An Insiders View of the Vertebrate Fossil Record: X-ray Computed Tomography of Vertebrate Microfossil Bonebeds from the Upper Cretaceous Judith River Formation, Montana

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Abstract

Vertebrate microfossil bonebeds (VMBs) are localized concentrations of small, disarticulated, and often taxonomically diverse vertebrate hardparts (e.g., teeth, scales, scutes, vertebrae, unidentifiable bone sand and bone pebbles). They are commonly studied in Mesozoic and Cenozoic records to recover otherwise rarely found small-bodied taxa, and to document relative taxonomic abundance and species richness in ancient vertebrate communities. We are using X-ray Computed Tomography (XRCT) to explore the taphonomy of a suite of richly fossiliferous VMBs in the Coal Ridge Member of the Upper Cretaceous (Campanian) Judith River Formation of north-central Montana. Vertebrate bioclasts in Judith River Formation VMBs are often found co-mingled with abundant invertebrate shell debris and plant fragments. Fortuitously, the bioclastic fraction of the site under investigation consists almost exclusively of vertebrate skeletal debris set in a silty claystone matrix—this particular site lacks invertebrate shell debris and preserves only a small amount of carbonaceous plant debris, making it somewhat less complicated than most of the other VMBs in our collection. Using an XRCT approach we are able to quickly observe in-situ hundreds of mm-scale vertebrate bioclasts in their original spatial orientations. Samples are scanned using a 225 kV microfocus system at the University of Minnesota XRCT lab, with 3-D volumes analyzed using Avizo Fire. This method allows us to directly observe the distribution, sorting, and orientation of bioclasts, along with other taphonomic attributes (such as breakage and potential associations) typically lost using traditional extraction methods such as soaking and sieving. This approach also allows characterization of the 3-D spatial orientation of vertebrate bioclasts in relation to associated molds (in this case, voids where mollusk shell debris has been dissolved). In addition to documenting various taphonomic attributes of VMBs in situ, this study tests the correlation between data derived from sieved collections and intact blocks of matrix scanned using XRCT.

Locality

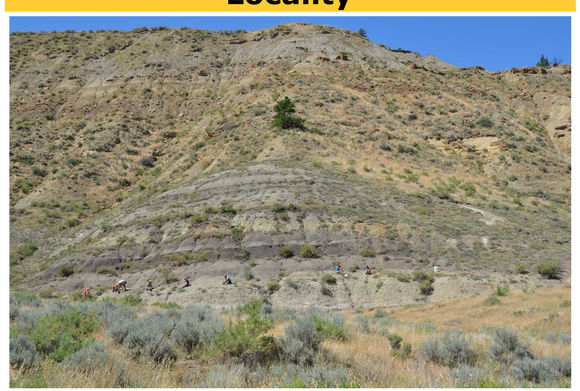

Figure 1. Outcrop view of locality UC-914 in the Coal Ridge Member of the Judith River Formation (Rogers et al. 2016). This pond/lake VMB accumulated in a coastal plain setting. Small resilient vertebrate fossils are preserved in association with carbonaceous debris along the full extent of the bed, which crops out near the base of exposures.

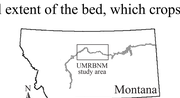

Figure 2. Location of study area in north-central Montana. Fossil matrix was collected from vertebrate microfossil bonebeds in the Upper Missouri River Breaks National Monument (UMRBNM).

Figure 3. Locations of six vertebrate microfossil bonebeds in the UMRBNM. Size and shape data were recovered from all six sites - two are described here using XRCT: UC-8303 and UC-914.

Project Description and Goals

Vertebrate microfossil bonebeds (VMBs)—localized concentrations of small resilient vertebrate hard parts—are commonly studied to recover otherwise rarely found small-bodied taxa, and to document relative taxonomic abundance and species richness in ancient vertebrate communities. VMBs are particularly abundant in terrestrial deposits of the Upper Cretaceous (Campanian) Judith River Formation of north-central Montana (see Figures 1-3). Previous work on VMBs in the Judith River Formation has focused on taphonomic comparisons of VMBs from different facies contexts, with the aim of documenting potential biases and reconstructing likely origins (Rogers and Brady 2010; Rogers et al. in press).

