SUPPLEMENTAL DATA

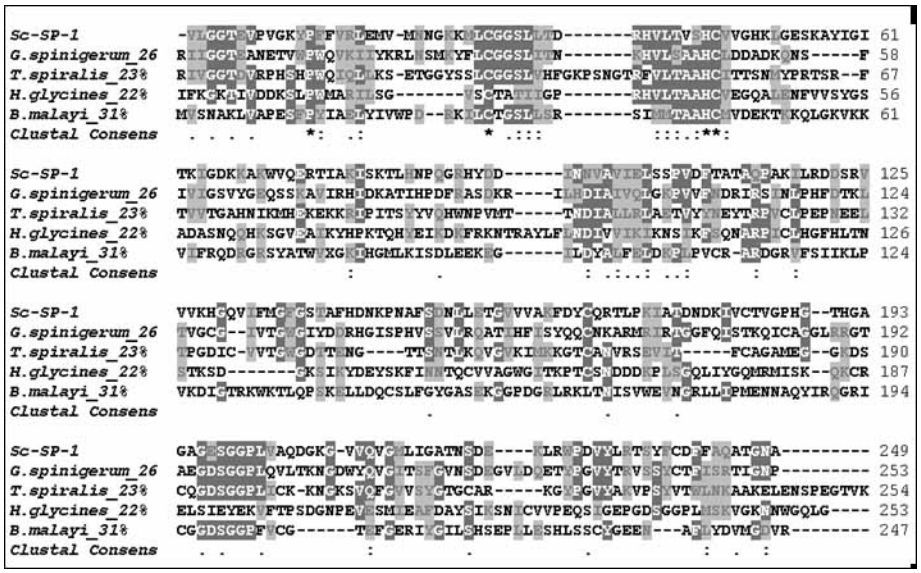
Table S1.

Identification of recombinant protein obtained in *E. coli* (54% sequence coverage) and native protein purified from ESPs (51% sequence coverage) by MALDI-TOF/TOF analysis. The peptides were obtained using trypsin and the mass spectra search was performed by MASCOT software. The following parameters were stated: missed-cleavage, one; peptide tolerance, 50 ppm; fragment mass tolerance, 0.3 Da; fixed modification, carbamidomethylation of cysteine; and variable modification, methionine oxidation.

Calc. Mass	Error (ppm)	Peptides	Ion Score	Score[1]
Recombinante Sc-SP-1				**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	

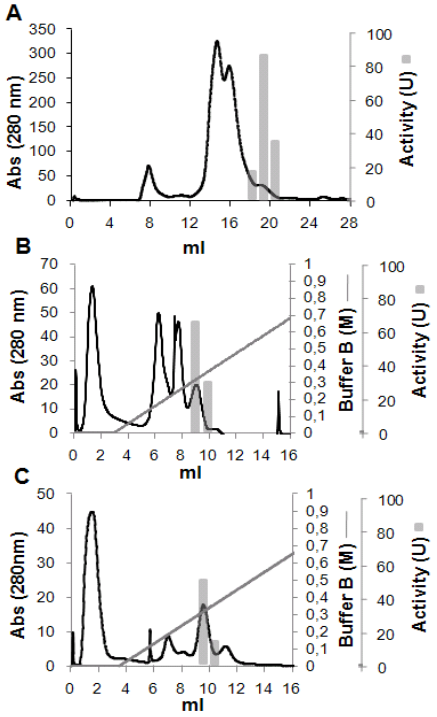
* peptides that were obtained the MS/MS sequences; 1, scores obtained with Mowse algorithm (scores >100 are significant with $p<0.05$); ppm –parts per million.

FIGURE S1.



