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Venom Composition Does Not Vary Greatly Between Different Nematocyst Types Isolated from the Primary Tentacles of *Olindias sambaquiensis* (Cnidaria: Hydrozoa)

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Abstract

In this quantitative proteomics study we determined the variety and relative abundance of toxins present in enriched preparations of two nematocyst types isolated from the primary tentacles of the adult medusa stage of the hydrozoan *Olindias sambaquiensis*. The two nematocyst types were microbasic mastigophores and microbasic euryteles, and these were recovered from the macerated tentacle tissues by using a differential centrifugation approach. Soluble protein extracts from these nematocysts were tagged with tandem mass tag isobaric labels and putative toxins identified using tandem mass spectrometry coupled with a stringent bioinformatics annotation pipeline. Astonishingly, the venom composition of the two capsule types was nearly identical, and there was also little difference in the comparative abundance of toxins between the two nematocyst preparations. This homogeneity suggested that the same toxin complement was present regardless of the penetrative ability of the nematocyst type. Predicted toxin protein families that constituted the venom closely matched those of the toxic proteome of *O. sambaquiensis* published four years

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previously, suggesting that venom composition in this species changes little over time. Retaining an array of different nematocyst types to deliver a single venom, rather than sustaining the high metabolic cost necessary to maintain a dynamically evolving venom, may be more advantageous, given the vastly different interspecific interactions that adult medusa encounter in coastal zones.