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

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Curriculum vitae

Bing Xie was born in Zaozhuang, Shandong Province, China. After completing his secondary education in Zaozhuang, he went to the city of Tai'an to attend Shandong Agriculture University for a four-year bachelor program. He gained two majors there: Agronomy and Computer Science. Since then, he became increasingly interested in the interdisciplinary field of bioinformatics. Then, he moved to Chongqing to pursue his master study at Southwest University in bioinformatics. After two years of study, he was employed by the Beijing Genomics Institute (BGI) as a bioinformatician. During his stay at the BGI, he was involved in the research of FishT1K and marine venom with multi 'omics' methods, including genomics, transcriptomics and proteomics. After BGI, he went to pursue his PhD studies in Leiden. He was supervised by Prof. M. K. Richardson in Leiden University and Dr. B. G. Fry in Queensland University. Both promotors are experts in the field of venomomics (venom studies). In his PhD work, he aimed at studying the evolution of toxins, and with a longer-term objective of developing animal venom toxins into novel therapeutics, by means of bioinformatics methods and functional assays. He also looked into the differential expression patterns of developmental genes in model animals. He is currently a postdoctoral fellow in the European Molecular Biology Laboratory – European Bioinformatic Institute (EMBL-EBI), Cambridge, UK, one of the world's leading bioinformatics institutes, to continue his passion for using bioinformatics to address major biological questions.

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