COMMUNITY PALEOECOLOGY AND BIOGEOGRAPHY OF THE JURASSIC (BAJOCIAN-OXFORDIAN) SUNDANCE SEAWAY IN THE BIGHORN BASIN OF WYOMING AND MONTANA, U.S.A.

by

KRISTOPHER MICHAEL KUSNERIK

(Under the Direction of Steven M. Holland)

ABSTRACT

The composition of marine communities is controlled by colonization of newly available habitat, development of community associations, and community variation in response to a gradient of environmental conditions. The Jurassic Sundance Seaway of the Bighorn Basin, Wyoming and Montana provides an ideal case study for determining the role of these factors on community composition and variation. The global provenance of taxa found in the Seaway support reconstructions depicting a single, northern entranceway. This, along with the Seaway's length and shallow depth, likely caused restrictions on taxa able to enter the Seaway under normal conditions, leading to communities with low diversity and low evenness. Ordination analysis suggests the primary factor controlling community composition was a complex gradient related to water depth. Secondary factors include substrate, salinity, and a carbonate to siliciclastic transition. These patterns are typical of Jurassic marine communities globally.

INDEX WORDS: Sundance Formation, Gypsum Spring Formation, fossils, quantitative analysis, ordination analysis

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DEDICATION

To my family, thank you for the love and support through this wild adventure called graduate school. I could not have done this without you.

And

To Andrea, I love you with all my heart.

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- The Thermopolis Independent Record
- The Tensleep Historical Museum

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CHAPTER 1

INTRODUCTION AND LITERATURE REVIEW

This thesis is best read as one chapter, given that it is written in the form of a manuscript intended for submission to the journal *PALAIOS*. The second chapter includes the discussion of the previous literature, geologic setting, methods, results, interpretation, discussion, and conclusions. The third chapter concludes the research.

The purpose of this study is to use the Jurassic marine record of the Bighorn Basin of Wyoming and Montana as a case study to understand how taxa colonize new habitat and organize into communities. Determining the initial source of a basin's fauna remains a relatively unexplored question in the fossil record, with most literature focusing on biotic invasions and dispersal into existing systems or the role of exchange between larger biogeographic provinces (Aberhan, 2001; Holland and Patzkowsky, 2007; Ávila et al., 2009; Dudei and Stigall, 2010; Oguz and Ozturk, 2011). Additionally, many environmental or biological factors have been hypothesized to drive community variation, including water depth, salinity, substrate, life habit, oxygen conditions, and environmental stress (Wright, 1973; Tang, 1996; de Gibert and Ekdale, 1999, 2002; Abdelhady and Fürsich, 2014).

This study uses the global occurrence of taxa to determine the geography of possible entrances to the Sundance Seaway. Implications of entranceway geography on the environments and taxa of the Seaway are discussed.

The fossil record of the Sundance Seaway within the Bighorn Basin provides an excellent case study of community variation. The 15 myr record of marine deposition, from initial flooding in the early Bajocian to its ultimate filling by terrestrial sediment in the Oxfordian, are preserved in the Gypsum Spring, Piper, and Sundance Formations (Parcell and Williams, 2005; McMullen et al., 2014). Access to communities from throughout the complete lifespan of a marine basin has been lacking in similar studies of community paleoecology (e.g., Holterhoff, 1996; Tang and Bottjer, 1996; Stanton and Dodd, 1997; Holland and Patzkowsky, 2004; Scarponi and Kowalewski, 2004).

CHAPTER 2

COMMUNITY PALEOECOLOGY AND BIOGEOGRAPHY OF THE JURASSIC (BAJOCIAN-OXFORDIAN) SUNDANCE SEWAWAY IN THE BIGHORN BASIN OF WYOMING AND MONTANA, U.S.A.[1]

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[1] Kusnerik, K.M. and S.M. Holland. To be submitted to *PALAIOS*

INTRODUCTION

The faunal composition of a marine basin is controlled by initial colonization of newly available habitat, subsequent development of community associations, and responses to changing environmental factors over the lifespan of the basin. While considerable study has been done on defining and delineating biogeographic provinces (Udvardy, 1975; Jablonski et al., 1985) or using provinces to answer larger questions (McKerrow and Cocks, 1986; Spalding et al., 2007; Sclafani and Holland, 2013), determining the source of a basin's fauna and the formation of a biogeographic province are less well known. Most similar studies focus on the impact of invasive taxa on communities or the role of exchange between larger biogeographic provinces (Aberhan, 2001; Holland and Patzkowsky, 2007; Ávila et al., 2009; Dudei and Stigall, 2010; Oguz and Ozturk, 2011).

Additionally, many environmental or biological factors are hypothesized to drive community variation, including water depth, salinity, substrate, life habit, oxygen conditions, and environmental stress (Wright, 1973; Tang, 1996; de Gibert and Ekdale, 1999, 2002; Abdelhady and Fürsich, 2014). The role of these factors has been found to vary between basins, environments, and communities (Holland and Patzkowsky 2004; Patzkowsky and Holland, 2012; Abdelhady and Fürsich, 2014; McMullen et al., 2014).

The Jurassic Sundance Seaway presents an ideal natural experiment on how marine communities form in a newly created seaway and develop over time. The entire 15 myr of the Seaway's geologically short history in the Bighorn Basin of Wyoming and Montana from initial flooding to an eventual transition to a terrestrial environment, is preserved (Parcell and Williams, 2005; McMullen et al., 2014). Access to a near complete record of the basin's lifespan can track the development of marine communities from initial colonization, development in response to changing factors, and final responses as the basin is filled. Similar studies of community development were limited to associations in preexisting, established ecosystems, lacking the initial formation and subsequent development of communities until the end of a basin's lifespan (see for example Holterhoff, 1996; Tang and Bottjer, 1996; Stanton and Dodd, 1997; Holland and Patzkowsky, 2004; Scarponi and Kowalewski, 2004).

This study used the global distribution of taxa present within the Sundance Seaway to determine the source of the basin's faunas, better understanding the biogeography of the Seaway in relation to the proto-Pacific. Implications of the Seaway's geography on faunal composition, diversity, and evenness were determined along with factors controlling community paleoecology near its southern terminus in Wyoming.

GEOLOGIC SETTING

The Sundance Seaway was a Jurassic, epicontinental sea that extended southward from the northern proto-Pacific Ocean and covered portions of western North America (Fig. 1; Imlay, 1948, 1957a; Kvale et al., 2001; Zakharov et al., 2002; Blakey, 2012, 2013, 2014). It was bounded by a volcanic arc to the west that separated it from the proto-Pacific Ocean, by the North American craton to the east, and by the ancestral Rockies uplift that separated it from the Gulf of Mexico (Kvale et al., 2001).

Most reconstructions of the Seaway depict a single, narrow entrance at approximately 55-60°N paleolatitude, with the Seaway stretching southward over 2000 km to modern Wyoming at approximately 35-40°N (Imlay, 1965b; Kvale et al., 2001; Massare et al., 2013; Blakey, 2013, 2014). One branching arm of the seaway, the Twin Creek Trough, continued farther south into Utah to approximately 30°N paleolatitude. The shape and extent of the Sundance Seaway is comparable to the modern Red Sea in length and width, though some reconstructions depict a wider southern terminus (Blakey, 2014). However, the Sundance Seaway was much shallower than the Red Sea, and it never exceeded 100 m at the deepest points, which would have been located along its western margin (Imlay, 1980; Kvale et al., 2001). The hypothesized single entrance, length, and shallowness would likely have inhibited extensive tidal exchange and would likely have allowed for strong gradients in temperature and salinity to develop along its length.

Throughout the Jurassic, North America drifted northward, driving the Bighorn Basin through a range of climatic and environmental conditions (May and Butler, 2012). At 35°N, during the early Jurassic, modern Wyoming would have fallen within the semiarid climatic zone. As North America moved northward, Wyoming would have entered the humid, temperate zone around 40°N, reaching the region during the middle Jurassic (Kvale et al., 2001).

The Sundance Seaway occupied a retro-arc foreland basin created by the subduction-generated volcanic arc to its west (Kvale et al., 2001; Parcell and Williams, 2005). Initial flooding spread southward from the northern proto-Pacific Ocean, reaching southeastern British Columbia during the early Jurassic (Imlay, 1957b). The Seaway continued to extend southward, reaching Wyoming during the lower Bajocian, as evidenced by deposition of marine sediments during this time (Imlay, 1957b, 1965b;

Bullock and Wilson, 1969; Brenner and Peterson, 1994; Guyer, 2000; Parcell and Williams, 2005). Marine deposition continued in this region throughout the Jurassic, until the late Oxfordian (Brenner and Peterson, 1994; Peterson, 1994; Uhlir et al., 2006; McMullen et al., 2014). In the late Oxfordian–early Kimmeridgian, the Seaway was filled with terrigenous sediment from the south, causing a transition from marine units into overlying, coastal plain deposits of the Morrison Formation (Brenner and Peterson, 1994; Peterson, 1994; Uhlir et al., 2006; McMullen et al., 2014).

In the Bighorn Basin of Wyoming and Montana, the marine Jurassic record is preserved in three Formations: Gypsum Spring (mid-late Bajocian), Piper (late Bajocian), and Sundance (Bathonian-Oxfordian); (Fig. 2; Imlay, 1965b; Guyer, 2000). The lowest unit, the Gypsum Spring Formation is divided into three units, (1) a basal unit of massive gypsum, anhydrite, red shale, and siltstone, (2) a middle unit of interbedded shales and fossiliferous limestone, and (3) an upper unit of red to grey shale and siltstone (Bullock and Wilson, 1969; Parcell and Williams, 2005). Only the middle unit of the Gypsum Spring Formation is fossiliferous. This upper unit is locally named the Piper Formation (Bullock and Wilson, 1969; Parcell and Williams, 2005). The Piper Formation is nonfossiliferous.

The Sundance Formation overlies the Gypsum Spring Formation, or the Piper Formation where it is mapped separately (McMullen et al., 2014). The Sundance Formation is divided into five members, in ascending order: Canyon Springs Member (middle Bathonian), Stockade Beaver Shale (late Bathonian), Hulett Member (Callovian), Redwater Shale (early-middle Oxfordian), and Windy Hill Sandstone (middle-late Oxfordian). Some authors (e.g. Imlay, 1956, 1980; Wright 1973) use an informal division into a “lower Sundance” which includes the Canyon Springs Member, Stockade Beaver Shale, and lower Hulett Member, and an “upper Sundance” which includes the upper Hulett Member, Redwater Shale, and Windy Hill Sandstone. All members of the Sundance Formation are fossiliferous.

This lower Sundance records deposition on a shallow-water carbonate ramp with siliciclastic mud in the offshore (McMullen et al., 2014). The Canyon Springs Member in the eastern Bighorn Basin is a shallow subtidal, skeletal to oolitic limestone with offshore mud preserved in the lowermost portion. The Stockade Beaver Shale is a deeper-water, offshore, siliciclastic mudstone. The carbonate, lower Hulett Member includes a range of facies representing shallow subtidal, ooid shoal, lagoonal, and eolian depositional environments (McMullen et al., 2014). The lower Hulett Member records overall shallowing on a carbonate ramp in arid to semi-arid conditions, as indicated by the abundance of ooids and presence of large eolian dunes.

The upper Sundance contains three facies associations, the predominantly siliciclastic, incised valley fill in the upper Hulett Member, a wave-dominated siliciclastic shelf in the Redwater Shale, and a tidal estuary in the Windy Hill Sandstone. The Redwater Shale contains three facies: (1) deep-water, offshore mudstones and siltstones deposited on a siliciclastic shelf, often with regionally traceable calcite-cemented concretions, (2) wave-ripple and current-ripple laminated sublitharenite to quartz arenite recording deposition in the shoreface, and (3) shell beds recording a lower oyster-dominant (*Liostrea*) bedset and an upper scallop-dominant (*Camptonectes*) bedset (McMullen et al., 2014).

The Windy Hill Sandstone contains three facies. These are: (1) lowermost, tidal channel deposits composed of densely packed, fragmented bivalves, (2) tidal bar facies, and, (3) a tidal sand flat facies. These facies occur in fining-upward parasequences, with most parasequences partially preserved as a result of channel migration (McMullen et al., 2014). The Windy Hill Sandstone grades upward into the overlying, terrestrial, late Jurassic Morrison Formation (early Oxfordian-early Thithonian); (Pipiringos, 1968; Imlay 1980; McMullen et al., 2014).

Five sequence boundaries, marking regional unconformities, divide the marine Jurassic of the Bighorn Basin (Fig. 2; Pipiringos, 1968; Pipiringos and O'Sullivan, 1978; Parcell and Williams, 2005; McMullen et al., 2014). The J1 sequence boundary denotes the base of the Gypsum Spring Formation, with the J1a separating the lowermost Gypsum Spring unit from the upper Gypsum Spring. The J2 sequence boundary marks the base of the Piper Formation, with the J2a and J2b marking the base of the Canyon Springs Member and Stockade Beaver Shale, respectively. The Stockade Beaver Shale and lower Hulett member are separated by the J3 sequence boundary, and the J4 separates the lower and upper Hulett Members. Finally, the J5 sequence boundary separates the Redwater Shale and the Windy Hill Sandstone (McMullen et al., 2014).

METHODS

Biogeographical Analysis

Most reconstructions depict the Sundance Seaway with a single, northern entranceway (Fig. 1; Imlay, 1980; Tang and Bottjer, 1996; Kvale et al., 2001; Hunter and Zonneveld, 2008; Massare et al., 2013; Blakey, 2014; McMullen et al., 2014). Taxa entering the Seaway through this northern route would have had to survive a range of conditions to colonize its southern terminus. Other reconstructions have depicted the Sundance Seaway with either a much wider single entranceway (Imlay, 1957a, 1965a), or additional entranceways at lower, sub-tropical latitudes (Levin, 2006; Blakey, 2012). Different entranceway configurations would create different faunal compositions within the Seaway.

The global provenance of taxa found within the Seaway, and their likely ability to enter at northern latitudes, is used to test the single, northern entranceway reconstruction. If the hypothesized single entranceway connected the Seaway to the proto-Pacific, the taxa present in the Sundance Seaway would likely have had northernmost Jurassic occurrences further north than entranceway latitudes, allowing entry via this route. Other possible entranceway configurations would result in different compositions of fauna. For example, the presence of additional, lower latitude entrances during the Seaway's lifespan would have allowed warmer-water taxa to enter the basin without dispersal through the cooler northern entrance.

Using previous literature on the fauna of the Sundance Seaway, a list of 90 macrofauna genera found in the Seaway was compiled (Appendix A; Miller, 1928; Black, 1929; Cooke, 1947; Imlay, 1948, 1964, 1965a, 1965b; Pipiringos, 1957; Love, 1958; Koch, 1962; Philip, 1963; Sohl, 1965; Wright, 1973, 1974; Hallam, 1977; Herrick and Schram, 1978; Perry, 1979; Blake, 1981, 1986; Calloman, 1984; Tang, 1996; Tang et al., 2000; Palmer et al., 2004; Wahl, 2005; Feldmann and Titus, 2006; Feldmann and Haggart, 2008; Feldmann et al., 2008; O'Keefe et al., 2009; Wilhelm and O'Keefe, 2010; Massare et al., 2013). Global Jurassic occurrences of these genera were downloaded from the Paleobiology Database, along with the taxonomic, geographic (both modern and paleogeographic), stratigraphic, lithologic, and bibliographic information for each occurrence (see Appendix B for download protocol). 13,709 occurrences were downloaded for analysis.

