Convergent molecular evolution of toxins in the venom of advanced snakes (Colubroidea)

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Stellingen behorende bij het proefschrift

Convergent molecular evolution of toxins in the venom of advanced snakes (Colubroidea)

1. An analysis pipeline combining different RNA-seq assemblers and manual curation can recover the most comprehensive and unbiased venom profile for venom studies (Chapter 2).
2. Kunitz-type toxin and SVMPs demonstrate a phylogenetic pattern of large clades belonging to snakes of the same family, which suggests that these toxins had not yet extensively diversified in the common ancestor of Colubroidea (Chapter 3 and Chapter 5).
3. Due to the relatively low number of sequences available from rear-fanged snakes, we still have limited knowledge about the phylogenetic history of other less 'famous' snake toxin families, such as AChE, ESP, HYAL, and RNase (this thesis).
4. The profile of snake venoms, and the reconstruction of their evolution history, can help elucidate predator-prey evolutionary arms races (this thesis).
5. The diversity of snake toxins produces a wide range of clinical effects and variable responses to antivenom that contribute to the global problem of snakebites.
6. Snake toxins have considerable potential in biochemical assays and in drug discovery design and development, so that we still need to utilize NMR and bioassay methods to learn more about them and utilize them.
7. With the rapid development of machine learning and use of AI algorithms, the biological function of newly discovered snake toxins can be precisely predicted.
8. Since snakes play an important role in environmental balance and bio-resources, we should pay more attention to protecting their habitats.
9. No matter what their PhD projects and future career, a course in speed reading of the scientific literature can be a valuable aid.
10. International PhD students who are living abroad and alone during the pandemic should take good care of their mental well-being.
11. Scientists in all fields can benefit from computer programming.
12. Bioinformatics is the cornerstone of contemporary biology.

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