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SUPPLEMENTAL DATA

METHODS

Sampling and Stratigraphy

All samples were collected from a single, continuous (~180 m long) outcrop of the Pierre Shale exposed on the Buffalo Gap National Grassland in Custer County, South Dakota, American Museum of Natural History (AMNH) locality 3504. Necessary permits for collection and removal of invertebrate fossil taxa were obtained from the Buffalo Gap National Grassland. In the field, sections were measured using a Jacobs staff noting changes in lithology and fauna. Using the bentonite for correlation, we traced ~100 m across the outcrop to non-seep associated sediments. The seep site is referred to as 3504A and the non-seep site as 3504D in the attached data spreadsheet.

Macroinvertebrate fossils were systematically collected above and below the bentonite at and away from the seep. In order to guarantee the collection of unweathered and in-situ material, exposures at the seep and non-seep site were initially benched 1.0 m back. Using the base of the bentonite bed as a datum point, individual fossils were collected from 0.125 m intervals up to 1.0 m above the bentonite and 0.5 m below at both localities. The bentonite was sampled as a single unit. A grid system was constructed to ensure systematic sampling. Each grid was 0.5 m across and 0.125 m in height. This was held consistent for all sampling. However, the depth at which the outcrop was benched varied between 0.4 m and 1.0 m for some horizons. The exact sampling dimensions were recorded for each horizon in order to calculate the total volume of sediment gone through, as bulk sediment samples were not collected. The exact dimensions for each sampled horizon can be found in the supplemental data file. At the seep site, we set up two grid systems on either side of the main micritic mass, each 0.5 m apart: the left side was denoted A, and the left as A'. The data from A and A' were combined following sample standardization (see section below as well as the supplemental data file).

Though the complete section exposed at AMNH loc. 3504 was measured, we focus on horizons below and above the bentonite for analysis. We refer to the bentonite bed as 0 m. Horizons sampled above and below are indicated by their distance from the top or bottom of the bentonite, respectively. Horizons above the bentonite are referred to as positive distances (ex. 0.125 m above) whereas horizons underlying the bentonite are referred to as negatives (ex. -0.125 m below).

Individual macroinvertebrate fossils were collected and wrapped on site and their stratigraphic positions were recorded. Large pieces of shale containing fossils were brought back to the lab where they were further broken apart to examine any additional fossil material. Since the presence of authigenic cemented carbonates at the seep may present a preservation bias, we avoided collecting fauna directly from the micritic mass of the seep 'core'.

The Pierre Shale exposed at the seep and non-seep localities are at approximately the same stratigraphic horizon and display identical lithologies. We find it valid to assume stratigraphic continuity between these two sites as well as similar sediment accumulation rates across the exposure at AMNH loc. 3504. We do not find evidence to suggest that our studied seep deposit formed any significant topography on the seafloor. Though seep fluids can/do escape the sediment, seep carbonates precipitate below to possibly very near the sediment-water interface in the sulfate-methane transition zone. Based on outcrop analysis, it appears that the seep was relatively flat. The bentonite does not appear disturbed or irregular when cross-cutting the seep, is laterally continuous, and maintains a constant thickness across the exposure, suggesting that these sections

were deposited along a flat profile of the seafloor. At most, there may have been a hardground at the seep formed by inoceramid shells cemented to seep carbonates precipitating close to the sediment-water interface, which is common at many seeps within the Pierre Shale. Additionally, some carbonates may be exposed by bottom currents, though this wouldn't likely result in any substantial topography. Lastly, based on the composition of the seep paleocommunity, it appears that in common with other WIS seeps (Meehan and Landman, 2016; Ryan et al., 2020), AMNH 3504 was mainly a soft-bottom habitat characterized by an increased abundance of typical Pierre Shale fauna.

Lastly, beds above and below the bentonite at both sites are lithologically consistent and fossils exhibit similar taphonomy, allowing for direct comparisons to be made between the two deposits. Although we did not perform petrographic analyses on fossil specimen, we do not observe any apparent mineralogical differences in specimens below or above the bentonite. The presence of ammonites (aragonitic shells) above and below the bentonite at the seep site suggest a diagenetic overprint is not a major control on our findings or interpretations. The lack of ammonites at the non-seep site is most likely due to habitat preference and not diagenesis, as we document a *Placenticeras* below the bentonite at this site. Inoceramid bivalve shells contain both aragonitic and calcitic layers, and *Inoceramus* are documented at both sites above and below the bentonite bed.

