Table 1 Full sequence of ponericin W5 (P82427) and its fragments. The full peptide corresponding to ponericin W5 and its fragments were identified in the venom of *N. villosa*. Isoforms of the full peptide and its fragments were also identified

Sequence	Condition	Mw (Da)	Peptide processing/Mutations
FWGALIKGAAKLIPSVVGLFKKKQ	Ponericin W5	2598.57	–
FWGALIKGAAKLIPSVVGLFKKKQ	Nv1; Nv2; Nv3; Nv4	2598.57	–
FWGALIKGAAKLIPSVVGLFKKK	Nv1;Nv3; Nv4	2470.51	Carboxypeptidase
FWGALIKGAAKLIPSVVGLFKK	Nv1	2342.42	Carboxypeptidase
FWGALIKGAAKLIPSVVGLF	Nv4	2086.23	Carboxypeptidase
FWGALIKGAAKLIPSVVGL	Nv2;Nv4	1939.16	Carboxypeptidase
FWGALIKGAAKLIPSVVG	Nv1; Nv3; Nv4	1826.08	Carboxypeptidase
FWGALIKGAAKLIPSVV	Nv1	1769.06	Carboxypeptidase
ALIKGAAKLIPSVVGLFKK	Nv4	1952.25	Endopeptidase
ALIKGAAKLIPSVVGLF	Nv1	1696.06	Endopeptidase
ALIKGAAKLIPSVVG	Nv4	1548.99	Endopeptidase
GAAKLIPSVVGLFKK	Nv1	1526.95	Endopeptidase
GAAKLIPSVVGLF	Nv4	1270.76	Endopeptidase
AAKLIPSVVGLF	Nv1;	1213.74	Endopeptidase
IPSVVGLFKK	Nv4	1342.83	Endopeptidase
PSVVGLFKKK	Nv3;	1101.69	Endopeptidase
IPSVVGLFK	Nv4	958.58	Endopeptidase
WGALIKGAAKLIPSVVGLFKKKQ	Nv1;	2451.50	Aminopeptidase
GALIKGAAKLIPSVVGLFKKKQ	Nv4	2265.42	Aminopeptidase
ALIKGAAKLIPSVVGLFKKKQ	Nv1;Nv4	2208.40	Aminopeptidase
IKGAAKLIPSVVGLFKKKQ	Nv1; Nv4	2024.28	Aminopeptidase
GAAKLIPSVVGLFKKKQ	Nv1; Nv2;Nv4	1783.10	Aminopeptidase
AAKLIPSVVGLFKKKQ	Nv1;Nv2; Nv4	1726.08	Aminopeptidase
PSVVGLFKKKQ	Nv1; Nv2; Nv4	1229.74	Aminopeptidase
FWGALIKGAAKLIPSVVG**M**FKKKQ	Nv1; Nv3; Nv4	2616.53	(Leu19Met)
FWGALIKGAAKLIPSVVG**M**	Nv3	1957.12	(Leu19Met)/carboxypeptidase
GALIKGAAKLIPSVVG**M**FKKKQ	Nv3	2283.38	(Leu19Met)/aminopeptidase
ALIKGAAKLIPSVVG**M**FKKKQ	Nv3	2226.36	(Leu19Met)/aminopeptidase
ALIKGAAKLIPSVVG**M**	Nv3	1566.95	(Leu19Met)/endopeptidase
GAAKLIPSVVG**M**FKKKQ	Nv1;Nv3	1801.06	(Leu19Met)/endopeptidase
FW*GALIKGAAKLIPSVVGLFKKKQ	Nv2; Nv4	2614.57	*Oxidation
FW*GALIKGAAKLIPSVVGL	Nv2	1955.16	*Oxidation/carboxypeptidase
FW*GALIKGAAK	Nv3	1176.66	*Oxidation/carboxypeptidase

Nv1: winter; Nv2: summer; Nv3 ground-dwelling ants; Nv4: arboreal ants
Bold letter indicates a mutation
* Indicates an oxidation

of the samples, or that this class of antimicrobial peptides might undergo enzymatic cleavages. This peptide processing seems to occur at both extremities of the peptide, suggesting the action of carboxypeptidases, aminopeptidases and/or endopeptidases (Table 1). This extensive proteolysis was observed only in ponericins and not in the other peptides identified in our work, suggesting an enzymatic preference to this peptide subfamily. In this way, it appears to be implausible that the peptide proteolysis observed is caused by sample degradation but it is, indeed, the result of post-translational modifications.

Toxin proteolysis was previously described and was related to the increase of the structural and molecular diversity of the venom protein repertoire [32]. Thus, with a single gene product cleaved in different positions, several other peptides with different targets and modes of action are produced, therefore generating an immense molecular repertoire with low energy costs [32].