The number of occurrences within the Paleobiology Database varies markedly among taxa. This may reflect the true abundance of a taxon or may reflect differences in the extent of sampling among taxa and locations. To determine if the northernmost global occurrence of a taxon is accurate, or simply reflects the amount of sampling, abundant taxa were resampled to 25 occurrences. This value is the average number of occurrences for taxa not occurring north of entranceway latitudes, which are typically less abundant than taxa with higher global northernmost occurrences. From 10,000 replicates of this resampling, 95% confidence intervals of the northernmost occurrence of each of the abundant taxa were calculated. All data analyses in this study were conducted in the open source statistical software R, version 3.0.2 (Appendix C; R Development Core Team, 2013). The global latitudinal range and northernmost occurrence of Sundance Seaway taxa was used to test whether they could have entered through the hypothesized single, northern entrance.

Fieldwork

To better capture variation in community composition across time and geographic space, fieldwork was conducted to acquire faunal abundances rather than simple presence/absence data as previous studies had done (Wright, 1973, 1974; Tang, 1996). Because the sequence stratigraphy of the Bighorn Basin of Wyoming and Montana had been previously interpreted by Parcell and Williams (2005) and McMullen et al. (2014), this region was selected for field sampling. This allowed data to be placed in a sequence stratigraphic context and correlated with depositional facies.

Thirteen localities within the Bighorn Basin were selected (Fig. 3) based on previous studies (McMullen et al., 2014) and by scouting via satellite imagery and in the field. For the purpose of sampling, the Redwater Shale was subdivided into four units: (1) a fossiliferous concretionary unit near the base, (2) mudstone prevalent through the unit, (3) an oyster (*Liostrea*) bedset that caps one parasequence, and (4) a scallop (*Camptonectes*) bedset that caps another parasequence near the top of the Redwater Shale.

Eighty-two samples for faunal censuses were collected from fossiliferous units in the Gypsum Spring Formation, Canyon Springs Member, Stockade Beaver Shale, Hulett Member, Redwater Shale, and Windy Hill Sandstone. The samples consist of a combination of bulk sampling, surficial sampling, small slabs, and field counts of exposed surfaces (Appendix D). A sample consisted of enough material to represent the typical faunal composition of the unit, approximately 1-3 gallon-sized bags in volume. Bulk samples were later sieved to 2 mm.

Sampling was designed to obtain an approximately equal number of censuses from each of the available units, although this goal was limited by outcrop exposure. Fifteen samples were obtained from the Gypsum Spring Formation, seventeen from the Canyon Springs Member, fifteen from the Stockade Beaver Shale, one from the Hulett Member, with five each from the Redwater Shale concretions, Redwater Shale oyster bedset, and Redwater Shale *Camptonectes* bedset, along with six samples from the Redwater Shale mud (for a combined Redwater Shale total of twenty-two samples), and twelve samples from the Windy Hill Sandstone.

Faunal censuses were conducted primarily in the lab, with each specimen identified to genus where possible. In most cases, genera in this region are monospecific. Identification was primarily conducted using a combination of Imlay (1964), Sohl (1965), and Cox et al. (1969).

The 82 samples contain a total of 14,550 specimens representing 49 taxa (Appendices E & F). To supplement field data, ecological data were compiled for each taxon encountered in the censuses using the Paleobiology Database (Appendix G).

Dominance and Diversity

To determine if the provenance of taxa influenced their abundance and distribution within field samples, taxa were separated into “Northern Taxa” or “Southern Taxa” based on their global northernmost occurrence in relation to the entranceway latitude. Those with a northernmost occurrence north of 54°N, the latitude of the Seaway’s single entranceway, are labeled “Northern Taxa” and were likely able to access the entranceway under normal conditions. Those with northernmost occurrences south of the latitude of the entranceway are labeled “Southern Taxa” and were presumably unable to freely exchange with the Seaway through the single entranceway under normal conditions. Median percent abundance and percent occupancy within samples was calculated for all taxa. Patterns and trends in these factors among the “Northern Taxa” were compared to those present in the “Southern Taxa.”

Quantitative Paleoecology

Numerous environmental factors are hypothesized to control community composition and variation within marine environments including water depth, salinity, substrate, life habit, oxygen conditions, and environmental stress (Wright, 1973; Tang, 1996; de Gibert and Ekdale, 1999, 2002; Abdelhady and Fürsich, 2014). A range of conditions along ecological gradients controls the presence and relative abundance of taxa with a community (Pearman et al., 2007; Patzkowsky and Holland, 2012). Understanding the environmental and ecological factors controlling taxa distribution is necessary to explain community variation through time (Patzkowsky and Holland, 2012). Ordination of the data allowed for identification of environmental and ecological factors driving variation in the composition of faunal communities of the Bighorn Basin region.

Prior to analysis, the abundance dataset was culled to reduce sampling biases for some taxa and samples. The abundances of the crinoid genera, *Isocrinus* and *Chariocrinus*, were reduced to one regardless of the number of columnal pieces, as it is impossible to estimate the number of individuals based on counts of columnals. This was also done with a taxon identified as round, elongate, calcitic serpulid tubes for similar reasons. Samples with fewer than twenty individuals were removed prior to analysis, as they may be nonrepresentative samples. With these changes, the final dataset contains 71 samples, 48 taxa, and 11,975 individuals. Following this culling, raw abundance was converted to percent abundance for each taxon within each sample to mitigate the effects of sample size.

Ordination Analysis

Ordination analysis was used to describe faunal gradients in the census data, and to determine relationships between the composition of fossil assemblages, lithofacies, and the ecology of taxa. Data were ordinated using Detrended Correspondence Analysis (DCA) and Non-Metric Multidimensional Scaling (nMDS) using the Community Ecology Package, VEGAN (Oksanen et al., 2013). Both DCA and nMDS have been used in similar studies to identify faunal gradients, and most often perform equally well (Patzkowsky and Holland, 2012). Both ordinations were conducted to allow comparison of their results, as each method may result in distortions of faunal gradients in some cases (Patzkowksy and Holland, 2012).

Detrended Correspondence Analysis was performed with the decorana function in VEGAN, using the default settings of no downweighting of rare taxa, 4 rescaling cycles, and 26 segments in rescaling.

To avoid local minima, Non-Metric Multidimensional Analysis was run with 100 random restarts using the metaMDS function in VEGAN. Dissimilarity between samples was measured using Bray-Curtis. Three dimensions were calculated without using any additional transformation, as the data were previously converted to percent abundance.

RESULTS

Biogeography

Given the 35-40° N paleolatitude of the Bighorn Basin during the Jurassic, the southern end of the Sundance Seaway was likely a warmer-water environment than its hypothesized single entranceway. As such, it would be expected to contain taxa suited to warmer water. If the Seaway had a single entranceway to the north, fauna in the southern part of the Seaway would have needed to tolerate colder conditions at the entranceway to be able to migrate to the southern terminus. If taxa present within the southern end of the Seaway do not occur globally at these northern latitudes, it would suggest that there must have been additional, more southerly entrances.

Of the 90 macroinvertebrates and vertebrates found in the Sundance Seaway, 88 are reported with occurrences in the Paleobiology Database. The remaining 2 taxa (*Bombur* and *Parastomechinus*) are reported in the Paleobiology Database, but lack any occurrence data. Of these 88 taxa, 39 (44.3%) occurred globally at latitudes at or north of 54°N, where the southernmost extent of the entranceway is hypothesized to have existed (Fig. 4; Blakey, 2014). The remaining 49 (55.7%) taxa are reported globally at latitudes to the south of the entranceway.

However, 4 of these 49 taxa have northernmost occurrences within 2° of the entranceway's southernmost extent. In some reconstructions that depict a wider entranceway, these taxa would be able to exchange freely with the Seaway under normal conditions, though this study will use the more recent, narrow entranceway reconstruction (Imlay, 1965a; Blakey 2012, 2014). There is likely uncertainty in the size of the entranceway as it is not preserved in the geological record and its size must be inferred.

Taxa with higher northernmost global occurrences, those found at or north of the entranceway, average a greater number of occurrences in the Paleobiology Database

(192) than taxa found only south of the entranceway (25). Taxa with higher northernmost occurrences also tend to span a wider geographic range, averaging 137°, than taxa occurring exclusively south of the entranceway, which average a range of 60°. Eurytopic “Northern Taxa” are more widely distributed globally than “Southern Taxa”, across a wider range of conditions, which would have allowed them a greater ability to tolerate conditions at the entranceway and along the length of the Seaway.

Resampling of taxa with more occurrences, typically “Northern Taxa,” to the rarity levels similar to “Southern Taxa” creates 95% confidence intervals of northernmost occurrence that drops south of the entranceway latitudes for many “Northern Taxa.” Of the 39 “Northern Taxa,” 18 have confidence intervals in which the northernmost occurrence may lie south of the entranceway. The confidence intervals of 13 did not fall south of entranceway latitudes. The remaining 8 “Northern Taxa” were not resampled since they already had less than 25 occurrences. Because of this effect, the large number of occurrences for “Northern Taxa” likely plays a role on the northernmost occurrence of the taxa. If “Southern Taxa” were sampled globally more frequently, it is possible that these taxa would have been found farther north. As such, it is conceivable that the taxa of the Sundance Seaway could have entered through a single, northern entranceway.

Occupancy and Abundance Comparison

“Northern” and “Southern” taxa show distinctly different patterns of occupancy and abundance in the field census data. On average, “Northern Taxa” vary widely in their percent occupancy, that is, the percentage of samples in which they occur is high, and they generally occur at low median abundances (Fig. 5). Conversely, “Southern Taxa” typically occur in few samples, but they occur at high abundances when they are present.

Of the 90 taxa previously reported from the Sundance Seaway, 49 (55%) are found in the field samples of this study. Twenty-four “Northern Taxa” (62% of “Northern Taxa” genera) are present within the samples. Many of these taxa are found in a large percentage of samples, including *Camptonectes* (55%), *Astarte* (52%), *Liostrea* (52%), *Pleuromya* (43%), *Gryphaea* (39%), and *Pachyteuthis* (35%); (Fig. 5). However, almost all “Northern Taxa” occur at median percent abundances below 20%. Although “Northern Taxa” are widespread throughout the southern terminus of the Seaway, overall median percent abundance for most “Northern Taxa” is low, as samples in which the taxa are abundant are balanced by samples in which the taxon is rare.

Seventeen “Southern Taxa” (35% of “Southern Taxa” genera) are found in the samples. Most “Southern Taxa” are rare, with only one taxon occurring in more than 8% of samples (Fig. 5). However, many “Southern Taxa” had large median percent abundances, dominating the samples in which they occur. These include *Corbicellopsis* (77%), *Procerithium* (61%), *Kallirhynchia* (25%), and *Mactromya* (23%). “Southern Taxa” are rarely present in samples, but they occur in high abundances when they are present.

There are two major exceptions to this trend. The oyster *Gryphaea* is part of the “Northern Taxa,” with a high percent occupancy, but possesses the highest median abundance (96%) of all genera studied. *Gryphaea* is found in a large number of samples, but maintains extremely high abundance, perhaps being suited to flourish at conditions represented in the samples.

The crinoid *Isocrinus* is part of the "Southern Taxa" with a percent occupancy unusually higher than other "Southern Taxa" (26%) and low median percent abundance (0.9%). While it's southern provenance likely caused *Isocrinus* difficulty in entering at northern latitudes and surviving conditions along the Seaway's length, once established in the southern terminus it was able to expand and establish populations across a wider range of locations than other "Southern Taxa."

These patterns are likely driven by the more eurytopic nature of "Northern Taxa" compared to "Southern Taxa." The ability of "Northern Taxa" to survive environmental gradients across a wide range of latitudes would have allowed for more frequent opportunities to colonize than for "Southern Taxa," which would have had fewer opportunities to enter the Seaway. When "Southern Taxa" do occur, they would have been well suited to likely warm-water conditions found near the Seaway's southern terminus, and able to establish the abundant populations found in some samples by this study.

Dominance and Diversity

Faunal samples from the Sundance typically have low diversity and low evenness (Fig. 6; Table 1). Average richness of all marine Jurassic samples was 5.3, with an average Simpson' D of 0.336, both relatively low.

This pattern is taken to the extreme in the Stockade Beaver Shale, where Simpsons's D averages 0.036 and richness averages 3.1. Only the single sample of the

Hulett Member, HU01, was less diverse and less even, with a Simpson's D of 0.035 and a richness of 2.

Most Redwater Shale samples also have low diversity and high dominance, except for the concretionary unit which averages the highest diversity (average richness of 8.2) and second highest evenness (average Simpson's D of 0.518) of all units. McMullen et al. (2014) also noted the Redwater concretions to be abundantly fossiliferous, even containing rare taxa, such as the ammonite *Cardioceras* that are not present in other Redwater Shale units.

The Canyon Springs Member is the second most diverse unit (average richness of 6.3), and has the highest evenness of all units (average Simpson's D of 0.56). The one outlier for the Canyon Springs Member is sample CS17, a monospecific *Liostrea* ostreolith. Previous work has also found such accumulations of *Liostrea* to be much lower in diversity compared with the Canyon Springs Member as a whole (Wilson et al., 1998).

While the marine record of the Sundance Seaway is typified by high dominance and low diversity, the dominant taxa change over time and across environments. In four units, a single taxon dominates in all samples from that unit. In Stockade Beaver Shale samples, the oyster *Gryphaea* averages 96% of individuals, and may be up to 99%. In the Redwater Shale mud, the belemnite *Pachyteuthis* averages 72%, with a maximum of 88% of individuals. Within the Redwater Shale oyster unit, the dominant taxon is *Liostrea*, averaging 65% of individuals and up to 89% in some samples. Finally, within the

Redwater Shale *Camptonectes* bedset, *Camptonectes* averages 88%, with a maximum of 95%, of individuals.

In other units, different beds or localities are dominated by different taxa. These taxa occur at levels of dominance comparable to the widespread dominance of other units, but are present in fewer samples. Within the Gypsum Spring Formation, different bedsets are dominated by *Pleuromya* (maximum: 96%), *Trigonia* (maximum: 97%), *Corbicellopsis* (maximum: 84%), and *Camptonectes* (maximum: 59%). A similar pattern is apparent in the Windy Hill Sandstone, with samples dominated by either *Liostrea* (maximum: 73%), *Camptonectes* (maximum: 46%), *Kallirhynchia* (maximum: 80%), or *Mactromya* (maximum: 77%).

Finally, in some units, some samples are dominated by a single taxon, whereas other samples have relatively high evenness and low dominance. Where a single dominant taxon is present, it varies by bed or locality in the unit. In the Canyon Springs Member, nine samples are dominated by a single taxa making up at least 50% of the sample: *Camptonectes* (maximum: 89%), *Liostrea* (maximum: 100%), *Pleuromya* (maximum: 60%), and *Procerithium* (maximum: 78%). However, in six samples from the Canyon Springs Member, no taxon represents over 50% of individuals. This trend is also present in the Redwater Shale concretions, where two samples are dominated by *Astarte* (78% and 86%), one sample is dominated by *Camptonectes* (62%), and the remaining two samples are not dominated by a single taxon.

Gradient Ecology

Although DCA and nMDS produced similar patterns (Table 2), each reveals different aspects of faunal variation. For the primary source of community variation, patterns in DCA were more apparent. For the secondary source of faunal variation, DCA and nMDS produced slightly differing patterns, though their axis scores are highly correlated.

DCA

Sample scores from the DCA ordination show partial overlap of many of the stratigraphic units, with separation of units into two broad clouds (Fig. 7). The smaller cloud has lower DCA1 scores and consists of a tight cluster of Stockade Beaver Shale and Hulett Member samples. This cluster results from the high dominance by highly abundant *Gryphaea* in both units, as the sample scores are similar to the taxon scores of *Gryphaea* (Fig. 8).

