**APPENDIX A; DIVERSIFICATION RATE ANALYSES USING DR AND BAMM**

**METHODS**

We assessed the historical dynamics of speciation and extinction among all species of the Corvides using two alternative methods, the Diversification Rate metric (DR [1]) and BAMM [2]. DR reflects the number of lineage splitting events from the root to the tip of the phylogeny, weighted by the relative timing of those events. This metric has been shown to be highly correlated with speciation rate estimates in birth-death simulations [1], but is limited in its representation of historical diversification, as it does not account for extinction, or the potential for diversification rates to vary through time [3-4]. However, given its consideration of branch length information in concordance with the species diversity arising from nodes throughout the lineage, DR does provide an effective index of the relative isolation of a species in the phylogeny, and is therefore likely to reflect the recent rate of diversification [4]. We estimated values of DR both on the MCC tree derived from Jønsson et al. [5], and on a phylogeny in which the missing species had been placed based on taxonomic information (see the main methods section and the original study for information about the tree building methodology).

In contrast to DR, BAMM uses a Reverse Jump Markov chain Monte Carlo (RJMCMC) algorithm to explore potential models of lineage diversification that vary in their rates of speciation and extinction. This method generates a posterior distribution of speciation and extinction rate values at any point in time along the phylogeny, such that BAMM evaluates a number of potential evolutionary rate shift scenarios that are sampled in proportion to their posterior probability. Each rate shift generates a cohort of taxa (all lineages downstream of the rate shift, assuming no further rate shifts) that share common rates of speciation and extinction.

We ran the BAMM analysis for a total of 10,000,000 generations, with a global sampling fraction of 0.85 to account for the species that had no DNA sequence available, and used BAMMtools [6] to estimate appropriate priors. We set an exponential hyperprior of 1.0 on the rate parameters of the Poisson distribution that governs the number of diversification rate shifts recorded throughout the phylogeny, exponential priors of initial speciation and extinction rates with values of 1.29, and a normal prior with a mean of 0 and a standard deviation of 0.02 as a shift parameter for the rate regimes. Following the analysis, we discarded the first 10% of all runs as a burn-in, after ensuring convergence of the RJMCMC algorithm by calculating the effective sample size. Subsequently, the present day rates of speciation were extracted for each species, which reflect the marginal density of speciation rates sampled across the tree [7, 8].

The results presented here illustrate the general trends of the diversification dynamics among the Corvides at the species-level, without further statistical analyses. We refrain from using methods that attempt to correct for the non-independence of these data points as a consequence of the shared evolutionary history among species, because both estimates of diversification (DR and BAMM) are derived from the structure of the phylogenetic tree itself. Unlike continuously evolving traits, in which we can account for the non-independence using a model of trait evolution (e.g. Brownian motion) in addition to a matrix of phylogenetic covariance (usually distance in branch lengths), we currently lack a formal statistical model that can describe and control for the expected variation in diversification rates (derived in this manner) across the phylogeny. Alternative methods [see 9] were unfortunately not appropriate for our data set given the relatively low number of species analysed and rate shifts recovered.

**RESULTS**

Contrasting the values of DR among the island/continental, habitat and migratory classifications, it is apparent that the main differences among species are predominantly within the island/continental classifications. Island and widespread species have higher DR values in contrast to continental species (Fig. A1). Differences in these same values among the habitat and migratory classifications were more negligible (Figs A2-3). These findings were consistent with those in which species that had no DNA sequence available at the time of the tree generation (and thus placed in the phylogeny based on taxonomic information) were excluded from the analysis (Fig A4-6). The results provided from the estimated values of DR were also in general concordance with those considering rates of speciation suggested by BAMM (Figs A7-9). From these results, it is apparent that many corvoid species share similar values of speciation rates, reflecting the low number of rate shifts recovered on the phylogeny (Fig A10). However, it is notable that of the four families that we consistently recover rate shifts for, three (Campephagidae, Monarchidae and Pachycephalidae) have diversified extensively throughout the Indo-Pacific archipelagoes and contain a relatively high proportion of island taxa (Fig. A11). These same families tend to have similar proportions of migratory and non-migratory species (except for Pachycephalidae; Fig A12), while there are no general trends when evaluating the habitat classifications. The Corvidae are predominantly found in open habitats, the Pachycephalidae and Monarchidae mainly in dense vegetation, and the Campephagidae in a mixture of habitat types (Fig. A13). These different trends may explain the similarity in DR values among the habitat classifications, and ultimately why we fail to detect any signature of habitat on the diversification dynamics of the Corvides. In summary, the results of these analyses suggest that the findings presented in Figure 3 (based on independent evolution of the character states among monophyletic groupings) may be general across all lineages of the Corvides.

