

RA: D. Tarkhnishvili et al.

RT: Phylogeography and evolution of anacondas

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Morphological trends and genetic divergence in anacondas, genus *Eunectes* Wagler, 1830 (Serpentes: Boidae)

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Supplementary material

Table S1. All_data – Specimens investigated morphometrically and genetically –
Label-Ids, taxon allocations, collection numbers, populations, approximate

geographical coordinates of historical sampling sites and geographic origin of individuals and raw measurement data used in this study. Regarding the use of acronyms for institutional resource collections in herpetology, we refer to the list in the appendix of Dirksen (2002) which was adapted from Leviton et. al. (1985).

Table S2. (a) primers used in the study, (b) Sequences used in this study (obtained from the available tissue samples (those marked by the asterisk), and downloaded from GenBank).

Table S3. Descriptives – Morphometric characteristics (nine body measurements, 11 scalation and 2 coloration pattern characters) of male (M) and female (F) anacondas. Ranges (RNG) followed by means (\bar{x}) and standard deviations (in parentheses), N = sample size. r – right side; l – left side. See “Materials and Methods” for further abbreviations.

Table S4. Percent variance explained and coefficients of individual traits loaded on the first four axes of a principal component analysis for ten body measurements, 11 scalation and two coloration pattern characters in individuals of *Eunectes* spp. Factor 1 is loaded by the contrast between the number of head stripes HS and dorsal blotches DB and most other characters, including total length TL. Factor 2 has positive loadings for the 10th subcaudal (10 SC) and 30th ventral scale width (30 V) and negative loadings for the number of scales on the head. Factor 3 is dominated by the contrast of the spurs length measured on the caudal side SpL and the number of orbital scales (Orb-re/li).

Table S5. Population samples, diploid sample sizes, proportion of variable marker loci (%pL), and total average expected heterozygosity or gene diversity (H_e) and its variance based on five variable RAPD markers showing 80 amplified bands in total.

Table S6. GenBank numbers of sequences for individual genes/ species.

Table S7. Genetic distance matrices among samples based on cytochrome b sequence analysis (proportion of substitutions: p-distance).

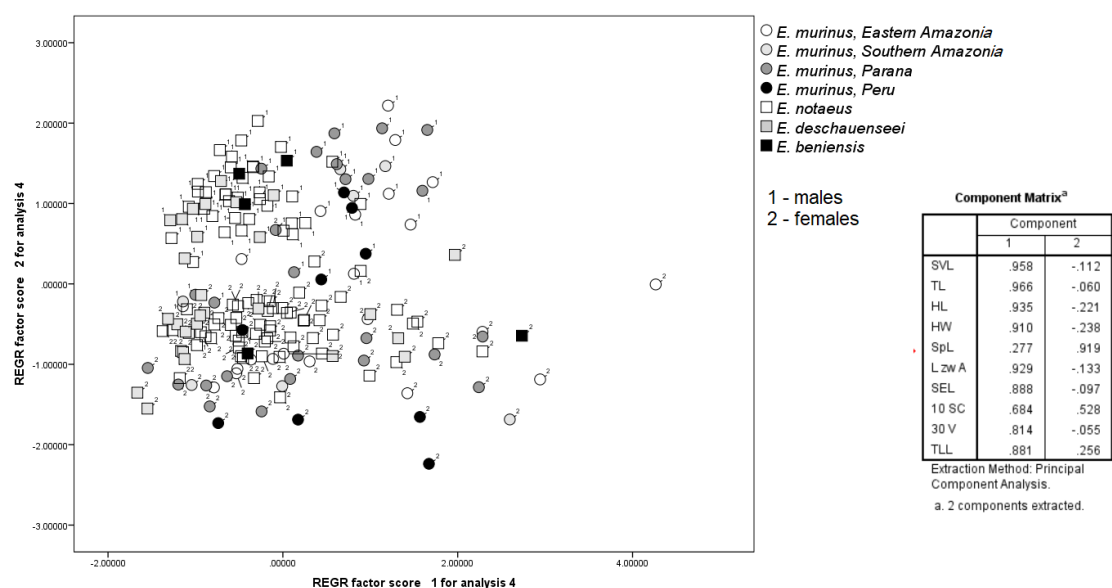
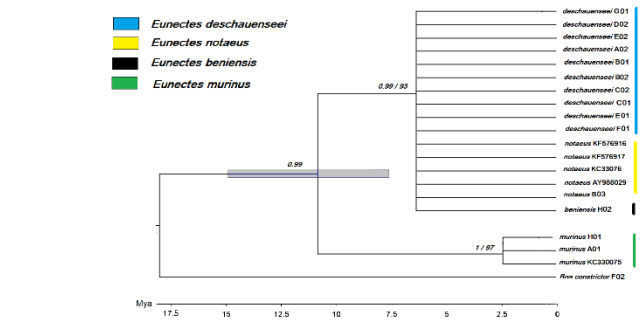
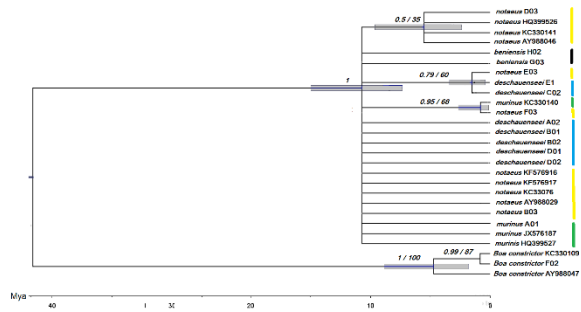
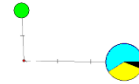