Overlap in the larger cloud of remaining units is driven primarily by the wide range of scores within the most variable units, specifically the Canyon Springs Member and Redwater Shale concretions. The larger diversity and lower dominance of these units drives their broader distribution of sample scores. When these units excluded, the remaining units separate along DCA1.

Overlapping Redwater Shale mud and Redwater Shale oyster units are found at lower DCA1 scores, though not as low as the tight cluster of Stockade Beaver Shale and Hulett Member scores. These two units show wider variation along DCA2, with Redwater Shale oyster samples averaging lower DCA2 scores than Redwater Shale mud samples, though there is still limited overlap of the two units. These units are similar in faunal composition, sharing most taxa though they differ in their dominant taxa, *Pachyteuthis* in Redwater Shale mud and *Liostrea* in Redwater Shale oyster. In both of these units, the second most abundant taxa are the dominant-taxa of the other unit (*Pachyteuthis* in Redwater Shale oyster and *Liostrea* in Redwater Shale mud). These units plot at scores similar to the species scores of their most dominant taxa (Fig. 8).

At intermediate DCA1 scores, there is an overlapping cloud of the highly variable Windy Hill Sandstone scores and a tight cluster of Redwater Shale *Camptonectes* scores. The Windy Hill Sandstone separates broadly along DCA2, though this is primarily driven by an outlier sample, dominated by the brachiopod *Kallirhynchia*. If this *Kallyrhynchia*-dominant sample is removed, the Windy Hill Sandstone still plots as a broad cloud, with the end-nodes defined by the dominant taxon (Fig. 8). The first of these, at lower DCA1 scores, contains samples dominated by *Liostrea*, at similar scores as the Redwater Shale oyster samples, though compositionally different enough not to overlap. The second node overlaps with the tight cluster of Redwater *Camptonectes* bedsets, and consists of those Windy Hill Sandstone samples similarly dominated by *Camptonectes*. Finally, at higher DCA1 and at the lowest DCA2 scores, are samples dominated by the bivalve *Mactromya*, with scores distinct from all other samples. The bivalve *Mactromya* is only found in these samples, where it is the dominant taxa, making these samples unlike any others collected. Similar beds were noted throughout the Windy Hill Sandstone, but could not be collected.

Finally, at high DCA1 and DCA2 scores is a broad cloud of Gypsum Spring Formation samples. Four taxa drive the separation of Gypsum Spring Formation samples into four end-nodes. *Corbicellopsis*-dominant samples plot as a tight cluster at the highest DCA1 scores of all samples. *Camptonectes*-dominant samples cluster at intermediate DCA1 and DCA2 scores, similar to Redwater Shale *Camptonectes* scores, but still compositionally different enough to prevent overlap. The remaining samples have higher DCA2 scores, with *Pleuromya*-dominant samples at higher scores than *Trigonia*-dominant samples.

DCA1

Correlating the stratigraphic units with their depositional environments determined by Parcell and Williams (2005) for the Gypsum Spring Formation and McMullen et al. (2014) for the Sundance Formation suggests that DCA1 is correlated with water depth. The lowest DCA1 scores correspond to the offshore, siliciclastic Stockade Beaver Shale, the deepest-water unit sampled. The next shallowest unit is the Redwater Shale mud, which is capped by the slightly shallower Redwater Shale oyster. These two units have higher DCA1 scores than the Stockade Beaver, but lower than all other units. The deeper Redwater Shale mud corresponds to slightly lower DCA1 values than the shallower Redwater Shale oyster.

Capping the entire unit, the Redwater Shale *Camptonectes* unit is shallower still, and with the decrease in depth corresponds to increased DCA1 scores. The shallow, estuarine Windy Hill Sandstone plots at similar DCA1 scores. Finally, the shallowest of all units, the evaporite/carbonate-rich shallow-subtidal Gypsum Spring Formation, scores have the highest DCA1 values. The marine Jurassic units of the Bighorn Basin track a gradient in depth along DCA1; with deeper units grading into progressively shallower units with increasing DCA1 scores. It is important to note these taxa were likely not responding directly to differences in water depth itself, but rather physical, chemical and biological conditions correlated with water depth (Patzkowsky and Holland, 2012).

Units at low average DCA1 scores are also tightly clustered, with little variation among samples along the primary axis. As DCA1 scores increase, units separate more broadly along the primary axis, likely encompassing a wider range of conditions. In deeper, offshore units, salinity, temperature, and other conditions may have been less subject to variation and remained fairly constant. In shallower water, salinity and temperature would be more likely to fluctuate, leading to extremes in conditions as evidenced by widespread evaporates in the Gypsum Spring Formation (Bullock and Wilson, 1969; Parcell and Williams, 2005). Correlated with water depth is a likely gradient from stenotopic conditions in deeper water to eurytopic conditions in shallow water.

Lower DCA1 scores also correspond to siliciclastic muds and shales, present in the Stockade Beaver Shale and various Redwater Shale units. Conversely, carbonate units present early in the history of the Seaway, such as the Gypsum Spring Formation and Canyon Springs Member have higher DCA1 scores. While such a gradient explains the end member units, those such as the siliciclastic Windy Hill Sandstone and Redwater Shale *Camptonectes* are found at intermediate DCA1 scores. An overall transition from older, carbonate units to younger, siliciclastic units can only be partially explained by increasing DCA1 scores.

Thus, in this study, DCA1 is correlated with a complex gradient of factors related to water depth, and the amount of variability in those conditions within the unit. Increasing DCA1 scores correlate with a decrease in water depth and wider fluctuation in environmental conditions. A gradient of the transition from older, carbonate units to younger, siliciclastic units may also be partly correlated with DCA1.

DCA2

The depositional facies of Parcell and Williams (2005) and McMullen et al. (2014) also suggest an interpretation of the second DCA axis, that it represents a gradient in salinity. Most of the Windy Hill Sandstone samples plot at low DCA2 scores (Fig. 7). These samples correlate to estuarine facies described by McMullen et al. (2014) in the eastern Bighorn Basin. These facies are likely influenced by increased freshwater input from terrestrial sources south and west of the Seaway (Uhlir et al., 1988; McMullen et al., 2014). Salinity within these estuarine facies was likely brackish to freshwater, depending on location. Lower DCA2 scores likely correlate with lower salinity levels, specifically the *Mactromya*-rich beds common in the Windy Hill Sandstone.

Samples from the Gypsum Spring Formation plot at high DCA2 scores. These samples correlate to restricted, shallow-subtidal facies (Parcell and Williams, 2005). Samples dominated by *Pleuromya*, those with the highest DCA2 scores in the Gypsum Spring Formation, are identified as hypersaline, restricted tidal flats (A.M. Clement, personal communication, 2015). Shallow water, where salinities would fluctuate between more normal marine and hypersaline, are apparent throughout the Gypsum Spring Formation by the widespread occurrence of evaporites, most notably gypsum (Parcell and

Williams, 2005). Salinity throughout the Gypsum Spring Formation likely fluctuated between fully marine and hypersaline, with higher DCA2 scores correlating with higher salinity levels.

Although most Windy Hill Sandstone samples plot at low DCA2 scores, a single sample from Cody, Wyoming, collected from a location farther west than any other samples, plots at the highest DCA2 scores, and is more in composition similar to Gypsum Spring Formation samples than any other Windy Hill Sandstone scores. The Sundance Seaway deepened to the west, suggesting more open-marine conditions to the west (Kvale et al., 2001; McMullen et al. 2014). While the Windy Hill Sandstone in the eastern Bighorn Basin is interpreted as estuarine facies, samples from the same may represent deeper-water or more open-marine facies (McMullen et al., 2014). This may explain the unique composition of this sample and its unusually high DCA2 scores compared to other Windy Hill Sandstone samples. Additional work is needed in these western areas to test this interpretation.

Lower DCA2 scores also correspond to harder substrate units, such as the shelly Redwater Shale oyster. Conversely, softer-bottom units, such as the tidal-flat Gypsum Spring Formation, have higher DCA2 scores. This separation of end-member units along DCA2 by substrate is also seen at a smaller scale between more similar units, such as the Redwater Shale mud and Redwater Shale oyster. There is a gradient between the harder, shellier Redwater Shale oyster bedset and the softer, muddier Redwater Shale mud with increasing DCA2 scores (Fig. 7). This gradient only partially explains separation of samples along DCA2, and does not account for units at intermediate scores.

Thus, DCA2 potentially correlates with a salinity and substrate gradient. Low DCA2 scores reflect lower salinities, with a gradational increase to marine or hypersaline conditions at high DCA2 scores.

Dominance and Diversity Patterns in the Ordinations

Patterns of dominance and diversity seen within each unit's samples are reflected within the DCA ordination. Units dominated by a single taxon correspond to a tight cluster of DCA sample scores, due to similar composition and levels of dominance. These units, the Stockade Beaver Shale, Redwater Shale mud, Redwater Shale oyster, and Redwater Shale *Camptonectes* plot at scores similar to the DCA species scores of their dominant taxa, *Gryphaea*, *Pachyteuthis*, *Liostrea*, and *Camptonectes* respectively (Fig. 7 & 8).

Those units where the dominant taxon differs by bed or locality plot as a broader range of scores due to the more variable composition of samples. These units, the Gypsum Spring Formation, Canyon Springs Member, Redwater Shale concretions, and Windy Hill Sandstone, plot over broader regions in the DCA ordination, suggesting each unit may preserve a wide range of conditions and faunal compositions.

Samples from these units tend to cluster around distinct end-nodes, with few samples between these nodes. Samples found at these end-nodes of each unit are dominated by one of the taxa identified previously as regionally dominant in the unit, with sample scores reflecting the corresponding species scores of the dominant taxon (Fig. 9).

The Gypsum Spring Formation contains bedsets dominated by one of four dominant bivalves: *Pleuromya*, *Trigonia*, *Camptonectes*, and *Corbecellopsis* (Fig. 9A). *Pleuromya* dominates eight samples, plotting at higher DCA2 scores, but within a narrow band of DCA1 scores. *Trigonia*-dominant samples plot at similar DCA1 scores as *Pleuromya*-dominant samples, but at increasingly lower DCA2 scores, reflecting a possible gradient between the two. *Corbicellopsis* dominates two samples, both from the same fieldsite, and they lie at the highest DCA1 scores of all samples. Finally, *Camptonectes*-dominant samples are found at intermediate DCA1 and DCA2 scores, at similar scores to other *Camptonectes*-dominant units, such as the Redwater Shale *Camptonectes* bedsets (Fig. 7).

Within the Canyon Springs Member, there are four regionally dominant taxa (three bivalves and one gastropod), although some samples are not dominated by a single taxon (Fig. 9B). *Procerithium*-dominant samples plot at higher DCA1 and DCA2 scores. *Pleuromya*-dominant samples plot at values similar to those *Pleuromya*-dominant samples within the Gypsum Spring Formation (Figs. 9A & 9B). *Liostrea*-dominant samples plot at much lower DCA1 and DCA2 scores than other Canyon Springs Member samples, at values similar to other *Liostrea*-dominant units such as the Redwater Shale oyster unit (Fig. 7). *Camptonectes*-dominant samples are found at similar intermediate DCA1 and DCA2 scores as in the Gypsum Spring Formation. A fifth node corresponds to a wider cluster of samples, in which there is no single dominant taxon, though which is abundant in *Gryphaea* and *Astarte*.

The Redwater Shale concretion unit contains three samples dominated by a single taxon. Two of these samples share a dominant taxon, *Astarte*, and both plot at similar intermediate DCA1 and DCA2 scores (Fig. 9C). Another sample is dominated by *Camptonectes*, and plots at scores similar to previous *Camptonectes*-dominant units (Figs. 7, 9A, and 9B). The remaining samples are not dominated by any single taxon and plot at scores similar to the species scores of their most abundant taxaon, *Kallirhynchia* and *Pholadomya* (Fig. 8). These low-dominance samples drive the broad separation of the Redwater Shale concretion unit.

Many bedsets in the Windy Hill Sandstone are dominated by *Liostrea* or *Camptonectes*, and plot at intermediate DCA1 and DCA2 scores, as in other *Liostrea*-dominant and *Camptonectes*-dominant units (Fig. 9D). However, in some samples the most abundant taxa is instead a more regionally dominant genus. Two samples were dominated by *Mactromya* and have high DCA1 and low DCA2 scores. Many similar bedsets were noted in the field but could not be counted. The *Kallirhynchia*rich sample plots at the highest DCA2 scores of all samples.

nMDS

Along most axes, nMDS reflects the same patterns as DCA (Table 2; Fig 10 & 11). Pearson correlation coefficients show MDS1 is strongly correlated with DCA1, and MDS2 is more correlated with DCA2. Higher axes show less agreement, but they also explain less variation. Although axis 2 of nMDS is highly correlated with DCA2, they appear to have somewhat different interpretations.

Along MDS axis 2, there is a life habit and mobility trend evident in species scores. Mobile taxa, on average, plot at higher MDS2 values than stationary taxa (Fig.

12A). Among mobile taxa, those that are facultatively mobile are, on average, found at higher MDS2 scores than slow or fast moving taxa.

This same trend is mirrored within life habit, where an increase in infaunalization correlates with increasing MDS2 taxon scores (Fig. 12B). Taxa living at the most elevated tiering level, upper-epifaunal, average the lowest MDS2 scores. This passes through a gradient of increasing infaunalization from epifaunal, lower epifaunal, semi-infaunal, infaunal, and deep infaunal life habits with increasing MDS2 scores. Nektonic taxa plot, on average, at intermediate MDS2 scores.

Thus, through a combination of these two patterns, it can be inferred that MDS2 correlates with a gradient of substrate consolidation. Lower MDS2 scores, those occupied by taxa that are stationary and epifaunal, correspond to firmer, shellier substrates, which would allow stationary taxa to cement or attach to the substrate and elevate themselves above the sediment-water interface. Taxa at intermediate MDS2 scores, which are fully mobile and semi-infaunal, are best suited to an intermediately consolidated substrate that would allow motion at or within the sediment-water interface. Higher MDS2 scores, occupied by mobile, infaunal taxa, correspond to less consolidated, muddier or sandier substrate. These softer substrates would have allowed taxa to move and survive infaunally, an impossible situation in harder, shellier substrates. Additional work is needed to determine the effects of taphonomy in preferentially preserving taxa of various life modes and mobility.

DISCUSSION

Biogeography

The global occurrence of Sundance Seaway taxa supports single-entranceway reconstructions (Fig. 1; Blakey, 2014). Accounting for the effects of sampling, most taxa had occurrences at, or near, the paleolatitude of this entranceway and could have entered the Seaway when conditions were favorable. The faunal population of the Sundance Seaway would not have needed other entranceways connecting to the proto-Pacific at more southern latitudes to produce the faunal assemblage found in the Bighorn Basin. However, this does not fully disprove the possibility that additional entranceways existed briefly over the history of the Seaway.

The geography of the Sundance Seaway and its single entranceway likely enhanced the restricted nature of the Seaway's taxa and environments. With a single connection to the proto-Pacific, its great length, and its shallow depth, the Seaway likely would have experienced limited tidal exchange. As a result, temperature and salinity would have been likely to show strong gradients across the entranceway and along the Seaway's length. Salinity and temperature would also likely have been more prone to fluctuation, along the shallower eastern and southern margins of the Seaway.

Because of its span into lower latitudes, southern portions of the Sundance Seaway, such as in those in modern Wyoming, were likely warmer than areas to the north. However, taxa most suited to these southern, warmer water environments would likely have been less able to enter the Seaway, owing to an inability to survive in the cooler waters at the northern entranceway.

