



**Fig. 2.** Relationships of the *Lanian excubitor* complex and its nearest relatives, estimated by Bayesian analysis of the mitochondrial cytochrome *b* gene and part of the mitochondrial control region D-loop (in total 1.3 kbp). The broad grey and black vertical bars denote the common division into a northern and southern group, respectively. The former is now usually treated *L. excubitor* s.s. and the latter as *L. meridionalis*. The vertical bar at the base of clade B indicates a unique synapomorphic single-base pair deletion in the D-loop alignment. The column on the far right gives the number of tandem repeats in the mitochondrial control region found in each individual in this study; “-” denotes missing data. Values at branches indicate, in sequence, posterior probability, maximum likelihood bootstrap and parsimony bootstrap (all  $\geq 0.50/50\%$ ); \* denote posterior probability or bootstrap value of 1.00/100%.