



Fig. 1. Majority rule (50%) consensus tree of Locustellidae based on unique mitochondrial cytochrome *b* haplotypes, inferred by Bayesian inference under the GTR+ Γ +I model. 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%. The species for which no subspecific names are given are monotypic (except *L. lanceolata*, see below). Bars and colour shading delimit clades discussed in text. *B.* = *Bradypterus*, *C.* = *Cincloramphus*, *D.* = *Dromaeocercus*, *E.* = *Eremiornis*, *L.* = *Locustella*, and *M.* = *Megalurus*. Numbers after names are sample identifiers (e.g. *davidi* Sichuan, China 1 + 2 means *davidi* samples 1 and 2 from Sichuan, China [same haplotype], and *sinensis* China EU016090 refers to GenBank number of sequence previously used in another study; see Appendix A). ¹On geographical grounds, most likely nominate subspecies, but samples collected during migration, so subspecies *hendersonii* cannot be eliminated.