## Snake venomics of the South and Central American bushmasters. Comparison of the toxin composition of *Lachesis muta* gathered from proteomic versus transcriptomic analysis

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We report the proteomic characterization of the venoms of two closely related pitvipers of the genus Lachesis, L. muta and L. stenophrys, and compare the toxin repertoire of the former revealed through a proteomic versus a transcriptomic approach. The protein composition of the venoms of L. muta and L. stenophrys, analyzed by a snake venomics approach, comprised 30-40 proteins of molecular masses in the range of 13-110 kDa and belonging, respectively, to only 8 and 7 toxin familiies in L. muta and L. stenophrys venoms. Both venoms contained a large number of bradykinin-potentiating peptides and a C-type natriuretic peptide, which comprised around 15% of the total venom proteins. In both species, the most abundant proteins were Zn2+-metalloproteinases (32-38%) and serine proteinases (25-31%), followed by PLA<sub>a</sub>s (9-12%), galactose-specific C-type lectin (4-8%), L-amino acid oxidase (LAO, 3-5%), CRISP (1.8%; found in L. muta but not in L. stenophrys), and NGF (0.6%). On the other hand, only six L. muta venom secreted proteins matched any of the previously reported 11 partial or full-length venom gland transcripts, and venome and transcriptome depart in their relative abundances of different toxin families. As expected from their close phylogenetic relationship, the venoms of L. muta and L. stenophrys share (or contain highly similar) BPPs, serine proteinases, a galactose-specific C-type lectin, and LAO. However, they dramatically depart in their PLA,s. Intraspecific quantitative and qualitative differences in the expression of PLA, molecules were found in the venoms of five L. muta specimens (3 from Bolivia and 2 from Peru) and an L. muta venom purchased from Sigma. These observations indicate that these class of toxins represents a rapidly-evolving gene family, and suggests that functional differences due to structural changes in PLA<sub>2</sub>s molecules among these snakes may have been a hallmark during speciacion and adaptation of diverging snake populations to new ecological niches, or competition for resources in existing ones. Our data may contribute to a deeper understanding of the biology and ecology of these snakes, and may also serve as a starting point for studying structure-function correlations of individual toxins.