



Fig. 2. Majority rule (50%) consensus tree of Locustellidae based on concatenated nuclear ODC, myoglobin, LDH and GAPDH and mitochondrial cytochrome *b* sequences, inferred by Bayesian inference, analysed in five partitions (four nuclear loci GTR+ Γ , cytochrome *b* GTR+ Γ +I). Colours of names indicate genus according to old taxonomy (Dickinson 2003; left) and new taxonomy proposed here (right; see Fig. 1 for explanation of abbreviations of generic names; *S.* = *Schoenicola*). Labelled bars denote clades as in Fig. 1. The four species for which only cytochrome *b* is available are in bold type. Posterior probabilities, and maximum likelihood and parsimony bootstrap values are indicated at the nodes, in this order; an asterisk represents posterior probability 1.0 or bootstrap 100%. *B. baboecala SA* and *B. baboecala Nig* refer to samples from South Africa (*transvaalensis/tongensis*) and Nigeria (*centralis*), respectively. ¹Node affected differently by different types of analyses (see Table 1). ²See Section 4 for recognition of non-monophyletic *Megalurus*.