

SUPPLEMENTARY MATERIALS AND METHODS FOR MANNION ET AL.: A TEMPERATE PALAEO-DIVERSITY PEAK IN MESOZOIC DINOSAURS AND EVIDENCE FOR LATE CRETACEOUS GEOGRAPHICAL PARTITIONING

Diversity and stratigraphic data

The unequal durations of our time slices is not expected to introduce bias into our analyses as we are investigating spatial, not temporal, patterns in diversity (temporal patterns preferentially employ equal-length time bins [Raup, 1975; Alroy *et al.*, 2001, 2008]; though see Butler *et al.*, 2011; Mannion *et al.*, 2011). Analysis of diversity patterns in time slices is analogous to the use of time slicing in biogeographic analyses of fossil data (Hunn & Upchurch, 2001; Upchurch & Hunn, 2002; Upchurch *et al.*, 2002).

Sampling data

Use of formation counts as a sampling proxy does not assume that all formations are equal, only that variation in weathering rates, outcrop area, thickness, lithostratigraphic research, and palaeontological sampling effort are distributed randomly and do not introduce systematic biases. Counts of fossiliferous formations form a proxy for: (1) the amount of rock available for fossil sampling, (2) the geographic extent of sampled formations (different sedimentary basins have different formations), (3) the heterogeneity of facies available for fossil sampling, and (4) the amount of geological study that has been undertaken (Raup, 1975; Peters & Foote, 2001; Peters & Heim, 2010; Upchurch *et al.*, 2011). The fossil record has been sampled over more than two centuries and historic collections are often sparsely documented. Thus, sampling effort can only rarely be measured directly and DBCs, as employed here, is an attempt to capture worker/collector effort. These collections represent independent samples of dinosaurs from

specific geographic and stratigraphic localities that have been as finely resolved as the published record allows (Mannion *et al.*, 2011). Although sampling proxies only provide an estimate of sampling effort, they are necessary in quantitative studies of ancient biotic diversity such as this one.

Statistical methods

Shareholder Quorum Subsampling (SQS [see Alroy, 2010a, b]) was performed on downloads of Mesozoic dinosaur data from *The Paleobiology Database* (PBDB; accessed June 2011) using built-in diversity tools within the PBDB. A separate download was carried out for each time- and palaeolatitudinal bin; generically indeterminate occurrences, form taxa and ichnofossils were all excluded. Analyses were conducted at the generic level. Following the recommendations of Alroy (2010a, b), the modified version of Good's u that counts one-reference taxa was used, the most common taxon was ignored, and taxa only occurring in the most diverse collection were excluded. 100 subsampling trials and three different quorum levels (0.40, 0.50, 0.60) were used, with congruent results obtained regardless of the level chosen.

In our multiple regression models, empty bins (bins containing zero DBCs or DBFs) interposed between sampled bins were initially retained to maintain the equal spacing of latitudinal bins implicit in the autoregressive models. The data were subsequently analyzed excluding all empty bins, retrieving similar results that are presented in the main text. Full results are presented in Appendix S2 in Supporting Information. All data were log₁₀ transformed prior to analysis in R version 2.10.1 (R Development Core Team, 2010), using the packages *lmtree* (Zeileis & Hothorn, 2002), *nlme* version 3.1-96 (Pinheiro *et al.*, 2009), *qpcR* version 1.2-7 (Spiess & Ritz, 2010) and *tseries* version 0.10-22 (Trapletti & Hornik, 2009). The Jarque-Bera and Breusch-Pagan tests indicated that the residuals were normally distributed in most cases, and

homoskedastic for the best models in almost all cases, which is not problematic (heteroskedasticity causes an overestimate of model fit, so homoskedasticity is only required for models that appear to fit the data well) (Burnham & Anderson, 2001).

Adjacent points in space are likely to have similar values of diversity, sampling and land area due to geographic proximity alone. This property is termed spatial autocorrelation and causes overestimation of the strength of the relationship between spatially-distributed variables, even when they are unrelated to each other (Burnham & Anderson, 2001). Because our spatial data series were one-dimensional, this problem is directly analogous to that of autocorrelation in time series data. To remove the potentially biasing effect of spatial autocorrelation, we tested each multiple regression model using autoregressive models of orders zero, one, and two using the 'gls' function of nlme version 3.1-96 (Pinheiro *et al.*, 2009). Models were selected using Akaike weights to identify the best combination of explanatory variables based on an information criterion (AICc) (Sugiura, 1978). This is a measure that rewards goodness of fit of the regression model (combination of explanatory variables) but penalises models incorporating higher numbers of variables. Thus, the best model is deemed to be one that explains the highest proportion of variation in taxic diversity using the fewest explanatory variables. The generalised coefficient of determination (R^2) (Maddala, 1983; Cox & Snell, 1989; Magee, 1990; Nagelkerke, 1991) was calculated manually from the output of the generalised least squares (GLS) analysis. This coefficient indicates the proportion of variance in taxic diversity explained by the combination of variables in the regression model.

Although we used linear regressions to model the relationships between sampling and diversity, the full relationship is more likely to be of inverse exponential form, 'levelling off' at a particularly high level of sampling. If this happened then we would find that increased sampling (e.g. through exploration of new formations) would yield few new taxa. However, this is not the

case for dinosaurs: inspection of the relationship between latitudinal sampling and observed palaeodiversity does not show a 'levelling off', so a linear model is adequate.

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