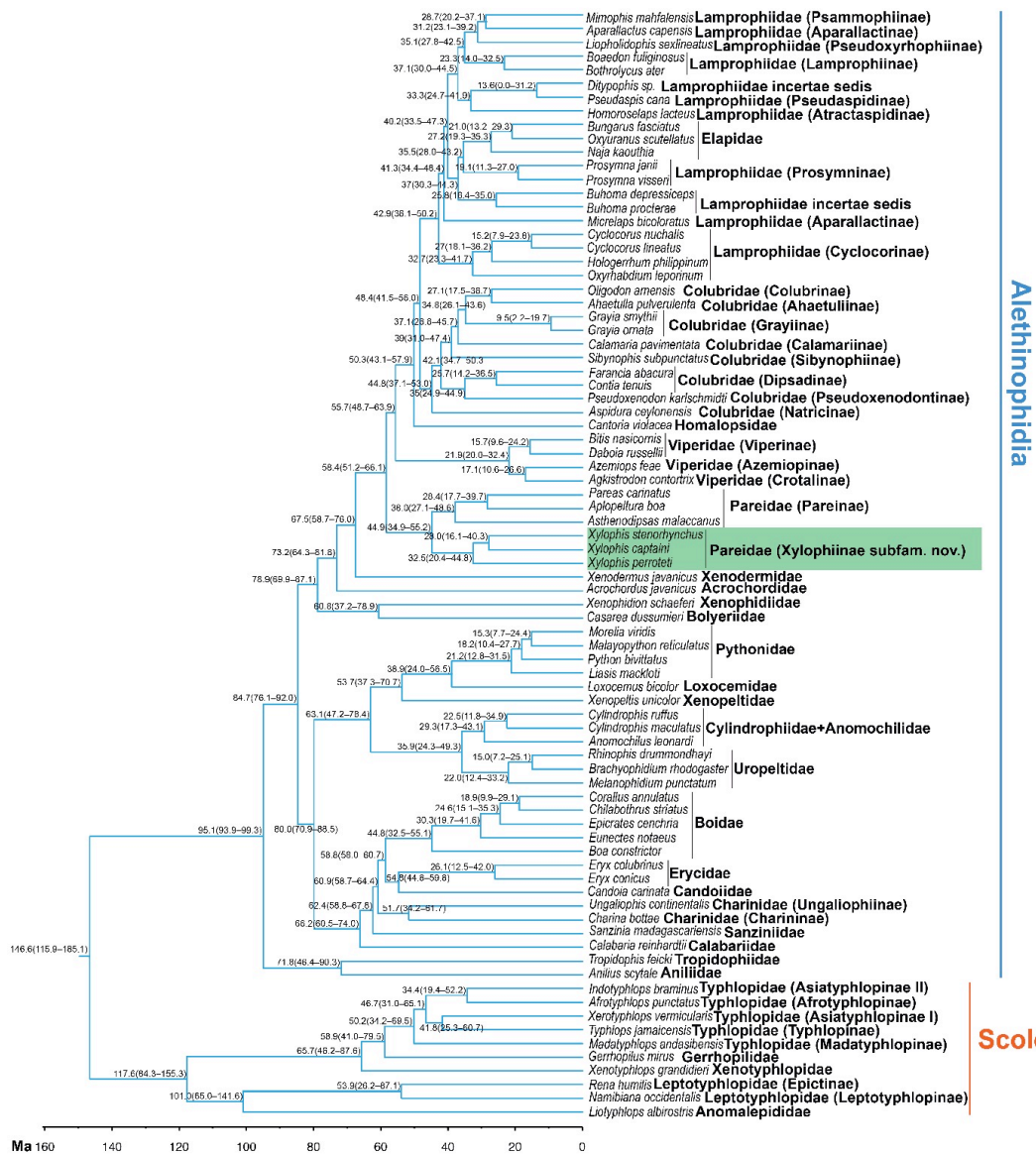


Figure S3. BEAST chronograms generated using concatenated gene sequence data for all families and subfamilies of snakes (81 taxa).

A. Concatenated dataset including all sites. Numbers at internal nodes indicate mean estimated node ages (and 95% highest posterior densities)



B. Concatenated dataset in which third codon position of the mitochondrial genes (nd4 and cyt b) are excluded. Numbers at internal nodes indicate mean estimated node ages (and 95% highest posterior densities)