Faunal Analysis and Sample Standardization

Samples were analyzed quantitatively for macroinvertebrate fossils at the AMNH. Pieces of shale containing fossils were broken apart to a size of ~3 cm using rock crushers and dental tools (picks). Fossils were identified to the species level (when preservation quality permitted) using a range of published literature (Richards, 1958; Gill and Cobban, 1966; Sohl, 1967; Speden, 1970; Cobban et al., 2006; Landman and Klofak, 2012). The total number of disarticulated bivalves that were identifiable at the genus level were halved and added to articulated bivalve totals. The total number of indeterminate bivalves were divided by 3. Inoceramids were an extremely common faunal component at both sites, however, most were poorly preserved and fragmented. We counted and measured all inoceramid fragments. If a fragment was greater than 6 cm, it was counted as a single individual *Inoceramus* sp., as this was the common size of articulated *Inoceramus* specimens at our study sites. Inoceramid fragments between a size of 1-2 cm were counted as 1/6 of an individual, 2-3 cm sized fragments as 1/3 of an individual, and so on. Fragments smaller than 1 cm were not included in our analysis See attached supplementary data for the exact quantities applied to each inoceramid size bin.

Using the collection dimensions for each horizon (see above), faunal abundances were standardized for each interval to represent a volume of 1 m^3. This was done by calculating the volume of sediment gone through at the outcrop. We then divided 1 m^3 by the total sediment processed ("x to m^3" column in supplemental data spreadsheet). The abundance of each taxon was then multiplied by this number and divided by 10 to produce standardized abundance data. Following data standardization per sediment volume, we combined the seep abundance data (A and A') for each horizon and halved the totals.

Standardized abundance, species richness, and Simpson's Diversity Index (Simpson, 1949) were calculated for all sampled horizons at both sites in order to reveal any faunal changes across horizons. We separate abundance into two parts: Total abundance (TA) reflects all fossils found, including those that were not able to be identified at the species or genus level, whereas species

abundance (SA) reflects the abundance of specimens that were able to be identified at the species level.

Species abundance data were used to calculate biodiversity (Simpson's D). However, Simpson's D places emphasis on abundant fauna. Seep ecosystems, both modern and ancient, tend to be characterized by an abundance of few, specialized taxa. For example, the seep fossil assemblages at AMNH loc. 3504 are dominated by lucinids and inoceramids. Likewise, these taxa dominate the fossil community at the non-seep site as well. Since abundant taxa can overwhelm potential or subtle patterns, species abundance data were standardized a second time where the most common taxon in each sample was given a value of 1 and all other taxa present within that sample were then scaled to it using the following equation (standardization to the maximum):

$$y_{Ai} = \frac{x_{Ai}}{\max(x_{Ai})} \quad (1)$$

where x_{Ai} is the abundance of species i in sample 'A'. The above equation was taken from Olszewski (2007) and based on Faith et al. (1987). The abundance of each species in each sample was standardized using this equation. Prior to calculating Simpson's D, a value of 1 was added to each taxon's transformed abundance to avoid a negative abundance when calculating Simpson's D. We also provide Simpson's D values for the seep and non-seep sites that were calculated prior to this abovementioned standardization (equation 1) in Table 2 below. A value of 1 was also added to each taxon's abundance when these values were calculated as well.

All standardization methods were held consistent for both the seep and non-seep sites. Due to the lack of fossils above the bentonite at the non-seep site, some horizons have Simpson's D values of 0. These 0 values indicate that there were either one or no taxa identifiable at the species level, as species abundance (SA), not total abundance (TA), was used to calculate diversity.

Stable Isotope Analysis

Seep associated carbonate concretions (SACs) were cut using a rock saw and were examined for evidence of post-depositional alteration (diagenesis, sparry calcite veins, weathering). Samples of micrite were taken from the center portion of the SAC in order to avoid overprinting from later-stage carbonate precipitation. Samples were analyzed for $\delta^{13}C$ (carb.) and $\delta^{18}O$ (carb.) at the UC Santa Cruz Stable Isotope Laboratory using standard techniques.

