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Bringing the evolutionary history of the world's deadliest toxins to light with genomics

Bacterial toxins are a broad category of molecules ranging from small organic compounds and peptides to large multi-domain or multi-meric enzymes. Several important diseases are caused primarily by the production of bacterial toxins, and yet paradoxically the same toxins have proven useful as therapeutics. The mechanistic details of intoxication have been

elucidated for many toxin families, but in general little is known about their evolution. As such, the availability of large sequencing data sets presents a unique opportunity to explore toxin sequence diversity and potentially gain key evolutionary insights. Using a bioinformatic approach, I present evolutionary studies of botulinum toxins, diphtheria toxins, and large clostridial toxins. In all cases, toxin families related to human diseases are broader than had been imagined previously. Genomics-derived toxin-related sequences possess unique functionality compared to their better characterized relatives, facilitate a deeper understanding of toxin functions, and potentially shed light on the evolution of human specificity.



