

The diversification of viperid venom genes highlights genomic mechanisms underlying transposon-mediated cis-regulatory element evolution

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Abstract

hAT-Tip100 transposable elements (TEs) are known to have been co-opted as regulatory loci (i.e., promoters and enhancers) for the snake venom serine protease (SVSP) gene family in a single viper species¹. This is notable because TEs are sequences that are usually silenced after insertion to protect against their many deleterious effects (e.g., disruption of normal gene regulation or protein-coding potential, ectopic recombination etc.). However, the process by which a normally silenced element becomes one that has a defined regulatory role is not well understood. Here, we leverage functional and comparative genomics applied to the hAT-Tip100 SVSP gene regulatory system of rattlesnakes to understand the genomic drivers of TE-driven regulatory element evolution.

