

ERRATUM

Morrow, E.H., Pitcher, T.E. & Arnqvist, G. (2003). No evidence that sexual selection is an 'engine of speciation' in birds. *Ecology Letters*, 6, 228–234.

We presented a comparative analysis of how species richness coevolves with sexual size dimorphism, sexual dichromatism and relative testes size in birds. The comparative method we employed (implemented in the computer program MacroCAIC) assumes that all, or at least nearly all, extant taxa are included in the analysis. This was not the case in our original contribution (see also Gage *et al.* 2002 who used MacroCAIC in two of their mammalian analyses) and the analyses reported there are therefore suspect. We are very grateful to Tim Barraclough for pointing out this error.

Since a complete phylogenetic hypothesis of all bird genera is not available at present, it is not possible to reanalyze the data at the generic level. However, a near complete family level phylogeny (incorporating 9564 of an estimated 9968 extant species) is available (Sibley & Ahlquist 1990) allowing us to include nearly all extant species in the analyses. Using this data, we generated phylogenetically independent contrasts of each of the three measures of sexual selection intensity and related this to relevant phylogenetically independent measures of species richness (termed Relative Rate Difference, RRD) (see our original contribution).

Tests of the slopes in regressions through the origin (see Isaac *et al.* 2003), using randomization tests (Manly 1991), failed to reveal significant associations between any of our three measures of sexual selection intensity and species richness (size dimorphism: $\beta = 0.049$, $SE_{\beta} = 0.272$, $t = 0.179$, $P = 0.57$; dichromatism: $\beta = -0.143$, $SE_{\beta} = 0.263$, $t = 0.544$, $P = 0.58$; relative testes size: $\beta = -0.018$, $SE_{\beta} = 0.263$, $t = 0.069$, $P = 0.47$). The results of these family level analyses are therefore qualitatively equivalent to those given in our original contribution, and the conclusions reported there are not altered by this reanalysis of our data.

REFERENCES

- Gage, M.J.G., Parker, G.A., Nylin, S. & Wiklund, C. (2002). Sexual selection and speciation in mammals, butterflies and spiders. *Proc. R. Soc. Lond. B*, 269, 2309–2316.
- Isaac, N.J.B., Agapow, P.-M., Harvey, P.H. & Purvis, A. (2003). Phylogenetically nested comparisons for testing correlates of species-richness: a simulation study of continuous variables. *Evolution*, 57, 18–26.
- Manly, B.F.J. (1991). *Randomization, Bootstrap and Monte Carlo Methods in Biology*. Chapman & Hall, London.
- Sibley, C.G. & Ahlquist, J.E. (1990). *Phylogeny and classification of birds. A Study in Molecular Evolution*. Yale University Press, London.