

ABSTRACT

We report the discovery of endogenous viral elements (EVEs) from Hepadnaviridae, Bornaviridae and Circoviridae in the speckled rattlesnake, *Crotalus mitchellii*, the first viperid snake for which a draft whole genome sequence assembly is available. Analysis of the draft assembly reveals genome fragments from the three virus families were inserted into the genome of this snake over the past 50 Myr. Cross-species PCR screening of orthologous loci and computational scanning of the python and king cobra genomes reveals that circoviruses integrated most recently (within the last approx. 10 Myr), whereas bornaviruses and hepadnaviruses integrated at least approximately 13 and approximately 50 Ma, respectively. This is, to our knowledge, the first report of circo-, borna- and hepadnaviruses in snakes and the first characterization of non-retroviral EVEs in non-avian reptiles. Our study provides a window into the historical dynamics of viruses in these host lineages and shows that their evolution involved multiple host-switches between mammals and reptiles.