Similar trends are seen in shallow, modern seaways including the Baltic Sea (Baker-Austin et al., 2013; Vali et al., 2013; Szymczycha et al., 2014; Vuorinen et al., 2015), Gulf of Bothnia (Baker-Austin et al., 2013; Vali et al., 2013; Vuorinen et al., 2015), and the Adriatic Sea (Lipizer et al., 2014). Along the 10° latitudinal range of the Baltic Sea and Gulf of Bothnia, summer sea surface temperatures vary from 18 to 23 °C (Baker-Austin et al., 2013). Sea surface salinity within the Baltic Sea varies from 0 to 25 psu, averaging 7.2-8.2 psu, while across the entranceway with the Kattegat region, salinities quickly reach levels of up to 36 psu (Bonsdorff, 2006; Baker-Austin et al, 2013). The rapid change in salinity across the entranceway of the Baltic Sea, likely drives a corresponding decrease in diversity of sub-littoral soft-sediment species. In the higher salinity regions of Skagerrak and Kattegat, 1,648 species are present, whereas an average of 18 species is present in lower salinity regions of the Baltic Sea (Bonsdorff, 2006).

Within the Adriatic Sea, summer sea surface temperature varies from 21 to 25 °C along its length (Lipizer et al., 2014). Sea surface salinity follows a similar pattern, ranging from 39 psu near the entrance to 30 psu at its northern terminus (Lipizer et al., 2014). Gradients in the Sundance Seaway were likely much stronger given the greater length of the Sundance Seaway and its north-south orientation. By way of comparison, the Sundance Seaway spanned approximately the equivalent of southern Alaska (60° N) to the north end of the Gulf of California (30° N).

In the modern Pacific, oceanic circulation along northwestern North America is driven by the North Pacific Gyre and the Aleutian Low (Latif and Barnett, 1996; Miller and Schneider, 2000). When the North Pacific Gyre is strong or the Aleutian Low weakened, warmer waters are transported from the tropics into the North Pacific by the

Kuroshio Current and Oyashio Extension (Latif and Barnett, 1996; Sawada and Handa, 1998). These oscillations in the North Pacific Gyre drive regional variation in water temperature, salinity, nutrients, and chlorophyll along the northwest coast of North America (Di Lorenzo et al., 2008).

During the Early to Middle Jurassic, the continents were surrounded by the ancestral Pacific Ocean (proto-Pacific or Panthalassa of some authors); (Kennett, 1977; Winguth et al., 2002; Arias, 2008). Recent oceanic models depict the northern proto-Pacific developing counter-clockwise rotating polar gyres and clockwise rotating subtropical gyres (Arias, 2008). At approximately 60°N, westerlies and the North Polar Current drove ocean circulation toward the western proto-Pacific (Arias, 2008). South of 60°N, trade winds and tropical easterlies would aid the North Panthalassa Current in transporting warmer water towards the eastern edge of the proto-Pacific (Arias, 2008). Along the eastern edge of the ocean, currents were turned southward by the weaker North-Western Gondwana Current (Arias, 2008). Older reconstructions of the proto-Pacific hypothesized simple or stagnant circulation (Kennett, 1977; Winguth et al., 2008), due to Pangaea preventing circum-global currents (Roth, 1989). In these reconstructions, the northern proto-Pacific is not supplied warmer water by any subtropical currents.

Oceanic circulation during the Early and Middle Jurassic was probably not that different than the modern Pacific. Conditions generated by the North Panthalassa Current are generally the same as those generated by the Kuroshio Current, and supplied the northwestern proto-Pacific with warmer water. As its entranceway sat north of the break of eastward circulating currents, the Sundance Seaway likely received limited circulation of warmer tropical water supplied by these currents under normal conditions, similar to the Pacific Northwest of North America (Fig. 13A).

Only eurytopic taxa, selected to survive a wide range of conditions, were likely to haven been able to both enter the cooler-water entrance to the Seaway and colonize to into its warmer southern area. “Southern Taxa” would have been able to enter the Seaway only when oceanic conditions were favorable, such as if the warmer water North Panthalassa Current shifted northward, expanding the range of warm water conditions into entranceway latitudes (Fig. 13B). Change in the position of the North Panthalassa Current would have controlled which taxa were able to enter the Seaway. While 62% of “Northern Taxa” reported from the southern Seaway were present in field samples, only 35% of “Southern Taxa” were found in the field samples of this study. The ability or inability to enter the Seaway under normal oceanic conditions controlled the relative proportions of these two groups of taxa, allowing more “Northern Taxa” than “Southern Taxa” to populate the Seaway’s southern reaches.

Survival across a range of conditions spanning the 2000 km distance from the entranceway to the terminus would have been difficult for most organisms living at northern latitudes, but less so for eurytopic taxa, such as the “Northern Taxa.” As evidenced by their wide global occurrence ranges, these taxa could survive a wide range of conditions and their high northernmost occurrences would have allowed access to the Seaway under normal oceanic conditions during the Jurassic (Figs. 4 & 13A). This allowed some “Northern Taxa” to establish widespread populations at the Seaway’s terminus, where they were typically found in a large percentage of field samples (Fig. 5).

"Southern Taxa," as warmer-water taxa, would have been able to enter the Seaway only when warm-water currents permitted (Fig. 13B). This prevented the "Southern Taxa" from generally invading the Seaway, instead limiting them to a small number of samples when present (Fig. 5). However, "Southern Taxa" that were able to colonize to the southern terminus were well equipped to flourish under the warm-water conditions, and therefore occur in larger average abundances than "Northern Taxa."

As North America shifted northward throughout the Jurassic, fewer of these warm-water episodes would have occurred at the entranceway to the Sundance Seaway (May and Butler, 2012). As fewer "Southern Taxa" were able to survive conditions necessary to reach the entranceway, already limited exchange of these taxa between the Seaway and proto-Pacific were completely starved. As "Southern Taxa" populations at the terminus were reduced or removed, more "Northern Taxa" were able to take their place, establishing widespread dominance. Older units, before significant northward shift of the continent, contain samples dominated by both "Northern Taxa" and the "Southern Taxa" (e.g., the "Northern Taxa" *Pleuromya, Trigonia,* and *Camptonectes* and the "Southern Taxa" *Corbicellopsis* in the Gypsum Spring Formation or the "Northern Taxa" *Pleuromya, Camptonectes,* and *Liostrea* and the "Southern Taxa" *Procerithium* in the Canyon Springs Member); (Figs 5 & 6). In the Gypsum Spring Formation and Canyon Springs Member, it was possible for "Southern Taxa" to establish dominance within an individual bedet (e.g., *Corbicellopsis* and *Procerithium*), a trend that disappeared in the Stockade Beaver Shale and younger units.

With increasing limitations over time on the ability of "Southern Taxa" to access the entranceway owing to the northward shift of the North American plate, dominant taxa shifted to include only “Northern Taxa” including *Gryphaea*, *Pachyteuthis*, *Liostrea*, and *Camptonectes* in the overlying Stockade Beaver Shale and Redwater Shale (Figs. 5 & 6). In the Windy Hill Sandstone, most samples are still dominated by the “Northern Taxa” *Liostrea* or *Camptonectes*, though a small number of scattered samples are dominated by the “Southern Taxa” *Kallirhynchia* or *Mactromya*. More eurytopic conditions within the shallower, brackish to freshwater estuarine unit may have allowed small, existing populations of these “Southern Taxa” the opportunity to establish dominance where previously unable or where “Northern Taxa” were less well-suited.

Trends in Sundance Seaway Dominance and Diversity

Faunal communities within the Sundance Seaway typically have low diversity and high dominance, often by a single taxon (Fig. 6). These dominant taxa changed over the lifespan of the Seaway, and they varied among units, and among individual beds and localities in some units.

These findings are consistent with similar studies of Sundance Seaway communities, such as those by Wright (1973, 1974), Tang (1996), and McMullen et al. (2014). These studies all recognized low diversity, high dominance assemblages within the Seaway with the same dominant taxa found in this study. Those units this study found to vary in dominance by bed or locality were also identified by these studies as containing multiple faunal associations or assemblages differing by lithofacies (Wright, 1973; McMullen et al., 2014).

All studies describe the widespread dominance by the oyster *Gryphaea* in the Stockade Beaver Shale (Wright, 1973; Tang, 1996, McMullen et al., 2014). They similarly identify unit-wide dominance by the belemnite *Pachyteuthis* within Redwater Shale mud (McMullen et al., 2014), by the oyster *Liostrea* within Redwater Shale oyster units (Wright, 1973, 1974; Tang, 1996; McMullen et al., 2014), and by the scallop *Camptonectes* within Redwater Shale *Camptonectes* units (Wright, 1973, 1974; Tang, 1996, McMullen et al., 2014). Wright (1973) also identifies an additional dominant taxon within the Stockade Beaver Shale the bivalve, *Meleagrinella*, which was found by this study but not at high dominance or abundance levels in any sample. In Wright's (1973, 1974) studies, *Meleagrinella* was found in abundance in southeast Wyoming, a region not sampled in this study.

These studies also identified similar dominant taxa in those units where dominance differed between individual beds or localities. In the Gypsum Spring Formation, faunal associations match those dominant-taxa communities identified in this study: *Camptonectes* (Wright, 1973; Tang, 1996), *Pleuromya* (Wright, 1973; Tang, 1996), *Trigonia* (Wright, 1973), and *Liostrea* (Tang, 1996). Within the Windy Hill Sandstone, these studies identified assemblages dominated by *Liostrea* and *Camptonectes*, similar to those found by this study (Wright, 1973; Tang, 1996, McMullen et al., 2014). Other taxa identified as dominant by this study, *Kallirhynchia* and *Mactromya*, were not previously reported as dominants. Instead, McMullen et al. (2014) found monospecific assemblages of *Ceratomya* (probably *Mactromya*) while Wright (1974) identified *Tancredia*-dominant assemblages. Neither of these communities was seen in this study, although *Tancredia* was observed uncommonly in samples of Windy Hill Sandstone.

Comparisons to the Overall Jurassic

Hallam (1977) described the Sundance Seaway as faunally impoverished. Studies of diversity in other regions during the Jurassic, including East Greenland (Fürsich, 1984a, 1984b), the Andean Basin (Aberhan and Fürsich, 1998), the Greater Caucasus Basin (Ruban, 2006, 2012) and Gebel Maghara, Egypt (Abdelhady and Fürsich, 2014, 2015), all show higher levels of diversity than the Sundance Seaway. However, high levels of dominance are also observed in some of those regions.

In the Jurassic of Milne Land, East Greenland, Fürsich (1984a, 1984b), identified 22 distinct benthic associations from 135 late Oxfordian-Kimmeridigian samples, containing approximately 24,000 specimens. These 22 associations range in richness from 1-38, with an average of 11.1, making East Greenland, on average, twice as diverse as the Sundance Seaway's average richness of 5.3 (Table 1).

Of the 22 associations of Jurassic East Greenland, 13 (59%) exhibit dominance by a single taxon that occurs in relative abundances greater than 50%. Dominant taxa are most commonly suspension-feeding bivalves, with occasional brachiopods or serpulid polychaetes. Fürsich (1984a) also identifies a number of low diversity associations, which correlate to low oxygen conditions, shifting substrate, or are driven by biotic interactions. Faunal associations vary vertically among beds, and laterally across the region (Fürsich, 1984b). East Greenland during the Jurassic displayed similar patterns in dominance and diversity as the Sundance Seaway. While overall diversity in East Greenland was much greater, dominance by a single taxon was present in 59% of associations and the dominant taxa varied between units, and over individual beds and localities within units.

In Middle to Upper Jurassic strata of Gebel Maghara, Egypt, Abdelhady and Fürsich (2014) identified a greater number of taxa (198) in a smaller number of specimens (9,130) than found in the Sundance Seaway. Abdelhady and Fürsich (2014) separate faunal associations into two groups: (1) low-stress, polyspecific assemblages and (2) high-stress, paucispecific assemblages. Low-stress polyspecific assemblages had higher diversity, and were deposited high-energy, firm substrate habitats dominated by brachiopods, solitary corals, and bivalves (Abdelhady and Fürsich, 2014). High-stress, paucispecific assemblages had lower diversity and were dominated by one or two taxa. Conditions in these high-stress environments varied in levels of oligotrophy, sedimentation rates, dysoxia, energy-levels, and overall restriction (Abdelhady and Fürsich, 2014). The average richness of Gebel Maghara faunal associations is 38.3, with an average Simpson's D of 0.642. In the paucispecific, low diversity associations, richness averaged 12 with an average Simpson's D of 0.433, still twice as diverse and with greater evenness than the Sundance Seaway (Table 1).

The Sundance Seaway is unusual in that low-stress, deep-water units, such as the Stockade Beaver Shale, exhibited the lowest diversity and highest dominance of all units, rather than the polyspecific assemblages expected in comparable low-stress, deep-water Egyptian assemblages. Additionally, shallow-water, eurytopic, high-stress units, such as the Gypsum Spring Formation, exhibited higher diversity and lower dominance, instead of being paucispecific, high-dominance assemblages as in Egypt.

These differences suggest that environmental stress plays a different role in the Sundance Seaway than in Egypt. Instead of allowing for greater diversity, low-stress environments maintained stenotopic conditions, allowing for one taxon that is well-suited to those conditions to establish dominance. In high-stress environments, fluctuations in conditions such as water level, temperature, and salinity prevented a single taxon from being well-suited for survival across an entire unit. In these units, multiple taxa established regional dominance where best suited along a gradient of conditions.

Trends in Sundance Seaway Gradient Ecology

Both DCA and nMDS identified the primary factor driving the distribution of fauna as a complex gradient reflecting conditions related to water depth (Fig. 7). DCA1 also potentially correlated with a separation of the carbonate Gypsum Spring Formation and lower Sundance Formation from the siliciclastic upper Sundance Formation. While DCA2 identified the secondary factor as potentially related to salinity, MDS2 correlated well with substrate, separating soft, muddy or sandy substrate at higher axis 2 scores from harder, shellier bottom conditions at lower axis 2 scores (Fig. 10).

Previous studies of the Sundance Seaway's community paleoecology include Wright (1973, 1974), Tang (1996), de Gibert and Ekdale (1999, 2002), Hunter and Zonneveld (2008), and McMullen et al. (2014). Most of these studies also identify the primary factor driving variation among marine communities of the Seaway as related to water depth.

In McMullen et al. (2014), non-metric multidimensional scaling of fossil assemblages in the Sundance Formation displays a gradient of depth along the primary axis from shallow subtidal and ooid shoals to offshore oyster and scallop bedsets. With the removal of the Stockade Beaver Shale, owing to the obscuring effects caused by its monospecific assemblages, the primary axis also separates the carbonate lower Sundance from the siliciclastic upper Sundance (McMullen et al., 2014). Both of these trends agree with the findings of this study.

Variation between the crinoid components of some Seaway communities also correlates well with water depth and related factors (Hunter and Zonneveld, 2008). Crinoid genera abundant in lower energy, offshore, marine facies (*Chariocrinus*) contrast with those abundant in higher energy, restricted, lagoonal facies (*Isocrinus*; Hunter and Zonneveld, 2008). This is somewhat different than the findings of this study in which *Isocrinus* and *Chariocrinus* have similar species scores in both ordinations, although *Isocrinus* always has lower axis 1 scores, corresponding to more deeper-water conditions than *Chariocrinus*.

In the field samples of this study, *Isocrinus* columnals are far more abundant (2,415) and common (26%) than *Chariocrinus* columnals (31 and 4%), possibly owing to shallow-water conditions in the eastern Bighorn Basin that correspond to the preferred environment of *Isocrinus*. However, in both ordinations, *Isocrinus* scores are more similar to deep-water, offshore samples than *Chariocrinus* scores. Further study of regions to the west of the Bighorn Basin are necessary to determine if the abundance of *Chariocrinus* increases in deeper-water regions of the Seaway.

