

Supplementary material legends

Figure S1. RAxML trees for concatenated data for 81 taxa, with three different alignment treatments for *16s*.

Figure S2. RAxML phylogeny highlighting relationships of the genus *Xylophis*.

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

Figure S4. Comparison of estimated mean divergence dates from BEAST analyses of data in which third codon positions of mitochondrial genes (*nd4* and *cytb*) are either included or excluded.

Table S1. GenBank accession and voucher numbers for gene sequences used in Maximum Likelihood analysis.

Table S2. Partitions and models of sequence evolution used in the Maximum Likelihood (ML) phylogenetic analyses.

Table S3. Partitions and models of sequence evolution used in the Bayesian (BEAST) phylogenetic analyses.

Table S4. Node calibration settings used in the BEAST analysis.

Table S5. Pairwise uncorrected genetic distances of *bdnf* gene sequences for 92 taxa. Values in bold are within family/subfamily genetic distances.

Table S6. Pairwise uncorrected genetic distances of *cmos* gene sequences for 308 taxa. Values in bold are within family/subfamily genetic distances.

Table S7. Pairwise Kimura 2-parameter genetic distances of *bdnf* gene sequences for 92 taxa. Values in bold are within family/subfamily genetic distances.

Table S8. Pairwise Kimura 2-parameter genetic distances of cmos gene sequences for 92 taxa. Values in bold are within family/subfamily genetic distances.