Here we dig a little deeper inside of VMBs, and explore key aspects of VMB taphonomy using X-ray Computed Tomography (XRCT). We compare the results of our preliminary XRCT analyses on intact blocks of fossiliferous matrix with data recovered via bulk sampling and sieving. This ongoing project has the potential to yield novel insights into the nature of Judith River VMBs. It also affords an opportunity to ground truth the XRCT method.

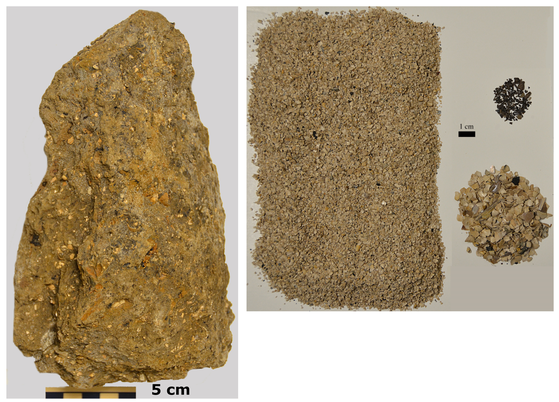

Figure 4. Blocks of fossiliferous matrix from sites UC-8303 (above), UC-914, and several other VMB localities were reduced to vertebrate and invertebrate bioclasts via sieving and sorting. Upon extraction, vertebrate bioclasts were set in frame for image capture and size analysis. Shape data were also collected from the vertebrate fraction.

Sieve Methods

Bulk samples of fossiliferous matrix collected from site UC-914 were processed using an automated sieve system designed at Macalester College. Eight nested sieve pairs with openings of 500 µm and 2 mm were washed concurrently, with 1 – 2 kg of material allocated to each pair. Sieve pairs were slowly submerged and drained in baths of standing water every 10 s until free of matrix. Remnant bioclasts in the 500 µm and 2 mm sieves were removed and sorted into vertebrate, invertebrate, and plant fractions under light microscopes. Each bioclastic fraction was weighed, and the invertebrate and plant fractions were stored for future study. Counts of vertebrate bioclasts were made during this initial sorting process. A representative subsample of approximately 1000 bioclasts from site UC-914 was studied in detail. The sizes of vertebrate bioclasts were documented using microscope-based image analysis (ImageJ; Rasband 1997–2015) to yield precise measurements of long axes down to the 500 µm recovery limit (see Figure 9 to right). The subsample was also characterized with regard to shape (see Figure 10 to right).

XRCT Methods

Samples from sites UC-914 and UC-8303 were scanned in the X5000 micro-CT machine located at the University of Minnesota XRCT lab. We used a 225-kV FeinFocus X-ray source to acquire 1080 projections using frame averaging to reduce noise. Samples were scanned using the following parameters: 160kV, 24.0 watts, and a framerate of 2.6 frames per second. The reconstructed volumes had a voxel size of 26 µm (isotropic) that we downsampled to 40 µm. The 16-bit slices were imported into Avizo Fire, filtered using a non-local means filter, and thresholded to select bones (see Figure 8). Using the label analysis module in Avizo Fire we measured the long, intermediate, and short axes of each bone. The smallest mesh size in the sieving method is 500 µm so we excluded all objects less than 500 µm in the XRCT analysis. We are focusing on UC-914 for this study but images from UC-8303 are included for comparison.

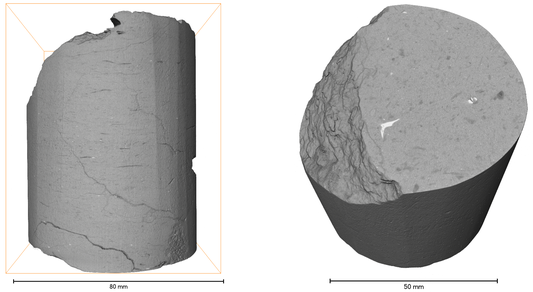

Figure 5. 3D volume renderings of UC-914. The image on the left shows the complete sample, the image on the right is cut to reveal bones and other higher density objects.