Though ordinations were not conducted, both Wright (1973, 1974) and Tang (1996) identified trends in life habit, mobility, and substrate preference driving variation among bivalves. Epifaunal, stationary bivalve-dominant communities established themselves on hard substrates, while mobile, infaunal bivalves were more common in shifting sandy or muddy substrates (Wright, 1973, 1974; Tang, 1996). In ichnofossil assemblages of the Arapian Shale and Carmel Formation, age-equivalents to the Sundance Formation in Utah, variation in trace fossil community composition is attributed to hypersalinity and poor bottom oxygenation in marginal, restricted settings (de Gibert and Ekdale, 1999, 2002). Both substrate and potentially salinity were identified by this study as potential secondary factors driving community variation.

Comparison to Overall Jurassic

Studies of paleoecology throughout the Jurassic globally have also found factors correlated to to water depth primarily driving community variation. A secondary driving factor relating to substrate consistency or sediment carbonate/siliciclastic content also plays a significant role in community variation (Kiessling and Aberhan, 2007; Abdelhady and Fürsich, 2014, 2015). In a diverse dataset of global Triassic-Jurassic marine samples, a complex gradient of water depth and carbonate/siliciclastic content was identified as the primary driving factor (Kiessling and Abherhan, 2007).

In Abdelhady and Fürsich (2014), detrended correspondence analysis of Bajocian-Oxfordian samples from Gebel Maghara, Egypt also identifies a gradient in water depth. Separation between deeper, low-energy open ramp and shallower, high-energy, restricted ramp depositional environments correlates to DCA axis 1. A gradient between hard to soft substrate correlates with DCA axis 2 (Abdelhady and Fürsich, 2014).

Other factors found to influence community variation throughout the Jurassic are bottom complexity (Kiessling and Aberhan, 2007), larval development (Abdelhady and Fürsich, 2015), life habit (Abdelhady and Fürsich, 2014, 2015; Danise et al., 2015), nutrient levels (Abdelhady and Fürsich, 2014; Danise et al., 2015), oxygen levels (Danise et al., 2013, 2015; Abdelhady and Fürsich, 2014), and, over wider scales, latitudinal zonation (Kiessling and Aberhan, 2007).

Comparisons to the Overall Phanerozoic

Throughout the Phanerozoic and across a wide geographic range, the majority of paleoecological studies have correlated water depth and related factors to be the primary driver of community composition (e.g., Horton et al., 1999; Holland et al., 2001; Holland and Patzkowsky, 2004, 2007; Patzkowsky and Holland, 2012; Chiba et al., 2014; Scarponi et al., 2014; Tyler and Kowalewski, 2014). In this respect, the primary pattern of community variation within the Sundance Seaway is consistent with the greater Phanerozoic pattern.

Other common environmental factors controlling composition during the Phanerozoic include feeding type (Scarponi et al., 2014), life habit (Holland et al., 2001; Scarponi et al., 2014), organic content/vegetation (Horton et al., 1999; De Francesco and Hassan, 2009), salinity (Horton et al., 1999; De Francesco and Hassan, 2009), sediment carbonate/siliciclastic content (Leonard-Pingel et al., 2012), substrate (Holland and Patzkowsky, 2007; Bush and Brame, 2010; Scarponi et al., 2014), temperature (Holland and Patzkowsky, 2004; De Francesco and Hassan, 2009), and turbidity (Holland and Patzkowsky, 2004; Bush and Brame, 2010). Many of these factors were identified as drivers of variation within the Sundance Seaway samples, and most that were absent are only easily identifiable in samples from the Recent or modern.

CONCLUSIONS

1. Global biogeographic distributions of fauna reported from the Sundance Seaway support the single, northern entranceway interpretation of the Seaway. This likely caused limited tidal circulation and, along with the Seaway's length and shallow depth, fostering gradients in temperature and salinity that likely controlled the taxa present in the Sundance Seaway.

2. Faunal communities in the Sundance Seaway are typically low diversity, with high dominance by a single taxon. This dominant taxon does not remain constant, and it varies among units, or among beds or localities within a unit. The restricted nature of the Seaway likely caused the lower richness and higher dominance levels when compared to other regions. Dominance and diversity in the Seaway was likely controlled by the ability of taxa to survive a range of conditions from the northern entranceway to the southern terminus. Eurytopic taxa, with occurrences at more northern latitudes globally, were more likely to colonize the Seaway in widespread, numerous populations. While less likely to survive conditions at the entranceway, when taxa with more southern provenances were able to colonize the southern terminus, they were well-suited to the warmer waters and flourished in high abundances.

3. Variation in community composition in the Sundance Seaway is primarily controlled by water depth and related factors. This may also include a transition from older, carbonate units to younger, siliciclastic units. Water depth has been found to be the most common primary driving factor in community variation throughout the Phanerozoic, including other studies of Jurassic Sundance Seaway communities.

4. Variation in community composition in the Sundance Seaway is secondarily controlled by substrate consistency and salinity may also play a role. These factors are both common secondary factors driving community variation, identified in many studies throughout the Phanerozoic.

CHAPTER 3

CONCLUSIONS

Global biogeographic distributions of fauna present in the Sundance Seaway support reconstructions of the Seaway depicting a single, northern entranceway. This likely limited circulation with the proto-Pacific and, combined with the Seaway's length and shallow depth, created temperature and salinity gradients that limited the diversity of taxa.

Faunal communities in the Seaway were commonly low diversity, with high dominance by a single taxon. This dominant taxon varies among units, and it varies among beds or localities within some units. Dominance and diversity in the Seaway was controlled by a taxon's ability to tolerate the range of conditions spanning from the northern entranceway to the southern terminus.

Eurytopic taxa, with global northernmost occurrences at higher latitudes, were more likely to tolerate these conditions and colonize the Seaway frequently "Southern Taxa," with more limited tolerances were less likely to enter the Seaway due to an inability to cope with normal conditions at the entranceway. However, when oceanic conditions varied and allowed these taxa to colonize the southern terminus, they were well-suited to the warmer waters and locally flourished in high abundances.

Variation in community composition within the Sundance Seaway was primarily controlled by a complex gradient of factors related to water depth. Secondary variation is correlated with substrate and potentially salinity. These trends are typical to those seen in similar studies through the Phanerozoic.

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TABLE 1—Richness and Simpson’s D of stratigraphic units based on samples analysis.

Stratigraphic Unit	**Mean Richness (minimum-maximum)**	**Mean Simpson's D (minimum-maximum)**
Gypsum Spring Formation	5.6 (3–8)	0.295 (0.036–0.606)
Canyon Springs Member	6.3 (1–9)	0.560 (0.000–0.833)
Stockade Beaver Shale	3.1 (2–5)	0.036 (0.010–0.097)
Hulett Member	2	0.035
Redwater Shale concretion	8.2 (6–11)	0.518 (0.250–0.750)
Redwater Shale mud	5.6 (3–8)	0.405 (0.221–0.667)
Redwater Shale oyster	6.2 (5–9)	0.404 (0.207–0.543)
Redwater Shale *Camptonectes*	4.6 (4–5)	0.214 (0.083–0.335)
Redwater Shale (total)	6.1 (3–11)	0.386 (0.083–0.750)
Windy Hill Sandstone	5.1 (4–7)	0.510 (0.353–0.716)
Average	5.3	0.336

TABLE 2—Pearson correlation coefficients of sample scores on all DCA and MDS axes.

	MDS1	**MDS2**	**MDS3**	**DCA1**	**DCA2**	**DCA3**	**DCA4**
MDS1	1.00	0.00	0.00	0.94	0.09	0.10	-0.45
MDS2		1.00	0.00	0.16	0.73	-0.36	-0.10
MDS3			1.00	0.11	-0.03	0.07	0.31
DCA1				1.00	0.16	0.08	-0.40
DCA2					1.00	-0.02	-0.17
DCA3						1.00	0.09
DCA4							1.00

TABLE 3—Taxon codes.

Code	Genus/other	Family	Order	Class
Asta	*Astarte*	*Astartidae*	*Carditita*	*Bivalvia*
Camp	*Camptonectes*	*Pectinoidae*	*Pectinida*	*Bivalvia*
Card	*Cardioceras*	*Cardioceratidae*	*Ammonitida*	*Cephalopoda*
Cera	*Ceratomya*	*Ceratomyidae*	*Pholadida*	*Bivalvia*
Cerc	*Cercomya*	*Laternulidae*	*Pandorida*	*Bivalvia*
Char	*Chariocrinus*	*Isocrinidae*	*Isocrinida*	*Crinoidea*
Clio	*Cliona*	*Clionaidae*	*Clavulina*	*Demospongea*
Corbi	*Corbicellopsis*	*Tancrediidae*	*Cardiida*	*Bivalvia*
Corbu	*Corbula*	*Corbulidae*	*Pholadida*	*Bivalvia*
echi	echinoid	unknown	unknown	*Echinoidea*
Erym	*Eryma*	*Erymidae*	*Decapoda*	*Malacostraca*
Gram	*Grammatodon*	*Parallelodontidae*	*Arcida*	*Bivalvia*
Gryp	*Gryphaea*	*Gryphaeidae*	*Ostreida*	*Bivalvia*
Hamu	*Hamulus*	unknown	*Serpulimorpha*	*Polychaeta*
Homo	*Homomya*	*Pholadomyidae*	*Pholadomyida*	*Bivalvia*
Hybo	*Hybodus*	*Hybodontidae*	*Hybodontiformes*	*Chondrichthyes*
Idon	*Idonearca*	*Cucullaeidae*	*Arcida*	*Bivalvia*
Isoc	*Isocrinus*	*Isocrinidae*	*Isocrinida*	*Crinoidea*
Isog	*Isognomon*	*Malleidae*	*Ostreida*	*Bivalvia*
Kall	*Kallirhynchia*	*Tetrarhynchiidae*	*Rhynchonellida*	*Rhynchonellata*
Lima	*Lima*	*Limidae*	*Pectinida*	*Bivalvia*
Lios	*Liostrea*	*Gryphaeidae*	*Ostreida*	*Bivalvia*
Loph	*Lopha*	*Ostreidae*	*Ostreida*	*Bivalvia*
Lyos	*Lyosoma*	unknown	*Archaeogastropoda*	*Gastropoda*
Mact	*Mactromya*	*Mactromyidae*	*Lucinida*	*Bivalvia*
Mele	*Meleagrinella*	*Oxytomidae*	*Pectinida*	*Bivalvia*
Micr	*Microeciella*	*Oncousoeciidae*	*Cyclostomata*	*Stenolaemata*
Modi	*Modiolus*	*Mytilidae*	*Mytilida*	*Bivalvia*
Myop	*Myophorella*	*Myophorelloidae*	*Trigoniida*	*Bivalvia*
nati	naticiform gastropod	unknown	unknown	*Gastropoda*
Nodo	*Nododelphinula*	*Nododelphinulidae*	*Amberleyoidea*	*Gastropoda*
Nucu	*Nucula*	*Nuculidae*	*Nuculida*	*Bivalvia*
Pach	*Pachyteuthis*	unknown	*Belemnitida*	*Cephalopoda*
Para	*Parastomechinus*	unknown	*Stomopneustoida*	*Echinoidea*
Phol	*Pholadomya*	*Pholadomyidae*	*Pholadomyida*	*Bivalvia*
Pinn	*Pinna*	*Pinnidae*	*Ostreida*	*Bivalvia*
Plat	*Playtmyoidea*	*Laternulidae*	*Pandorida*	*Bivalvia*
Pleu	*Pleuromya*	*Pleuromyidae*	*Pholadida*	*Bivalvia*
Proc	*Procerithium*	*Procerithiidae*	*Sorbeoconcha*	*Gastropoda*
Pron	*Pronoella*	*Arcticidae*	*Cardiida*	*Bivalvia*

Pros	*Prososphinctes*	unknown	*Ammonitida*	*Cephalopoda*
Quen	*Quenstedtia*	*Quenstedtiidae*	*Cardiida*	*Bivalvia*
rou	round serpulid	*Serpulidae*	*Canalipalpata*	*Polychaeta*
serp	serpulid	*Serpulidae*	*Canalipalpata*	*Polychaeta*
Stom	*Stomechinus*	*Stomechinidae*	*Stomopneustoida*	*Echinoidea*
Tanc	*Tancredia*	*Tancrediidae*	*Cardiida*	*Bivalvia*
Trig	*Trigonia*	*Trigoniidae*	*Trigoniida*	*Bivalvia*
Tylo	*Tylostoma*	*Tylostomatidae*	*Stromboidea*	*Gastropoda*
Vaug	*Vaugonia*	*Myophorelloidae*	*Trigoniida*	*Bivalvia*

FIGURE 1—Paleogeography of western North America during the Middle Jurassic (modified from Blakey, 2014).


60° N
Proto-Pacific Ocean
Siberia
Europe
North America
Africa
South America
India
Antarctica
Australia
Land
Shallow marine
Deep marine
Sundance Seaway
Belt Island
Field area
Twin Creek Trough
Sheridan Arch
30° N
North America

FIGURE 2—Chronostratigraphic and lithostratigraphic framework of the Gypsum Spring Formation, Piper Formation, Sundance Formation, and Morrison Formation in the Bighorn Basin of Wyoming and Montana (modified from McMullen et al., 2014).

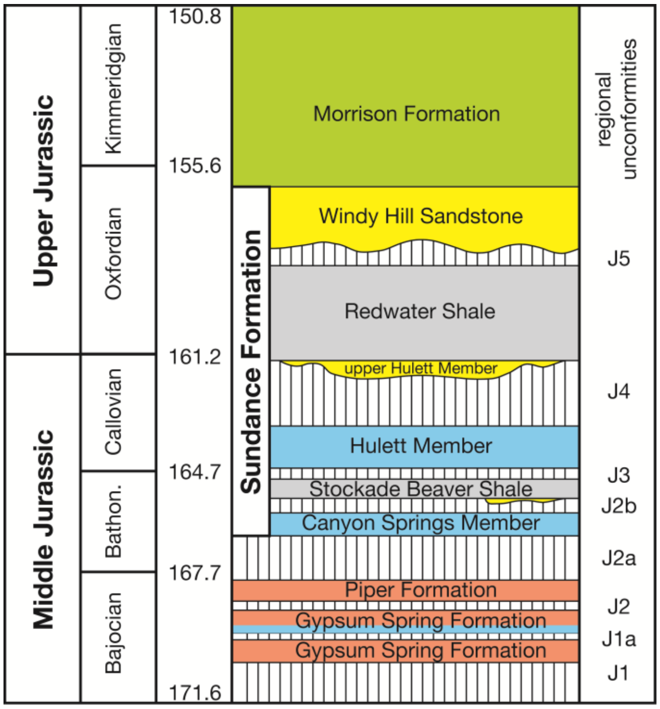

Upper Jurassic
Middle Jurassic
Kimmeridgian
Oxfordian
Callovian
Bathon.
Bajocian
150.8
155.6
161.2
164.7
167.7
171.6
Sundance Formation
Morrison Formation
Windy Hill Sandstone
Redwater Shale
upper Hulett Member
Hulett Member
Stockade Beaver Shale
Canyon Springs Member
Piper Formation
Gypsum Spring Formation
Gypsum Spring Formation
regional unconformities
J5
J4
J3
J2b
J2a
J2
J1a
J1

FIGURE 3—Location of field sites in the Bighorn Basin of Wyoming and Montana.

