

Supplementary Table 1. Models of evolution selected by AIC and applied for partitioned, model-based phylogenetic analyses.

Partition	AIC Model	Number of Characters
NADH 1, 1 st codon position	GTR + Γ	322
NADH 1, 2 nd codon position	GTR + Γ	322
NADH 1, 3 rd codon position	GTR + Γ	322
NADH 2, 1 st codon position	GTR + Γ	287
NADH 2, 2 nd codon position	GTR + Γ	287
NADH 2, 3 rd codon position	GTR + Γ	287
ATP8	HKY + Γ	157
ATP6	GTR + Γ	682
COXII and COXIII	GTR + Γ	177
All tRNAs (Lys, Leu, Ile, Gln, Trp, Ala, Asn)	GTR + Γ	518
BDNF	GTR + Γ	715
α -enolase	GTR + Γ	261
GapD	GTR + Γ	372
PTGER4	HKY + Γ	490
R35	GTR + Γ	689

VARIABLE CHOICE FOR MORPHOMETRIC SIZE CORRECTION

In order to explore whether head length is an appropriate measure with which to

standardize morphometric variables, and in doing so account for body size allometry, we first conducted a multivariate correlation analysis of all variables to determine which morphometric variable was most highly correlated with all measures of body size. We then conducted three sets of analyses using three different variables to correct for size. Following the methods of Lande (1978), Wiens and Slingluff (2001), and Brandley et al. (2008), we calculated measurements of relative limb and body sizes by regressing independent contrasts of limb and body-length measurements against contrasts in head length, snout–vent length, and midbody width. Each regression line was forced through the origin following Felsenstein (1985) and the standardized residuals were saved as variables. Relative measurements in each of the three sets of size-corrected morphometric variables (head-length-corrected, snout–vent-length-corrected, midbody-width-corrected) were subsequently used in bivariate and multivariate analyses. For all sets of analyses, the Benjamini and Hochberg (1995) method for controlling the false discovery rate (FDR) was applied to determine significant *P*-values (Verhoeven et al. 2005). SPSS 18.0 was used for all statistical analyses and JMP 8 was used for graphical output.

LITERATURE CITED

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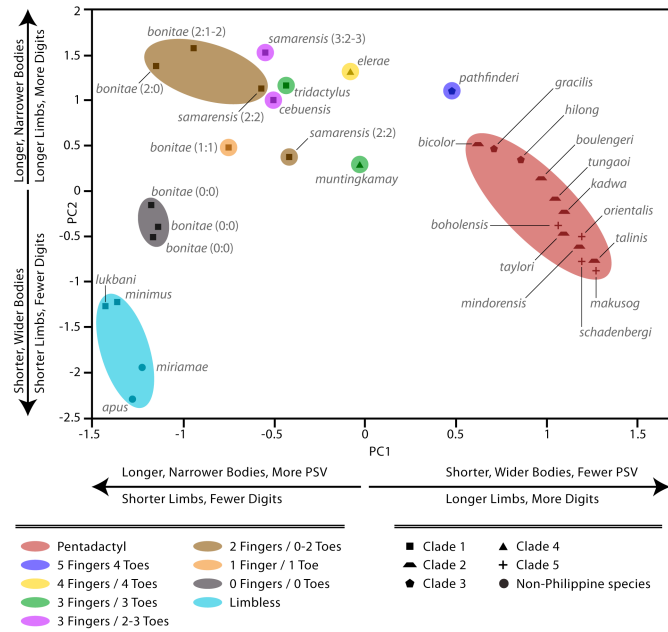
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Supplementary Figure 1. Multivariate plot of morphometric and meristic data showing variable loadings for the first and second components for a non-phylogenetic PCA. Colored spheres indicate body form groups among *Brachymeles*, with shapes referring to labeled phylogenetic clades in Figure 1.