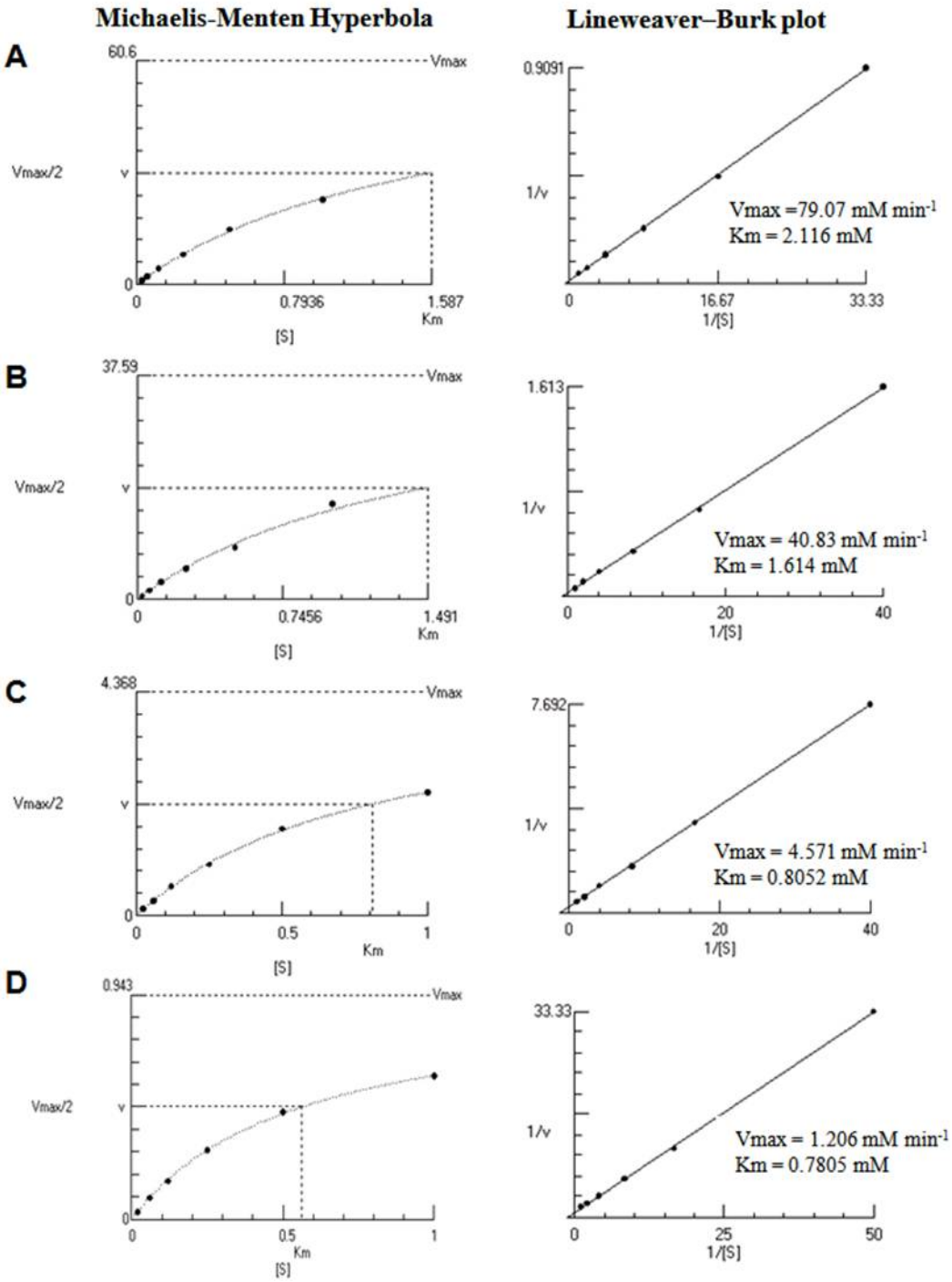
Comparison of the Sc-SP-1 deduced amino acid sequence with the amino acid sequences of selected homologous molecules. Alignment of catalytic domains of nematode serine proteases family. Percentages represent identity with Sc-SP-1. The sequences were *Brugia malayi* (NCBI Accession XP_001900587), *T.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

FIGURE S2.



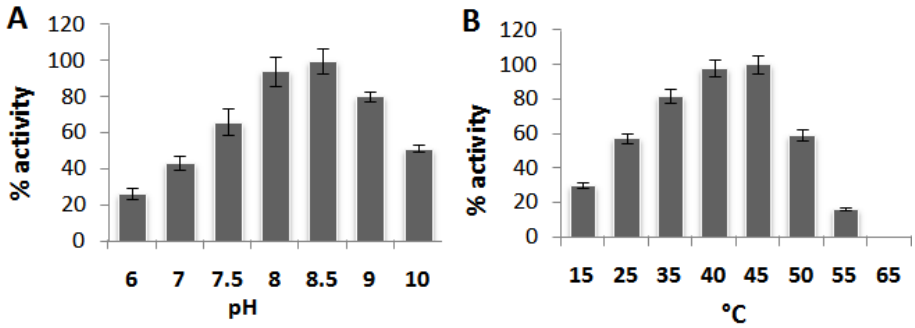
Chromatographic profiles of native protease purification from ESPs of the S. carpocapsae parasitic stage. Three steps were sequentially run: Gel filtration (**A**); Hitrap SP (**B**) and Mono S (**C**). proteolytic activity was measured in the substrate AAPF-pNA. Vertical grey bars indicate proteolytic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

FIGURE S3.



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

FIGURE S4.



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