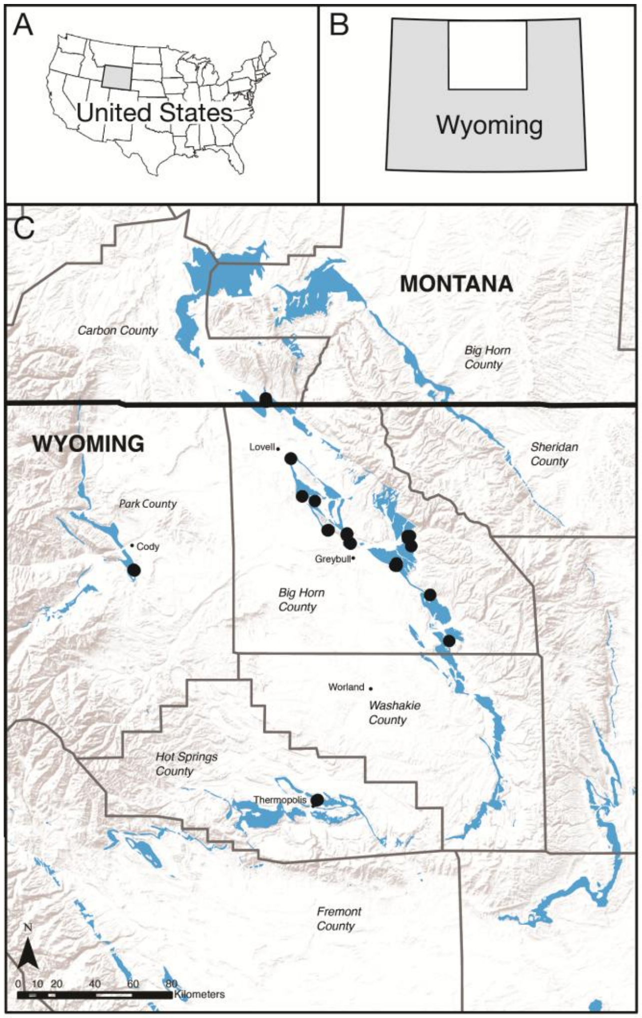

A
United States
B
Wyoming
C
MONTANA
Carbon County
Big Horn County
Sheridan County
WYOMING
Lovell
Park County
Cody
Greybull
Big Horn County
Worland
Washakie County
Hot Springs County
Thermopolis
Fremont County
N
0 10 20 40 60 80
Kilometers

FIGURE 4—Global paleolatitudinal occurrence of Sundance Seaway taxa.

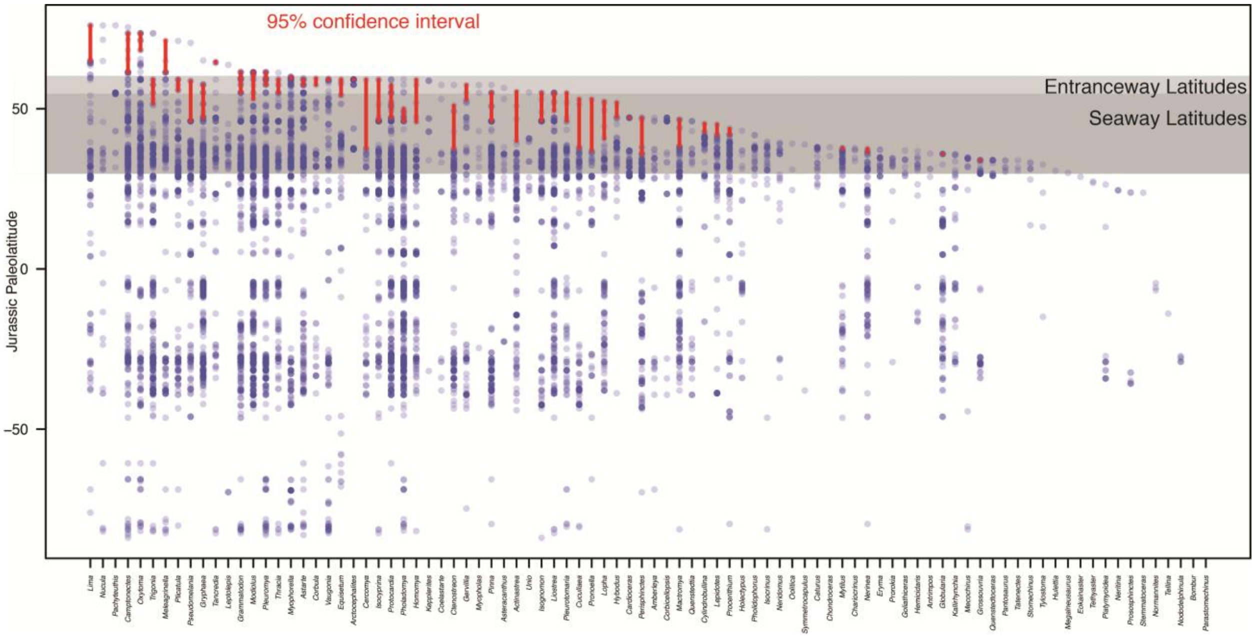

95% confidence interval
Entranceway Latitudes
Seaway Latitudes
Jurassic Paleolatitude
50
0
−50
Lima
Nucula
Pachyteuthis
Camptonectes
Oxytoma
Trigonia
Meleagrinella
Plicatula
Pseudomelania
Gryphaea
Tancredia
Leptolepis
Grammatodon
Modiolus
Pleuromya
Thracia
Myophorella
Astarte
Corbula
Vaugonia
Equisetum
Arctocephalites
Cercomya
Isocyprina
Protocardia
Pholadomya
Homomya
Kepplerites
Coelastarte
Ctenostreon
Gervillia
Myopholas
Pinna
Asteracanthus
Actinastrea
Unio
Isognomon
Liostrea
Pleurotomaria
Cucullaea
Pronoella
Lopha
Hybodus
Cardioceras
Perisphinctes
Amberleya
Corbicellopsis
Mactromya
Quenstedtia
Cylindrobullina
Lepidotes
Procerithium
Holectypus
Pholidophorus
Isocrinus
Neridomus
Oolitica
Symmetrocapulus
Caturus
Chondroceras
Mytilus
Chariocrinus
Nerinea
Eryma
Prorokia
Goliathiceras
Hemicidaris
Antrimpos
Globularia
Kallirhynchia
Mecochirus
Grossouvria
Quenstedtoceras
Pantosaurus
Tatenectes
Stomechinus
Tylostoma
Huletia
Megalneusaurus
Eokainaster
Tethyaster
Platymyoidea
Neritina
Prososphinctes
Stemmatoceras
Normannites
Tellina
Nododelphinula
Bombur
Parastomechinus

FIGURE 5—Comparison of median percent abundance and percent occupancy of taxa within samples.

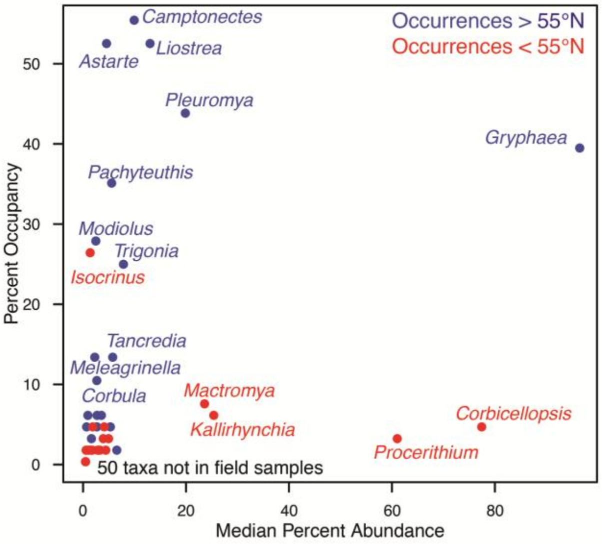

Occurrences > 55°N
Occurrences < 55°N
Camptonectes
Liostrea
Astarte
Pleuromya
Gryphaea
Pachyteuthis
Modiolus
Trigonia
Isocrinus
Tancredia
Meleagrinella
Corbula
Mactromya
Kallirhynchia
Corbicellopsis
Procerithium
50 taxa not in field samples
Percent Occupancy
0
10
20
30
40
50
Median Percent Abundance
0
20
40
60
80

FIGURE 6—Relative abundances of taxa within samples. Taxa in blue have global occurrences at or above 55°N, taxa in red have global occurrences below 55°N, taxa in black have unknown global occurrences during the Jurassic.

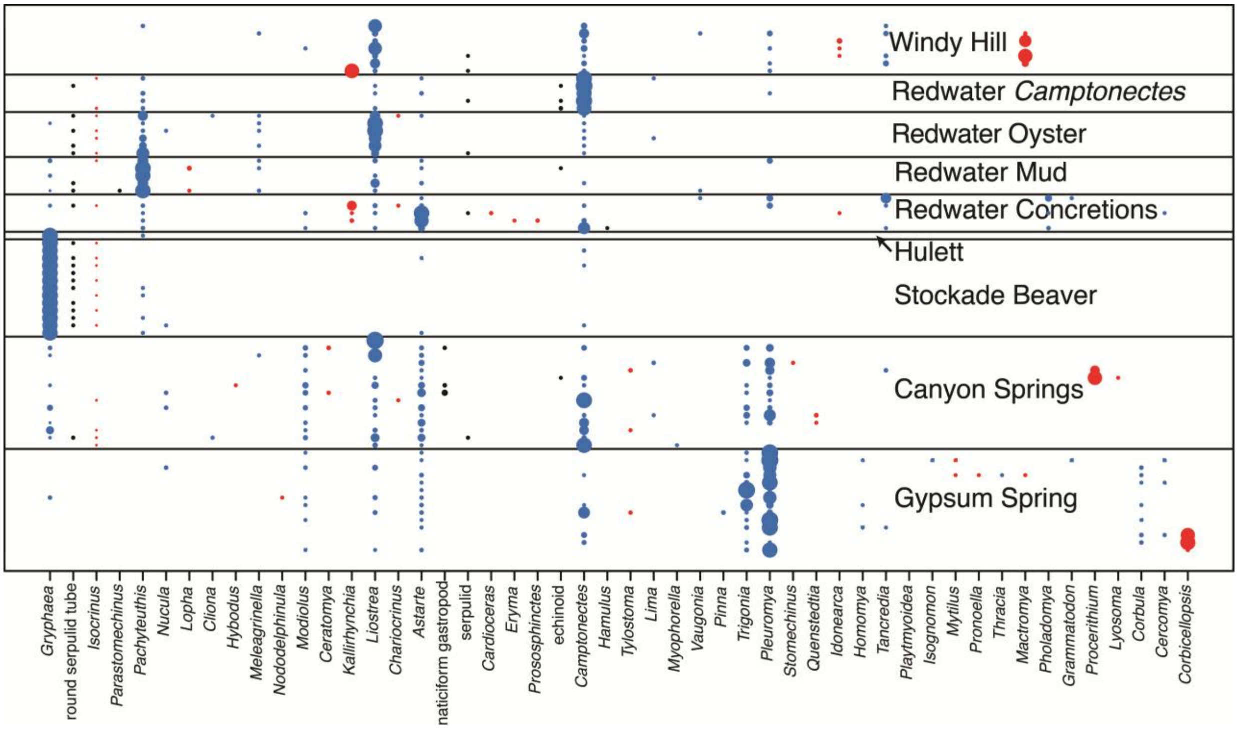
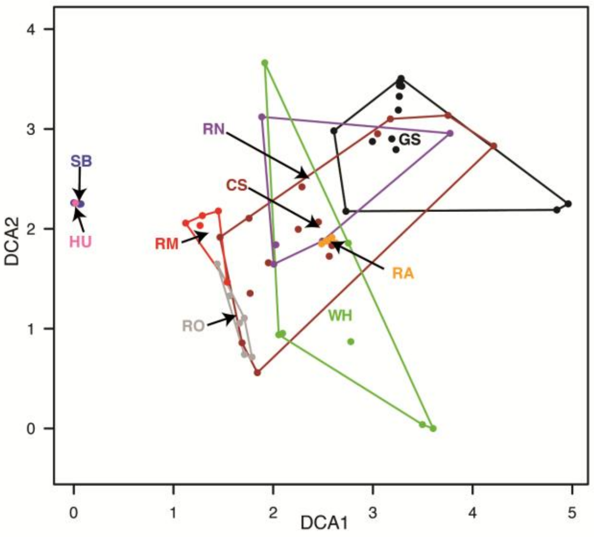

Windy Hill
Redwater *Camptonectes*
Redwater Oyster
Redwater Mud
Redwater Concretions
Hulett
Stockade Beaver
Canyon Springs
Gypsum Spring
Gryphaea
round serpulid tube
Isocrinus
Parastomechinus
Pachyteuthis
Nucula
Lopha
Cliona
Hybodus
Meleagrinella
Nododelphinula
Modiolus
Ceratomya
Kallirhynchia
Liostrea
Chariocrinus
Astarte
naticiform gastropod
serpulid
Cardioceras
Eryma
Prososphinctes
echinoid
Camptonectes
Hamulus
Tylostoma
Lima
Myophorella
Vaugonia
Pinna
Trigonia
Pleuromya
Stomechinus
Quenstedtia
Idonearca
Homomya
Tancredia
Playtmyoidea
Isognomon
Mytilus
Pronoella
Thracia
Mactromya
Pholadomya
Grammatodon
Procerithium
Lyosoma
Corbula
Cercomya
Corbicellopsis

FIGURE 7—DCA sample scores, with convex hull around each stratigraphic unit. Centroid of each unit is indicated by position of unit name (CS: Canyon Springs Member; GS: Gypsum Spring Formation; HU: Hulett Member; RA: Redwater Shale *Camptonectes*; RM: Redwater Shale mud; RN: Redwater Shale concretions; RO: Redwater Shale oyster; SB: Stockade Beaver Shale; WH: Windy Hill Sandstone).



4
3
2
1
0
DCA2
0
1
2
3
4
5
DCA1
RN
GS
SB
CS
HU
RM
RA
WH
RO

FIGURE 8—DCA species scores. See Table 3 for taxon codes.

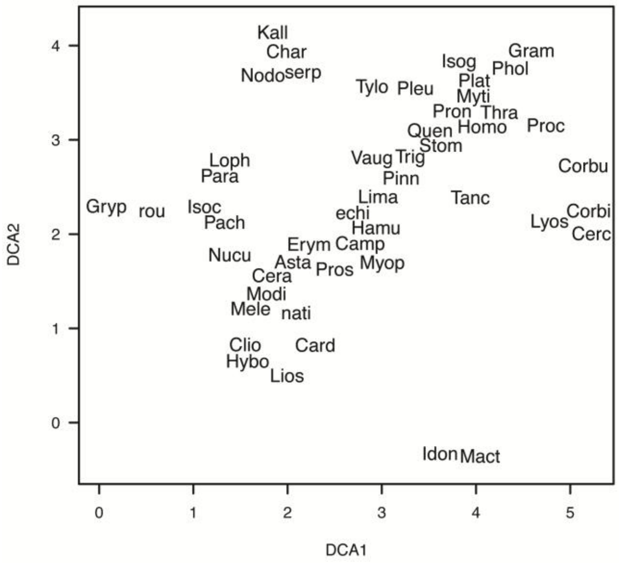

DCA2
DCA1
0
1
2
3
4
5
Kall
Char
Nodo
serp
Tylo
Pleu
Isog
Gram
Phol
Plat
Myti
Pron
Thra
Quen
Homo
Proc
Stom
Loph
Para
Vaug
Trig
Corbu
Pinn
Gryp
rou
Isoc
Pach
Lima
echi
Hamu
Tanc
Lyos
Corbi
Cerc
Nucu
Erym
Camp
Asta
Cera
Pros
Myop
Modi
Mele
nati
Clio
Card
Hybo
Lios
Idon
Mact

FIGURE 9—Detail of DCA sample scores for selected units with species scores shown by position of taxon names. A) Gypsum Spring Formation; B) Canyon Springs Member; C) Redwater Shale concretions; D) Windy Hill Sandstone.

