

## THE VENOM OF SO-CALLED “NON-VENOMOUS” SNAKES: INSIGHTS FROM COMPARATIVE TRANSCRIPTOMIC ANALYSIS OF TWO COLUBRIDAE SPECIES

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The snakes traditionally considered to be dangerous to man are restricted to three families summing 20% of the world species, whereas the Colubridae family alone has 60% of leaving species. This family is not used to be associated with poisoning events, nevertheless, rear-fanged species are capable of producing venom and are reported to cause severe disturbs in man. In order to investigate their unknown arsenal of toxins, we perform an Expressed Sequence Tags (ESTs) based transcriptomic analysis of two common Brazilian species. We extract mRNA from Duvernoy's (venom) glands, constructed plasmid cDNA libraries, and generated 2194 ESTs from *Philodryas olfersii* and over 500 ESTs from *Waglerophis merremii*. The ESTs were independently clustered and annotated, and then compared. The profile of *P. olfersii* revealed 5 toxin classes common in Viperidae snakes: Metalloproteases (15.4%), Serine proteases (2.6%), C-type lectins (1.7%), Crisps (3.0%), and C-type natriuretic peptides (6.6%). The analysis of *W. merremii* revealed two additional toxins: a venom peptidase and, most interestingly, a three-finger like toxin, which is a putative neurotoxin common in the Elapidae snakes. These results support the new evidences that the arsenal of Colubridae is very similar to that of other families and may have evolved early. Support: FAPESP.