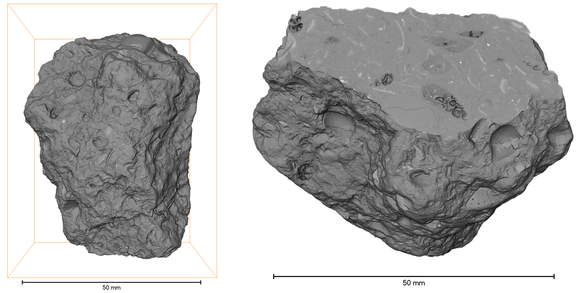

Figure 6. 3D volume renderings of UC-8303. The image on the left shows the complete sample, the image on the right is cut to reveal shells, bones, molds, and other higher density objects.

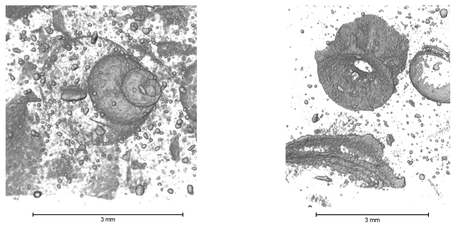

Figure 7. Close up view of a gastropod (left) and osteichthyan fish vertebra (right). These specimens are preserved in the block of intact matrix illustrated above in Figure 6.

Results

We are in the early stages of developing the XRCT method but the results are very promising. The scanning and analysis procedures are simple and fast. For a better comparison we need to scan more samples so that the bone yields are similar (see Table 1). We are still working to determine the best sample size to scan and the necessary resolution for the analysis. Most of the error in the XRCT analysis results from erroneous bone identification in the thresholding step, and we think it likely that scanning smaller samples (resulting in higher resolution) will provide better results. For this study we compared XRCT analysis with previous sieving results. The next step is to sieve the scanned samples to further test and confirm the XRCT results.

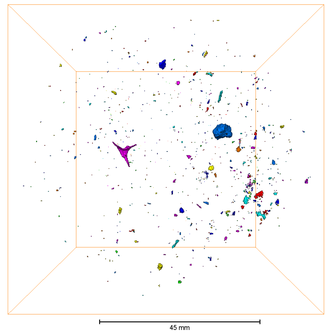

Figure 8. 3D rendering of bones preserved in sample UC-914. This is accomplished by thresholding and removing objects smaller than 500 µm. Different colors represent discrete objects and do not correlate to size or other measures. The large pink bone is the same bone visible in Fig. 5 (right).

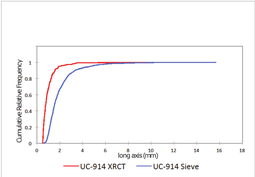

Figure 9. Size distributions of vertebrate bioclasts in UC-914 recovered via bulk sampling and sieving (blue). The mean long axis of recovered specimens is 2.0 mm. The size distribution of potential vertebrate bioclasts based on XRCT analysis (red) is provided for comparison.

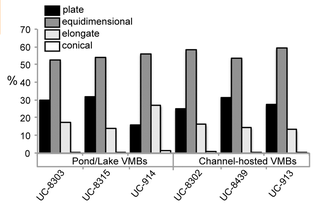

Figure 10. Shape distributions of sieve-based subsamples of VMBs. These show great consistency across sites, with equidimensional bioclasts dominating in all localities. The only notable outlier is site UC-914, which has a disproportionate abundance of elongate elements relative to the other five sites. Shape distributions from XRCT data show a disproportionate amount of elongate bones, most likely related to the thresholding error previously mentioned.

UC-914	Sieve Recovery	XRCT Imaging
Total Bones documented	1067	287
Minimum (long axis)	0.58 mm	0.50 mm
Maximum (long axis)	15.7 mm	10.1 mm
Mean	2.0 mm	1.0 mm
SD	1.4	0.8
Bone yield/Kilogram	187/kilogram	323/kilogram

Table 1. Comparison of bone size and yield using sieve recovery and XRCT imaging for sample UC-914.

Acknowledgements and References

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