Prior to analysis, 40-60 micrograms of solid sample were vacuum-roasted for one hour at 65°C. Samples were analyzed for $\delta^{18}O$ and $\delta^{13}C$ via acid digestion using an individual vial acid drop ThemoScientific Kiel IV carbonate device interfaced to a ThermoScientific MAT-253 dual-inlet isotope ratio mass spectrometer (IRMS). Samples were reacted at 75°C in orthophosphoric acid (specific gravity = 1.92 g/cm3) to generate carbon dioxide and water. Non-condensable gases were pumped away, and the CO_2 analyte was then cryogenically separated from water, finishing with the introduction of pure CO_2 into the IRMS via the dual inlet. Raw data were corrected against samples of calibrated in-house granular Carrara Marble standard reference material and granular NBS-18 limestone international standard reference material. The in-house Carrara Marble was extensively calibrated against NIST Standard Reference Materials (NBS-19, NBS-18, and LSVEC) and further calibrated in intercomparison studies with international laboratories. Raw data were also corrected for offset from the international standard PDB (PeeDee Belemnite) for $\delta^{18}O$ and $\delta^{13}C$ and corrected for instrument specific source ionization effects. Two aliquots of powdered Atlantis II calcium carbonate were run "as-a-sample" to monitor quality control and long-term performance. Precision of Atlantis II at UCSC SIL is 0.05‰ for both $\delta^{18}O$ and $\delta^{13}C$. Isotopic data are reported relative to the Vienna Pee Dee Belemnite (VPDB) standard.

Supplementary Table 1: $\delta^{13}C_{(carb.)}$ and $\delta^{18}O_{(carb.)}$ of seep associated concretions (SACs) from the seep deposit at AMNH locality #3504.

Description	AMNH LOC.	$\delta^{13}C$ (‰VPDB)	$\delta^{18}O$ (‰VPDB)
SAC	3504	-36.03	-1.76
SAC	3504	-33.11	-3.03

Supplementary Table 2: Diversity metrics per sampled horizon (in meters with respect to proximity from the bentonite) for the seep and non-seep deposit at AMNH locality number 3504. Simpson's D is the biodiversity metric and is shown in two parts: Std. Simpson's D are values calculated using maximum standardized species abundance data (see equation 1 above and attached excel spreadsheet) whereas the second set of Simpson's D values were calculated using the species abundance (SA) and species richness (R) in the columns below. TA is total abundance and TA Error is the standard error on for total abundance.

	Seep						Non-seep					
Horizon (m)	Std. Simpson's D	Simpson's D	TA	TA Error	SA	R	Std. Simpson's D	Simpson's D	TA	TA Error	SA	R
1.0 m	0.987	0.6662	288.9	5.99	49.3	13	0	0	13.9	1.62	6.9	1
0.875 m	0.9873	0.568	227.8	4.96	123.2	13	0.66	0.626	16.6	0.90	4.9	2
0.75 m	0.898	0.5146	106.1	5.42	37.3	4	0	0	5.1	0.00	0	0
0.625 m	0.93	0.4778	171	6.26	75.5	5	0	0	13.4	0.62	1.8	1
0.5 m	0.957	0.602	80.7	3.31	38.2	7	0.681	0.596	12.9	0.44	6.1	2
0.375 m	0.975	0.684	91.8	3.87	66.2	9	0	0	7.4	0.99	0	0
0.25 m	0.9307	0.553	72.2	3.44	36.2	5	0	0	9.1	0.67	2.6	1
0.125 m	0.9288	0.7419	105.7	3.88	37.8	5	0.8	0.763	14.0	0.13	7.9	3
0 m	0.895	0.613	31.13	2.08	21.8	4	0.685	0.550	9.9	0.52	6.9	2
-0.125 m	0.947	0.664	91.2	3.24	54.8	6	0.9226	0.841	53.2	0.72	34.4	6
-0.25 m	0.9608	0.6933	114.9	3.29	54.8	7	0.888	0.727	41.3	0.69	20.6	5
-0.375 m	0.6752	0.2711	71.7	5.48	25.1	2	0.8222	0.687	27.9	0.67	12.9	3
-0.5 m	0.6857	0.5327	36.8	1.66	8.3	2	0.9637	0.839	95.9	2.02	41.6	8

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