURE S1**.

15

Sc-SP-1	- GGT VPVGK P F DEMV-M NG K LCGGSL DRHVLTV HC VGHK GESKAYIGI	61
G.spinigerum_26	R GGT ANETV PWQ YKRL SM YFLCGGSL N HVL AAHC DDADK NSF	58
T.spiralis_23%	R GGT VRPHSHPWQ L KS-ETGGYSSLCGGSL HFGKPSNGTRFVLTAAHC TTSN YPRTSRF	67
H.glycines_22%	IFKGKTIVDDKSLPWMA SG SCTA GPRHVLTAAHC EGQA NFVVSYGS	56
B.malayi_31%	M SNAKLVAPES P IA YIVWP K LCTGSL RSI TAAHC VDEKT KQLGKVKK	61
Clustal Consens	*: .: * .::: :::.:**:	
Sc-SP-1	TK GDK A WYQ RTIA SKTL NP G HY D N AVID SSPVD TATA AK LRD SR	125
G.spinigerum_26	I GSVYG QSS A IRHIDKATIHPDF AS KRI DIA VOIG PVVF DRIRS NOPHF TK	124
T.spiralis_23%	T TGAHNIKME KEKK PITS YV HWNPVMTTNDIA LA TVY EYTRP CIPEP EE	132
H.glycines_22%	ADASNO H SGVOA KYHPKTOH EI D FRKNTRAYLF NDIV KNS KF ONARP CUHGFHLTN	126
B.malayi_31%	V FRQD G SYATW XG IHGMLKISDLEEK G LDYA F D 2 PVCR-ARDGR FSIIKLP	124
Clustal Consens		
SC-SP-1	VVKHOQV FMC CS AFHDNKPNAFS NEL TO VVA FDY QRTLP ADDNCK VCTVGPH THGA	193
G.spinigerum_26	VGCG VTG GIYD RHGISPHVS VUR AT HE SYQQ NKARM RAGGEQ STKQICA GL GT	192
T.spiralis_23%	PGDIC- VTG CD T NGTTS TK VG KI KGT A VRS V TFCAGAMEGG DS	190
H.glycines_22%	TKSDK I YDEYSKFI TQCVVAGWG TKPT S DDD P QLIYGQMRMISKO CR	187
B.malayi_31%	VKDICTRKWKTLQP K LLDQCSLFGYGAS K GPDG LRKLT ISVWE NCRLL PMENNAQYIR GRI	194
Clustal Consens		
Sc-SP-1	GAS SEGEL AQDEKS-VVOVS LIGATNSD LR EDVVL T Y CDF ATSA	249
G.spinigerum 26	AEGDSGGPLQVLTKNCDWY VG T CVNSD GV DET PGVYT VSS CTFISRTIGNP	253
T.spiralis_23%	CQGDSGGPL CK-KNCKSVQFG V GTGCARKG PGVYA VPS VT AAKELENSPEGTVK	254
H.glycines_22%	ELSIEYEK FTPSDGNPEV SM E DAYSI SN CVVPEQS GEPGD GGPL VGK NWGQLG	253
B.malayi_31%	CGCDSGGPF CGT FCERI CILSHSEP L SHLSSC GEE AF YDVMG VR	247
Clustal Consens	그는 것이 가지 않는 것이 많이	

16 17 18

18 Comparison of the Sc-SP-1 deduced amino acid sequence with the amino acid sequences of 19 selected homologous molecules. Alignment of catalytic domains of nematode serine proteases 20 family. Percentages represent identity with Sc-SP-1. The sequences were *Brugia malayi* (NCBI 21 Accession XP_001900587), *T. spiralis* (AAK16520), *Heterodera glicines* (CAA74206), 22 *Gnathostoma spinigerum* (ACA30304) and *C. elegans* (NP_500999). Identical residues are marked 23 with "*", conserved substitutions with " : " and semi-conserved substitutions with " . " below the 24 sequences

25

26 27 FIGURE S2.







- Chromatographic profiles of native protease purification from ESPs of the S. carpocapsae
- 30 parasitic stage. Three steps were sequentially run: Gel filtration (A); Hitrap SP (B) and Mono S
- 31 (C). proteolytic activity was measured in the substrate AAPF-pNA. Vertical grey bars indicate 32 proteolytic activity in the fractions.
- 33





Kinetic activity of native and recombinant Sc-SP-1. Kinetic activity of native and recombinant 38 39 proteins was measured against AAPF-pNA substrate (A and C) and against AAPM-pNA (B and D).

40 FIGURE S4.





42 pH °C
43 pH and temperature dependence of Sc-SP-1. Enzymatic activity was measured with 0.1 mM of
44 the purified enzyme on the AAPF-pNA substrate in buffers ranging from pH 6 to 10 (A). The
45 optimal temperature determined in optimal pH buffer and on the AAPF-pNA substrate (B).

46