Special Issue

Venom Gene Evolution: Past, Present and Future

Message from the Guest Editor

Ongoing advances in sequencing platforms have generated a tremendous wealth of data, and their impact on the research of venom gene evolution has already been documented. A simplistic picture of venom genes emerging via duplication followed by a neofunctionalization is being questioned, with multiple high-profile studies participating in this exciting scientific debate. Many crucial questions remain open: Do venom genes share a common origin pattern? Are there any genomic or protein structure effects that increase the chance of a gene being weaponised into venom? Do venoms evolve repeatedly within the same clade or is it a predominantly singular event within each of the venomous taxa? And many more. Some of these questions can be answered already, some might be ripe for a machine learning approach, yet some might remain forever open. The aim of this Special Issue is to provide a snapshot of the field of venom gene evolution and to serve as a topical roadmap of the field in the future.

Keywords
- venom genes evolution
- current state of venom genetics
- patterns in venom evolution

Guest Editor

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Toxinology is an incredibly diverse area of study, ranging from field surveys of environmental toxins to the study of toxin action at the molecular level. The editorial board and staff of *Toxins* are dedicated to providing a timely, peer-reviewed outlet for exciting, innovative primary research articles and concise, informative reviews from investigators in the myriad of disciplines contributing to our knowledge on toxins. We are committed to meeting the needs of the toxin research community by offering useful and timely reviews of all manuscripts submitted. Please consider *Toxins* when submitting your work for publication.

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