SUPPLEMENTARY DATA 1—Detailed methods of data collection.

Data collection for this project proceeded in two phases. In the first phase, the USGS topographic maps used by the UW, USGS and JHU expeditions to record the location and extent of localities in the Willwood Formation were scanned. The maps were linked to form a single map of the central part of the Bighorn Basin, from which the outlines of the localities were digitized, and GIS was used to calculate the two-dimensional areas of each locality. In the second phase, locality attributes and specimen data were collected and linked with the locality areas. Descriptive statistics for each locality were then calculated.

PHASE ONE

There were 20 USGS topographic maps used by the UW, USGS and JHU expeditions to record localities. These were scanned using an HP DesignJet 800PS 42-inch plotter at 150 dpi. The resulting tiff files were opened in ArcMap 9.1 and referenced to the USGS quadrangle key map grid using the georeferencing tool. All rectified images were held to a Root Mean Square (RMS) value of ≤13. Hand drawn polygons representing fossil localities were digitized by creating shapefiles and tracing by hand the outlines from the geotiffs, thus creating geospatially referenced vectors. Each vector was identified by locality number. More than 1000 localities were digitized and a subset of 385 localities was targeted for this project, including only those tied directly to the Bown et al. (1994) master composite stratigraphic section that had catalogued mammal specimens in the Smithsonian National Museum of Natural History (NMNH) collections. Only one locality was excluded due to outline error that likely arose during the initial phase of site identification onto the USGS topographic map. A few additional localities were not clearly labeled on the maps and require further study to identify.

ArcMap was used to calculate the area in squared meters for each locality vector. The error of the area estimates was minimal as all locality outline digitizing was done by the second author for consistency, and error due to digital rectification was only $\pm 13 m^2$. There were several very small FMC and NWC localities ($<500\ m^2$); however, none of these localities appeared to be the result of incorrect digitization. It is possible that some of the outlines on the topographic maps are inaccurate, but this cannot be tested with the present data and must await further exploration in the field. For this project, it was assumed that all locality areas were valid estimates. Although most of the localities in the Willwood Formation have some degree of elevation, the fossil layers themselves are limited to a few vertical meters (see text). Thus, a two-dimensional model was adequate for this study.

PHASE TWO

In the second phase of data collection, specimen data for the subset of 385 localities were compiled in an Access database. Specimens included only dental remains collected by surface prospecting, identifiable to the species level and catalogued in the NMNH collections. The length and width of all complete lower first molars were measured using digital calipers. These data were exported to MS Excel and linked with corresponding locality data, including stratigraphic meter level, associated creek drainage, and relative paleosol maturity rank (T.M. Bown, unpublished data, 1989; Bown and Beard, 1990; Bown et al., 1994). For each locality, sample size and species richness were then compiled. For all localities with 60+ specimens, species richness was also rarefied to a standardized sample size of 50 specimens using software downloaded from the University of Georgia Stratigraphy Lab web page (http://www.uga.edu/~strata/software/Software.html). Log-transformed occlusal surface areas

were calculated for all measured lower first molars as follows: SA = LN(l*w), where SA is the occlusal surface area, l is the length, and w is the width of the lower first molars.

The two-dimensional locality surface areas calculated by ArcMap were then exported to MS Excel and linked with the specimen and locality data by locality number. Species densities were calculated for each locality as follows: SD = E(S)/A, where SD is species density, E(S) is rarefied richness, and A is area (km^2). A summary of the locality data is presented in Appendix 2, excluding those relative paleosol development stages that are currently unpublished.

REFERENCES

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