

THE ROLE OF THE GIBBON FOSSIL RECORD IN PREDICTING RANGE CHANGES AND PHYLOGENY

H.J. Chatterjee

Research Department of Genetics, Evolution and Environment, Darwin Building, Gower Street, University College London, UK

Presenter's Email: h.chatterjee@ucl.ac.uk

The tempo and mode of gibbon phylogeny was estimated using a supermatrix approach comprising 7 mitochondrial genes (6,138 nucleotides) across 11 species, as part of an order wide estimate of primate phylogeny (Chatterjee, et al. 2009). Bayesian phylogenetic analysis was performed on the mitochondrial species-level supermatrix using an unconstrained Felsenstein model implemented by *MrBayes* 3.1 and the phylogeny and divergence times were co-estimated using the software *BEAST* 1.4.7. Results suggest the following divergence patterns across gibbons: (Symphalangus,(Nomascus,(Hoolock, Hylobates))). The fossil record was used to inform the specification of 11 minimum age constraints in order to calibrate the age estimates for primate divergences across the entire tree; results suggest a mean date estimate of 10.3 million years ago for the Hylobatidae clade. Given the pattern and timing of gibbon evolution across the Hylobatidae, further analyses were undertaken to predict range changes for a subset of gibbon species in China. The fossil record was used in combination with vegetation, climate and human population data to understand how species respond to environment changes over time. The study provides a framework for using the primate fossil record in tandem with multiple lines of evidence to address questions pertaining to phylogeny, patterns of speciation, conservation and range shifts in response to environmental change.

Keywords: gibbons, phylogeny, supermatrix, fossil