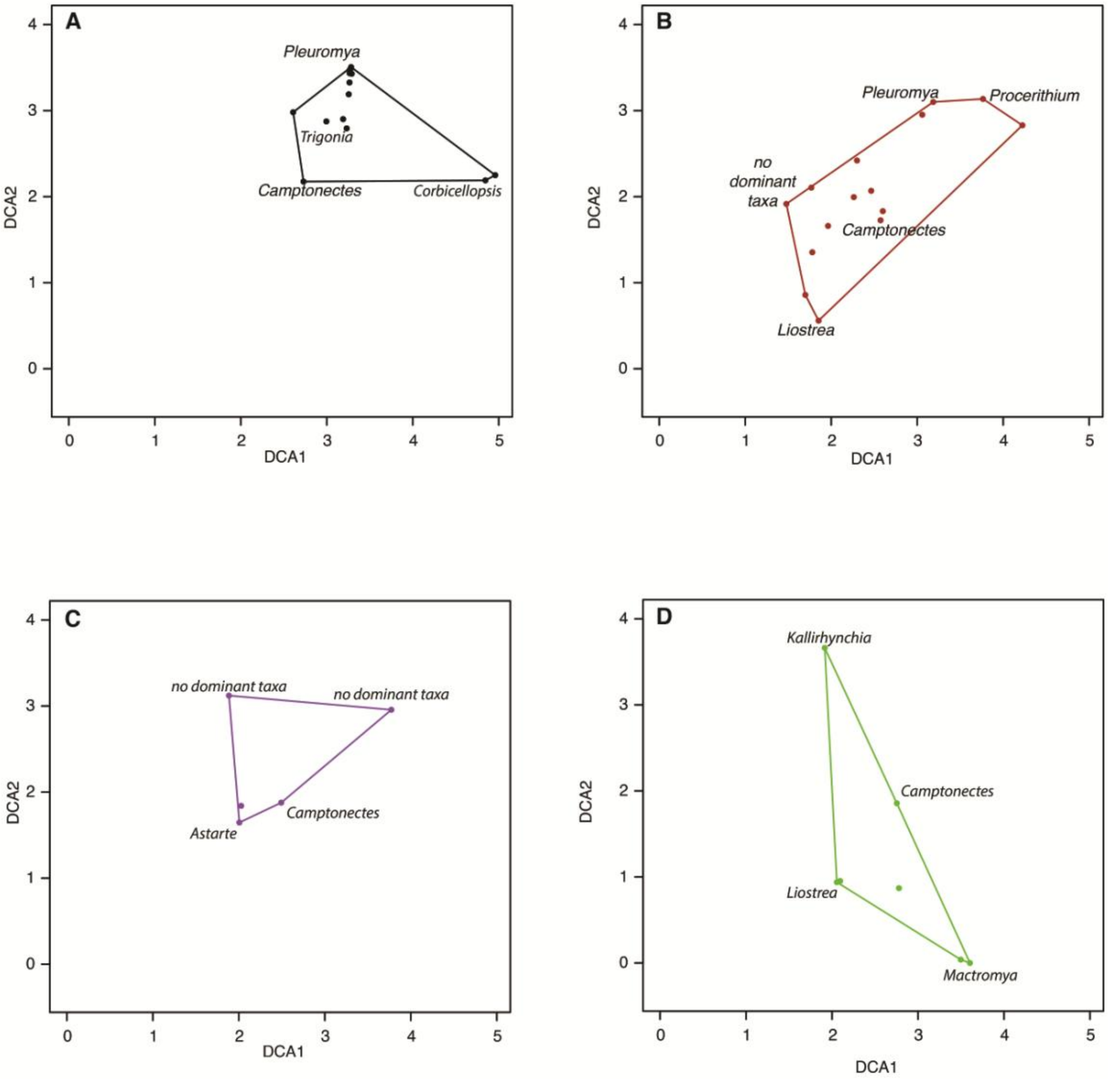
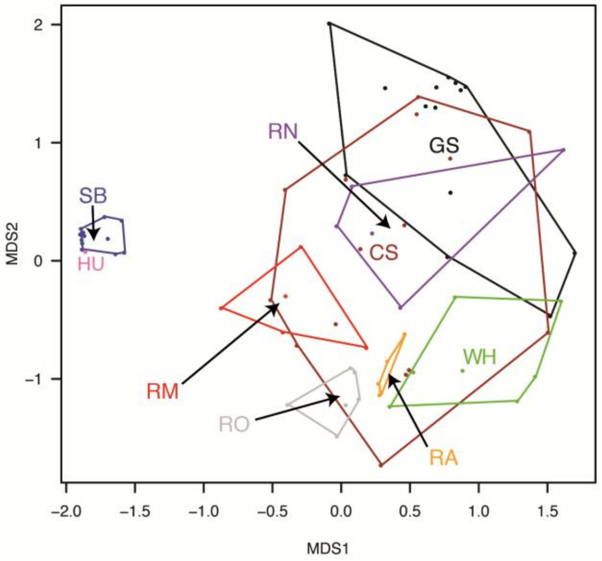

A
Pleuromya
Trigonia
Camptonectes
Corbicellopsis
B
Pleuromya
Procerithium
no dominant taxa
Camptonectes
Liostrea
C
no dominant taxa
no dominant taxa
Camptonectes
Astarte
D
Kallirhynchia
Camptonectes
Liostrea
Mactromya
DCA1
DCA2
0
1
2
3
4
5

FIGURE 10—nMDS sample scores, plotted as in Figure 7.



SB
HU
RN
GS
CS
RM
RO
RA
WH
MDS1
MDS2
−2.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
2
1
0
−1

FIGURE 11—nMDS species scores. See Table 3 for taxon codes.

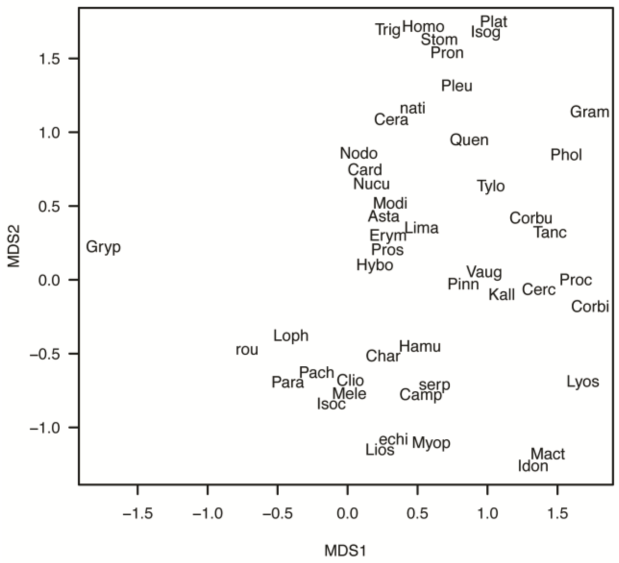

Plat
Trig
Homo
Isog
Stom
Pron
Pleu
nati
Cera
Gram
Quen
Nodo
Phol
Card
Nucu
Tylo
Modi
Asta
Corbu
Lima
Tanc
Erym
Pros
Gryp
Hybo
Vaug
Proc
Pinn
Cerc
Kall
Corbi
Loph
rou
Hamu
Char
Pach
Clio
serp
Para
Lyos
Mele
Camp
Isoc
echi
Myop
Lios
Mact
Idon
1.5
1.0
0.5
0.0
−0.5
−1.0
MDS2
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
MDS1

FIGURE 12—nMDS species scores coded by A) life habit and B) mobility.

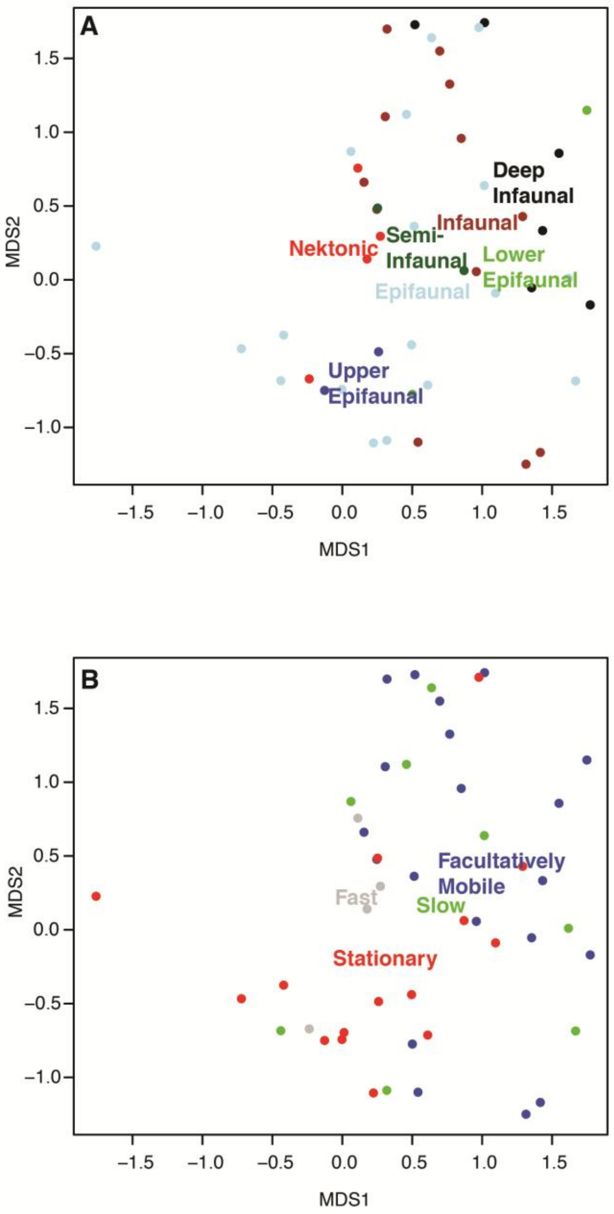
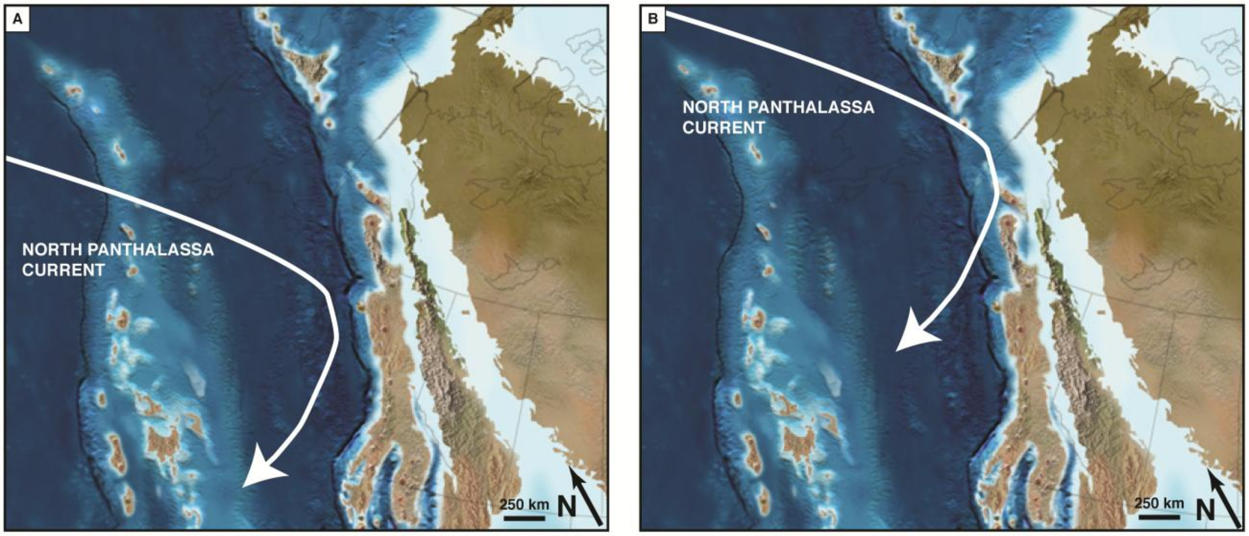

A
Deep
Infaunal
Infaunal
Nektonic
Semi-
Infaunal
Lower
Epifaunal
Epifaunal
Upper
Epifaunal
MDS1
MDS2
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
B
Facultatively
Mobile
Fast
Slow
Stationary

FIGURE 13—Jurassic proto-Pacific circulation as hypothesized by Arias (2008). A) Normal conditions preventing warmer water influence on the Seaway entranceway; B) Northward shift of the North Panthalassa Current allowing warm water influence on the Seaway entranceway (modified from Blakey, 2013).


A
NORTH PANTHALASSA CURRENT
250 km
N
B
NORTH PANTHALASSA CURRENT
250 km
N

APPENDIX A

LIST OF SUNDANCE SEAWAY TAXA

Actinastrea
Amberleya
Antrimpos
Arctocephalites
Astarte
Asteracanthus
Bombur
Camptonectes
Cardioceras
Caturus
Cercomya
Chariocrinus
Chondroceras
Coelastarte
Corbicellopsis
Corbula
Ctenostreon
Cylindrobullina
Eokainaster
Equisetum
Eryma
Gervillia
Globularia
Goliathiceras
Grammatodon
Grossouvria
Gryphaea
Hemicidaris
Holectypus
Homomya
Hulettia
Hybodus
Cucullaea
Isocrinus
Isocyprina
Isognomon
Kallirhynchia
Kepplerites
Lepidotes
Leptolepis
Lima
Liostrea
Lopha
Mactromya
Mecochirus
Megalneusaurus
Meleagrinella
Modiolus
Myopholas
Myophorella
Mytilus
Neridomus
Nerinea
Neritina
Nododelphinula
Normannites
Nucula
Ooliticia
Oxytoma
Pachyteuthis
Pantosaurus
Parastomechinus
Perisphinctes
Pholadomya
Pholidophorus
Pinna
Platymyoidea
Pleuromya
Pleurotomaria
Plicatula
Procerithium
Pronoella
Prorokia
Prososphinctes
Protocardia
Pseudomelania
Quenstedtia
Quenstedtoceras
Stemmatoceras
Stomechinus
Symmetrocapulus
Tancredia
Tatenectes
Tellina
Tethyaster
Thracia
Trigonia
Tylostoma
Unio
Vaugonia

APPENDIX B

CODE FOR DOWNLOADING PALEOBIOLOGY DATABASE OCCURRENCES

```
#! /bin/bash

rm results.txt

while read TAXON ; do

   curl
http://paleobiodb.org/data1.1/occs/list.txt?limit=all\&interval=Jurassic\&base_name=$TAXON\&show=coords,attr,loc,prot,time,strat,stratext,lith,lithext,geo,rem,ent,entname,crmod >> results.txt

done < taxa.txt
```

