

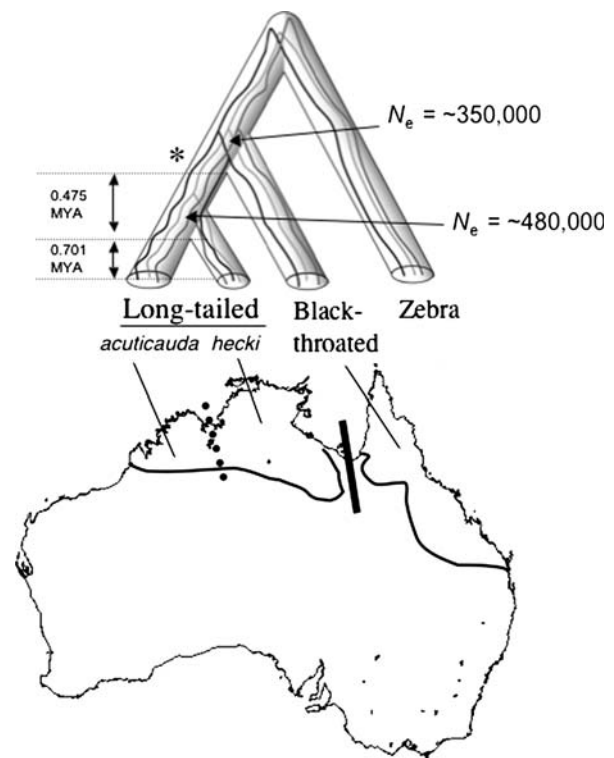
## Genomics and ornithology

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**Erratum to: J Ornithol (2007) 148 (Suppl 1):S27–S33**  
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Figure 3 was printed incorrectly. The correct version of Fig. 3 is given here.



**Fig. 3** Species tree analysis of Australian Grassfinches (*Poephila*) made possible by multilocus sequencing. The analysis is based on 30 anonymous, noncoding loci presented in Jennings and Edwards (2005) and re-analyzed by Liu and Pearl (2007). *Top* Phylogenetic relationships of four finch species. The asterisk indicates an estimated confidence (posterior probability) of the species tree branch at 0.88. Species divergence times for the ingroups are indicated, as are estimated effective population sizes. The 95% confidence limits (CI) on the *P. hecki*–*acuticauda* divergence are 0.18–0.72 MYA, with a confidence limit on effective size of the ancestral population of ~48,000–~1,195,000. *P. cincta* is estimated to have diverged 1.18 MYA (CI: 0.95–1.46 MYA), with an ancestral effective size confidence range of ~201,000–~580,000. *Bottom* Geographic ranges of species analyzed, with the Carpentarian (*solid*) and Kimberley/Arnhemland (*dotted*) barriers indicated

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