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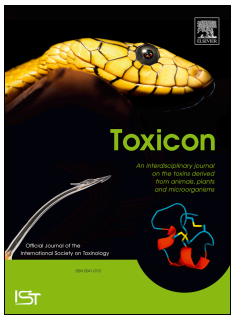

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SHORT COMMUNICATION

Multi-copy venom genes hidden in *de novo* transcriptome assemblies, a cautionary tale with the snakelocks sea anemone *Anemonia sulcata* (Pennant, 1977)

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Abstract

Using a partial transcriptome of the snakelocks anemone (*Anemonia sulcata*) we identify toxin gene candidates that were incorrectly assembled into several Trinity components. Our approach recovers hidden diversity found within some toxin gene families that would otherwise go undetected when using Trinity, a widely used program for venom-focused transcriptome reconstructions. Unidentified hidden transcripts may significantly impact conclusions made regarding venom composition (or other multi-copy conserved genes) when using Trinity or other *de novo* assembly programs.

Keywords

Next Generation Sequencing**;** Trinity; Sodium Channel Toxins; sea anemone venom;

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