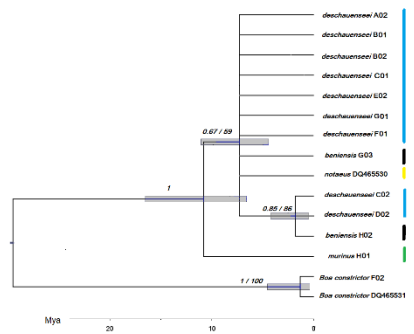
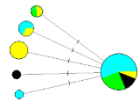
Figure S1. Principal Component analyses based on 10 morphometric traits (the first two PCA axes and component matrix shown).



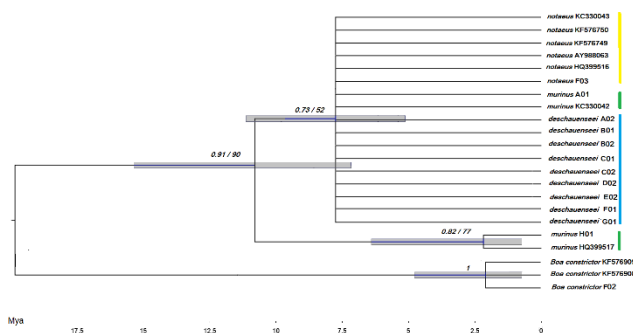
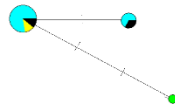
a (BDNF)



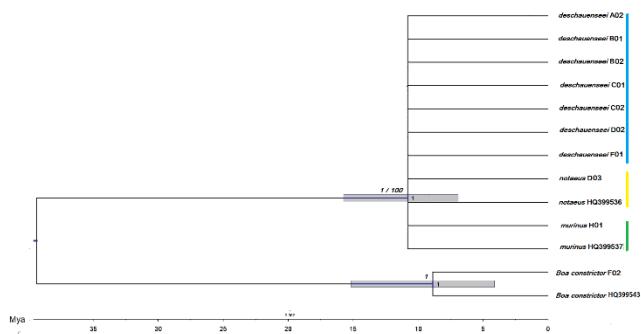
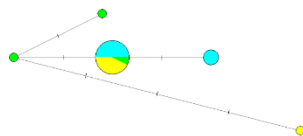
b (NT3)



c (ODC)



d (RAG)



e (C-mos)



Figure S2. Phylogenetic trees (left) and haplotype networks (right) based on the analysis of nuclear gene sequences. Bayesian inference tree is shown; the nodes with the posterior probability support below 0.5 are shown as unresolved. Above the nodes, posterior probabilities are shown, and bootstrap values inferred from ML analysis with RaxML if exceeding 50. The boxes indicate 95% HPD intervals for the estimated split times. Haplotype/ allele networks: size of the pies are proportional to the number of individuals/ alleles. (a) BDNF, (b) NT3, (c) ODC, (d) RAG-1, (e) C-mos.

File S1. Clickable Google Earth kml-file to map the approximate sites of the study area where the specimens were sampled for the morphometric and genetic analysis (cf. Appendix 1; anaconda_AMREP_sites.kml).

File S2. STRUCTURE input file for the RAPD analysis (anaconda_RAPD_structure_inputfile.txt).