

## Abstract

With a worldwide distribution and diversification into almost 400 species, Viperidae is considered one of the evolutionarily most successful families of snakes. The group is of broad scientific and public interest for its medical importance and is popular amongst reptile enthusiasts. The evolutionary success of the family is attributed to various key innovations; traits that have emerged throughout its evolutionary history that significantly contributed to increased rates of diversification. These include the distinctive solenoglyphous dentition, viviparity and heat-sensing pits found in the Crotalinae subfamily.

In order to accurately assess the impact of these evolutionary novelties, it is essential to have a well-sampled and robust phylogeny. In this study, I have combined genomic data obtained from UCE (ultra-conserved elements) sequences with Sanger-sequenced loci to construct a topology that incorporates as many species as possible. The resulting tree encompasses 95 % of the currently recognized species, with genetic data having been generated for several species for the first time. Subsequently, I then use the phylogeny to estimate diversification rates within the family and to examine its correlation with the emergence of key innovations and macroecological variables such as distribution area sizes, inhabited elevation, and body size.

As a result, this study provides insights into the evolutionary history and diversification patterns of viperids, shedding light on the factors that have contributed to its remarkable success as one of the most diverse snake families on the planet.