



**Fig. 3.** Tree based on the complete concatenated dataset (cytochrome *b*, LDH, ODC and myoglobin), analysed by Bayesian inference. Pie charts indicate support in the four single-locus analyses (see explanation in upper left corner of figure). Squares on the right indicate indels shared among taxa in the alignments of the non-coding regions. Numbers in squares indicate size of indels: + means insertion and deletion. Names in bold refer to subgenera as defined by Helbig and Seibold (1999). Taxa marked with an asterisk (\*): only *cyt b* was available. Taxon marked with a circle (°): only ODC and *myo* were available.