

Figure S6. Results of Bayesian species tree analysis of the complete character matrix. Shown is the maximum clade credibility tree derived from a single MCMC analysis (5 · 10⁸ generations, sampled every 1 · 10⁴) using *BEAST v1.6.1 (Drummond et al. 2006, 2007), with two temporal constraints: a uniform distribution of [5.1,0] Ma on the node uniting *Paroreomyza* and *Oreomystis*, and a normal distribution with $\mu=21.0$ and $\sigma=3.9$ on the root node (see text for justification). Numbers associated with nodes are estimated Bayesian posterior probabilities (after removal of the first 5 · 10⁷ generations as burn-in), and bars at each node are 95% highest posterior density intervals for divergence times.