**REFERENCES**

1. Jetz W, Thomas GH, Joy JB, Hartmann K, Mooers AØ. 2012 The global diversity of birds in space and time. *Nature* **491**, 444-448.
2. Rabosky DL. 2014. Automatic detection of key innovations, rate shifts, and diversity-dependence on phylogenetic trees. *PLoS One* **9**, e89543.
3. Rabosky D. 2009 Ecological limits and diversification rate: alternative paradigms to explain the variation in species richness among clades and regions. *Ecol. Lett*. **12**, 735-743.
4. Kennedy JD, Wang Z, Weir JT, Rahbek C, Fjeldså J, Price TD. 2014. Into and out of the tropics: the generation of the latitudinal gradient among New World passerine birds. *J. Biogeogr*. **41**, 1746-1757.
5. Jønsson KA, Fabre P, Kennedy JD, Holt BG, Borregaard MK, Rahbek C, Fjeldså J. 2016. A supermatrix phylogeny of corvoid passerine birds (Aves: Corvides). *Mol. Phylogenet. Evol*. **94**: 87-94.
6. Rabosky DL, Grundler M, Anderson C, Shi JJ, Brown JW, Huang H, & Larson JG. 2014 BAMMtools: an R package for the analysis of evolutionary dynamics on phylogenetic trees. *Methods. Ecol. Evol.* **5**, 701-707.
7. Rabosky DL, Title P, Huang H. 2015 Minimal effects of latitude on present-day speciation rates in New World birds. *Proc. R. Soc. B.* **282***,* 20142889.
8. Rabosky DL, Matute DR. 2013 Macroevolutionary speciation rates are decoupled from the evolution of intrinsic reproductive isolation in Drosophila and birds. *Proc. Natl Acad. Sci. USA.* **110***,* 15354-15359.
9. Rabosky D.L, Huang H. 2016 A robust semi-parametric test for detecting trait-dependent diversification. *Syst. Bio.* **65**, 181-193.

**Figure A1.** Boxplots illustrating differences in the values of DR among 782 species of the Corvides. Variation in these values are highlighted among taxa that undertake seasonal movement (generally > 1,000 km) compared to those that are more sedentary. The numbers of species in the migratory and non-migratory classes are shown in parentheses.

****

**Figure A2**. Boxplots illustrating differences in the values of DR among 782 species of the Corvides. Variation in these values are highlighted among taxa that are distributed on islands, continents or are widespread (present on both islands and continents). The numbers of species in the island, continental and widespread classes are shown in parentheses.



**Figure A3**. Boxplots illustrating differences in the values of DR among 782 species of the Corvides. Variation in these values are highlighted among species found in open, dense or mixed habitat types. The numbers of species in the open, dense or mixed classes are shown in parentheses.

****

**Figure A4.** Boxplots illustrating differences in the values of DR among the 662 corvoid species sampled in the phylogeny of Jønsson et al. [5]. Variation in these values are highlighted among taxa that undertake seasonal movement (generally > 1,000 km) compared to those that are more sedentary. The numbers of species in the migratory and non-migratory classes are shown in parentheses.



**Figure A5**. Boxplots illustrating differences in the values of DR among the 662 corvoid species sampled in the phylogeny of Jønsson et al. [5]. Variation in these values are highlighted among taxa that are distributed on islands, continents or are widespread (present on both islands and continents). The numbers of species in the island, continental and widespread classes are shown in parentheses.



**Figure A6**. Boxplots illustrating differences in the values of DR among the 662 corvoid species sampled in the phylogeny of Jønsson et al. [5]. Variation in these values are highlighted among species found in open, dense or mixed habitat types. The numbers of species in the open, dense or mixed classes are shown in parentheses.



**Figure A7**. Boxplots illustrating present day speciation rates (estimated from BAMM) among 662 species of the Corvides. Variation in these values are highlighted among taxa that undertake seasonal movement (generally > 1,000 km) compared to those that are more sedentary. The numbers of species in the migratory and non-migratory classes are shown in parentheses.



**Figure A8**. Boxplots illustrating present day speciation rates (estimated from BAMM) among 662 species of the Corvides. Variation in these values are highlighted among taxa that are distributed on islands, continents or are widespread (present on both islands and continents). The numbers of species in the island, continental and widespread classes are shown in parentheses.



**Figure A9**. Boxplots illustrating present day speciation rates (estimated from BAMM) among 662 species of the Corvides. Variation in these values are highlighted among species found in open, dense or mixed habitat types. The numbers of species in the open, dense or mixed classes are shown in parentheses.



**Figure A10**. Mean rates of speciation estimated among five groups of corvoid birds. Four of these groupings represent families (Campephagidae, Corvidae, Monarchidae and Pachycephalidae) that were consistently recovered to have increased rates of speciation by BAMM, whereas the final group represents the remaining lineages that are diversifying at the background rate. Error bars represent the standard deviation of the mean speciation rates estimated across 4,500 post-burnin samples from BAMM.



**Figure A11**. Proportion of overall corvoid species diversity distributed on islands, continents or in both areas within four families of corvoid birds (Campephagidae, Corvidae, Monarchidae and Pachycephalidae) that were consistently recovered to have increased rates of speciation by BAMM.



**Figure A12**. Proportion of overall corvoid species diversity that are migratory or non-migratory within four families of corvoid birds (Campephagidae, Corvidae, Monarchidae and Pachycephalidae), that were consistently recovered to have increased rates of speciation by BAMM.



**Figure A13**. Proportion of overall corvoid species diversity found in open, dense or mixed habitat types among four families of corvoid birds (Campephagidae, Corvidae, Monarchidae and Pachycephalidae) that were consistently recovered to have increased rates of speciation by BAMM.

