

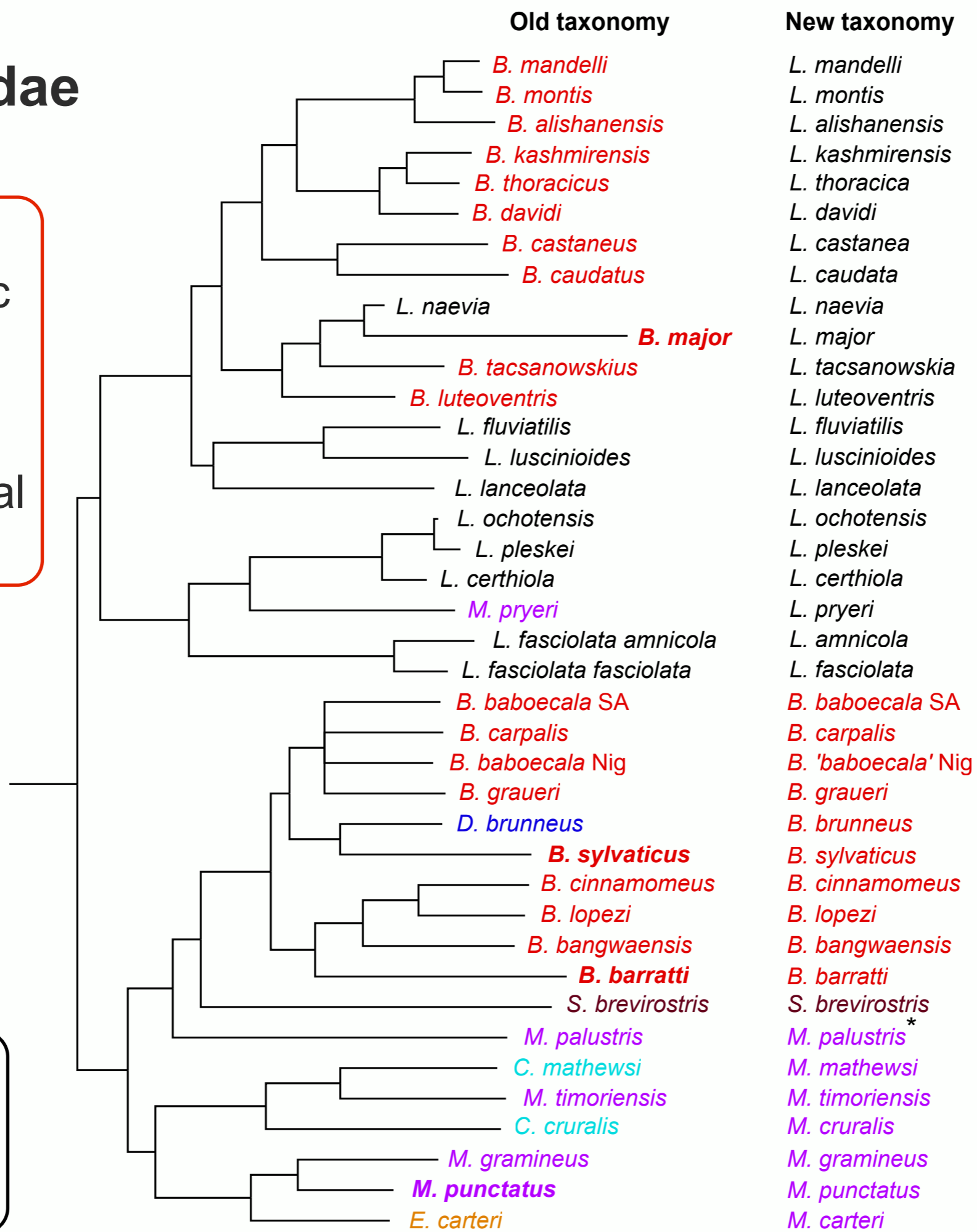
Locustellidae

Non-monophyletic genera

Complex morphological evolution

Alström et al. 2011. *Molecular Phylogenetics and Evolution* 58: 513–526.

Paintings: Brian Small. From Kennerley & Pearson. 2010. Reed and bush warblers. London: Christopher Helm; and Wikipedia (bottom)



Eurasia



Africa, Madagascar



Orient-Australia

Phylogeny of the family Locustellidae – multiple unexpected relationships revealed

The phylogeny of most of the species and multiple subspecies in the Old World family Locustellidae was inferred using mitochondrial and nuclear DNA. The phylogeny strongly disagrees with the current taxonomy at the generic level, and we propose a revised classification that recognizes four instead of seven genera. In addition, we show that several taxa presently treated as subspecies or as monotypic species as well as a few taxa recognized as separate species are in need of further taxonomic work.

The family Locustellidae (formerly Megaluridae) is widely distributed in Africa, Eurasia, Australasia and Oceania, and comprises several different genera, with generally slight morphological divergence among the different species. We used mitochondrial and nuclear DNA to infer the relationships of most of the species and many subspecies in this family, using both traditional phylogenetic methods as well as a recently developed Bayesian species tree method (BEST).

All of the genera for which more than one species are included in the analyses are inferred to be non-monophyletic. In particular, the large genus *Bradypterus* is found to be highly non-monophyletic, as it is separated into a Eurasian clade that also includes the genus *Locustella* (one of the latter nested within the traditional *Bradypterus*) and *Megalurus pryeri* and an African clade that includes the rest of the species as well as the Malagasy *Dromaeocercus brunneus*.

We propose that *Locustella*, all Asian *Bradypterus* and *Megalurus pryeri* be treated as *Locustella*, whereas the name *Bradypterus* be restricted to the African *Bradypterus* and *Dromaeocercus brunneus*.

Some taxa that are currently treated as conspecific appear to be sufficiently divergent in cytochrome *b* to warrant species status, although this needs to be confirmed by independent data: *Locustella fasciolata fasciolata* vs. *L. f. amnicola*; *Bradypterus baboecala tongensis*/*B. b. transvaalensis* vs. *B. b. centralis*/*B. b. elgonensis*; *Bradypterus lopezi mariae*/*B. l. usambarae* vs. *B. l. ufipae*; and *Megalurus palustris toklao* vs. *M. p. forbesi*.

Also the monotypic *Locustella* (formerly *Bradypterus*) *luteoventris* needs further study in the light of our results.

The divergences between the two species pairs *Locustella pleskei*–*L. ochotensis* and *Locustella* (formerly *Bradypterus*) *mandelli*–*L. montis* are so slight that their status as separate species need to be studied further.

We also report convergence problems for the recently developed species tree method BEST, despite up to 1×10^9 iterations.

Alström, P., Fregin, S., Norman, J.A., Ericson, P.G.P., Christidis, L. & Olsson, U. 2011. Multilocus analysis of a taxonomically densely sampled dataset reveal extensive non-monophyly in the avian family Locustellidae. *Molecular Phylogenetics and Evolution* 58: 513–526.