APPENDIX C

R CODE

```
library(vegan)

#Read matricies into R
AbundanceCounts<-read.table("AbundanceCounts.csv", header=TRUE,
sep=",", row.names=1) #Abundance Count
FaunaMatrix<-read.table("FaunaMatrix.csv", header=TRUE, sep=",",
row.names=1) #Faunal data matrix
SampleMatrix<-read.table("SampleMatrix.csv", header=TRUE, sep=",",
row.names=1) #Sample data matrix
TaxaList<-read.table("taxa.csv",header=TRUE,sep=",")
TaxaNames<-TaxaList[2]
PBDBresults<-read.table("results.csv",header=TRUE,sep=",",row.names=1)
PBDBtaxalist<-read.table("PBDBtaxalist.csv", header=FALSE,sep=",")
#TaxaList sorted by northernmost occurrence rank order
#Expanded Abundance Count dataset. Taxa from lit. review were added to
sample abundances. Abundances of all taxa not field in samples is zero.
PBDBwithFieldAbundances<-
read.table("AbundanceCountsWithPBDBTaxa.csv",header=TRUE, sep=",",
row.names=1)

#Editing/Culling of Matrix
#Replace abundances of all crinoid columnals (Isocrinus & Chariocrinus) with
1 individual
AbundanceCounts$Isoc[AbundanceCounts$Isoc>0]<-1
AbundanceCounts$Char[AbundanceCounts$Char>0]<-1

#Replace abundances of all round tube serpulid with 1 individual
AbundanceCounts$rou[AbundanceCounts$rou>0]<-1

#Remove samples under abundances of 20, remove corresponding samples
from sample matrix
AbundanceOver20<-AbundanceCounts[rowSums(AbundanceCounts)>20,]
SampleOver20<-SampleMatrix[rowSums(AbundanceCounts)>20,]

#Remove species without any occurrences after previous removal
AbundanceOver20<-cullMatrix(AbundanceOver20, minOccurrences=1,
minDiversity=1)
FaunaOver20<-FaunaMatrix[,colnames(FaunaMatrix) %in%
colnames(AbundanceOver20)]
```

```
#Percent Abundance transformation
AbundanceOver20.t1<-decostand(AbundanceOver20, method="total")

#Run an MDS of all data
AbundanceOver20.t1.MDS<-metaMDS(AbundanceOver20.t1,
distance="bray", k=3, trymax=100, autotransform=FALSE)
#3 dimensions, distance is bray-curtis, transformation is not taken as data
previous transformed
AbundanceOver20.t1.MDS.dataframe<-
as.data.frame(AbundanceOver20.t1.MDS$points)
#flips MDS1 and MDS2 to better match DCA axes,
AbundanceOver20.t1.MDS.dataframe$MDS1<- -
AbundanceOver20.t1.MDS.dataframe$MDS1
AbundanceOver20.t1.MDS.dataframe$MDS2<- -
AbundanceOver20.t1.MDS.dataframe$MDS2

#Run a DCA on all data
AbundanceOver20.t1.DCA<-decorana(AbundanceOver20.t1)

#Seperate Formations/Members/Groupings for later use
GypsumSpringAbundance<-AbundanceOver20[grep("GS-
*",rownames(AbundanceOver20.t1)),]
cullGypsumSpringAbundance<-
cullMatrix(GypsumSpringAbundance,minOccurrences=1)
GypsumSpringOnly<-as.data.frame(AbundanceOver20.t1[grep("GS-
*",rownames(AbundanceOver20.t1)),])
cullGypsumSpringOnly<-cullMatrix(GypsumSpringOnly, minOccurrences=1)
SampleGypsumSpringOnly<-as.data.frame(SampleOver20[grep("GS-
*",rownames(SampleOver20)),])
FaunaGypsumSpringOnly<-FaunaOver20[,colnames(FaunaOver20) %in%
colnames(cullGypsumSpringOnly)]

CanyonSpringsAbundance<-AbundanceOver20[grep("CS-
*",rownames(AbundanceOver20.t1)),]
cullCanyonSpringsAbundance<-
cullMatrix(CanyonSpringsAbundance,minOccurrences=1)
CanyonSpringsOnly<-as.data.frame(AbundanceOver20.t1[grep("CS-
*",rownames(AbundanceOver20.t1)),])
cullCanyonSpringsOnly<-cullMatrix(CanyonSpringsOnly, minOccurrences=1,
minDiversity=1)
```

```
SampleCanyonSpringsOnly<-as.data.frame(SampleOver20[grep("CS-
*",rownames(SampleOver20)),])
FaunaCanyonSpringsOnly<-FaunaOver20[,colnames(FaunaOver20) %in%
colnames(cullCanyonSpringsOnly)]

StockadeBeaverAbundance<-AbundanceOver20[grep("SB-
*",rownames(AbundanceOver20.t1)),]
cullStockadeBeaverAbundance<-
cullMatrix(StockadeBeaverAbundance,minOccurrences=1)
StockadeBeaverOnly<-as.data.frame(AbundanceOver20.t1[grep("SB-
*",rownames(AbundanceOver20.t1)),])
cullStockadeBeaverOnly<-cullMatrix(StockadeBeaverOnly,
minOccurrences=1)
SampleStockadeBeaverOnly<-as.data.frame(SampleOver20[grep("SB-
*",rownames(SampleOver20)),])
FaunaStockadeBeaverOnly<-FaunaOver20[,colnames(FaunaOver20) %in%
colnames(cullStockadeBeaverOnly)]

HulettAbundance<-AbundanceOver20[grep("HU-
*",rownames(AbundanceOver20.t1)),]
cullHulettAbundance<-cullMatrix(HulettAbundance,minOccurrences=1)
HulettOnly<-as.data.frame(AbundanceOver20.t1[grep("HU-
*",rownames(AbundanceOver20.t1)),])
SampleHulettOnly<-as.data.frame(SampleOver20[grep("HU-
*",rownames(SampleOver20)),])

RedwaterMudAbundance<-AbundanceOver20[grep("RM-
*",rownames(AbundanceOver20.t1)),]
cullRedwaterMudAbundance<-
cullMatrix(RedwaterMudAbundance,minOccurrences=1)
RedwaterMudOnly<-as.data.frame(AbundanceOver20.t1[grep("RM-
*",rownames(AbundanceOver20.t1)),])
cullRedwaterMudOnly<-cullMatrix(RedwaterMudOnly, minOccurrences=1)
SampleRedwaterMudOnly<-as.data.frame(SampleOver20[grep("RM-
*",rownames(SampleOver20)),])
FaunaRedwaterMudOnly<-FaunaOver20[,colnames(FaunaOver20) %in%
colnames(cullRedwaterMudOnly)]

RedwaterConcAbundance<-AbundanceOver20[grep("RN-
*",rownames(AbundanceOver20.t1)),]
cullRedwaterConcAbundance<-
cullMatrix(RedwaterConcAbundance,minOccurrences=1)
```

```
RedwaterConcOnly<-as.data.frame(AbundanceOver20.t1[grep("RN-
*",rownames(AbundanceOver20.t1)),])
cullRedwaterConcOnly<-cullMatrix(RedwaterConcOnly, minOccurrences=1)
SampleRedwaterConcOnly<-as.data.frame(SampleOver20[grep("RN-
*",rownames(SampleOver20)),])
FaunaRedwaterConcOnly<-FaunaOver20[,colnames(FaunaOver20) %in%
colnames(cullRedwaterConcOnly)]

RedwaterCampAbundance<-AbundanceOver20[grep("RA-
*",rownames(AbundanceOver20.t1)),]
cullRedwaterCampAbundance<-
cullMatrix(RedwaterCampAbundance,minOccurrences=1)
RedwaterCampOnly<-as.data.frame(AbundanceOver20.t1[grep("RA-
*",rownames(AbundanceOver20.t1)),])
cullRedwaterCampOnly<-cullMatrix(RedwaterCampOnly, minOccurrences=1)
SampleRedwaterCampOnly<-as.data.frame(SampleOver20[grep("RA-
*",rownames(SampleOver20)),])
FaunaRedwaterCampOnly<-FaunaOver20[,colnames(FaunaOver20) %in%
colnames(cullRedwaterCampOnly)]

RedwaterOysterAbundance<-AbundanceOver20[grep("RO-
*",rownames(AbundanceOver20.t1)),]
cullRedwaterOysterAbundance<-
cullMatrix(RedwaterOysterAbundance,minOccurrences=1)
RedwaterOysterOnly<-as.data.frame(AbundanceOver20.t1[grep("RO-
*",rownames(AbundanceOver20.t1)),])
cullRedwaterOysterOnly<-cullMatrix(RedwaterOysterOnly,
minOccurrences=1)
SampleRedwaterOysterOnly<-as.data.frame(SampleOver20[grep("RO-
*",rownames(SampleOver20)),])
FaunaRedwaterOysterOnly<-FaunaOver20[,colnames(FaunaOver20) %in%
colnames(cullRedwaterOysterOnly)]

WindyHillAbundance<-AbundanceOver20[grep("WH-
*",rownames(AbundanceOver20.t1)),]
cullWindyHillAbundance<-cullMatrix(WindyHillAbundance,minOccurrences=1)
WindyHillOnly<-as.data.frame(AbundanceOver20.t1[grep("WH-
*",rownames(AbundanceOver20.t1)),])
cullWindyHillOnly<-cullMatrix(WindyHillOnly, minOccurrences=1)
SampleWindyHillOnly<-as.data.frame(SampleOver20[grep("WH-
*",rownames(SampleOver20)),])
```

```
FaunaWindyHillOnly<-FaunaOver20[,colnames(FaunaOver20) %in%
colnames(cullWindyHillOnly)]

#Rank percent abundance for each Member
GypsumSpringAbundanceTotal<-
sort(colSums(cullGypsumSpringAbundance),decreasing=TRUE)
GypsumSpringAbundanceTotal<-
t(as.data.frame(GypsumSpringAbundanceTotal))
GypsumSpringPercentAbundance<-
t(decostand(GypsumSpringAbundanceTotal, method="total"))
GypsumSpringPercentAbundance

CanyonSpringsAbundanceTotal<-
sort(colSums(cullCanyonSpringsAbundance),decreasing=TRUE)
CanyonSpringsAbundanceTotal<-
t(as.data.frame(CanyonSpringsAbundanceTotal))
CanyonSpringsPercentAbundance<-
t(decostand(CanyonSpringsAbundanceTotal, method="total"))
CanyonSpringsPercentAbundance

StockadeBeaverAbundanceTotal<-
sort(colSums(cullStockadeBeaverAbundance),decreasing=TRUE)
StockadeBeaverAbundanceTotal<-
t(as.data.frame(StockadeBeaverAbundanceTotal))
StockadeBeaverPercentAbundance<-
t(decostand(StockadeBeaverAbundanceTotal, method="total"))
StockadeBeaverPercentAbundance

HulettAbundanceTotal<-
sort(colSums(cullHulettAbundance),decreasing=TRUE)
HulettAbundanceTotal<-t(as.data.frame(HulettAbundanceTotal))
HulettPercentAbundance<-t(decostand(HulettAbundanceTotal,
method="total"))
HulettPercentAbundance

RedwaterConcAbundanceTotal<-
sort(colSums(cullRedwaterConcAbundance),decreasing=TRUE)
RedwaterConcAbundanceTotal<-
t(as.data.frame(RedwaterConcAbundanceTotal))
RedwaterConcPercentAbundance<-
t(decostand(RedwaterConcAbundanceTotal, method="total"))
RedwaterConcPercentAbundance
```

```
RedwaterMudAbundanceTotal<-
sort(colSums(cullRedwaterMudAbundance),decreasing=TRUE)
RedwaterMudAbundanceTotal<-
t(as.data.frame(RedwaterMudAbundanceTotal))
RedwaterMudPercentAbundance<-t(decostand(RedwaterMudAbundanceTotal,
method="total"))
RedwaterMudPercentAbundance

RedwaterOysterAbundanceTotal<-
sort(colSums(cullRedwaterOysterAbundance),decreasing=TRUE)
RedwaterOysterAbundanceTotal<-
t(as.data.frame(RedwaterOysterAbundanceTotal))
RedwaterOysterPercentAbundance<-
t(decostand(RedwaterOysterAbundanceTotal, method="total"))
RedwaterOysterPercentAbundance

RedwaterCampAbundanceTotal<-
sort(colSums(cullRedwaterCampAbundance),decreasing=TRUE)
RedwaterCampAbundanceTotal<-
t(as.data.frame(RedwaterCampAbundanceTotal))
RedwaterCampPercentAbundance<-
t(decostand(RedwaterCampAbundanceTotal, method="total"))
RedwaterCampPercentAbundance

WindyHillAbundanceTotal<-
sort(colSums(cullWindyHillAbundance),decreasing=TRUE)
WindyHillAbundanceTotal<-t(as.data.frame(WindyHillAbundanceTotal))
WindyHillPercentAbundance<-t(decostand(WindyHillAbundanceTotal,
method="total"))
WindyHillPercentAbundance

#Plots
#set which MDS axes to use in plots
axisx=1 #x-axis plots MDS1
axisy=2 #y-axis plots MDS2

#Sample scores plotted by formation
GypsumSpring<- -
as.data.frame(AbundanceOver20.t1.MDS$points[grep("GS-
*",rownames(AbundanceOver20.t1.MDS$points)),])
```

```
CanyonSprings<- -
as.data.frame(AbundanceOver20.t1.MDS$points[grep("CS-
*",rownames(AbundanceOver20.t1.MDS$points)),])
StockadeBeaver<- -
as.data.frame(AbundanceOver20.t1.MDS$points[grep("SB-
*",rownames(AbundanceOver20.t1.MDS$points)),])
Hulett<- -as.data.frame(t((AbundanceOver20.t1.MDS$points[grep("HU-
*",rownames(AbundanceOver20.t1.MDS$points)),])))
row.names(Hulett)<-"HU01"
RedwaterCamp<- -
as.data.frame(AbundanceOver20.t1.MDS$points[grep("RA-
*",rownames(AbundanceOver20.t1.MDS$points)),])
RedwaterMud<- -as.data.frame(AbundanceOver20.t1.MDS$points[grep("RM-
*",rownames(AbundanceOver20.t1.MDS$points)),])
RedwaterConc<- -as.data.frame(AbundanceOver20.t1.MDS$points[grep("RN-
*",rownames(AbundanceOver20.t1.MDS$points)),])
RedwaterOyster<- -
as.data.frame(AbundanceOver20.t1.MDS$points[grep("RO-
*",rownames(AbundanceOver20.t1.MDS$points)),])
WindyHill<- -as.data.frame(AbundanceOver20.t1.MDS$points[grep("WH-
*",rownames(AbundanceOver20.t1.MDS$points)),])

windows()
plot(AbundanceOver20.t1.MDS.dataframe$MDS1,
AbundanceOver20.t1.MDS.dataframe$MDS2, xlab="MDS1", ylab="MDS2",
type="n", las=1, main="Sample Scores- Formation")
points(GypsumSpring$MDS1, GypsumSpring$MDS2, pch=16, col="black")
points(CanyonSprings$MDS1, CanyonSprings$MDS2, pch=16, col="brown")
points(StockadeBeaver$MDS1, StockadeBeaver$MDS2, pch=16, col="blue")
points(Hulett$MDS1, Hulett$MDS2, pch=16, col="hot pink")
points(RedwaterCamp$MDS1, RedwaterCamp$MDS2, pch=16, col="orange")
points(RedwaterMud$MDS1, RedwaterMud$MDS2, pch=16, col="red")
points(RedwaterConc$MDS1, RedwaterConc$MDS2, pch=16, col="purple")
points(RedwaterOyster$MDS1, RedwaterOyster$MDS2, pch=16, col="grey")
points(WindyHill$MDS1, WindyHill$MDS2, pch=16, col="green")

centerx<-mean(GypsumSpring[,axisx])
centery<-mean(GypsumSpring[,axisy])
text(centerx, centery, labels="GS", cex=1, col="black")
polypoints<-chull(GypsumSpring)
polypoints<-c(polypoints, polypoints[1])
lines(GypsumSpring[polypoints,], col="black")
```

```
centerx<-mean(CanyonSprings[,axisx])
centery<-mean(CanyonSprings[,axisy])
text(centerx, centery, labels="CS", cex=1, col="brown")
polypoints<-chull(CanyonSprings)
polypoints<-c(polypoints, polypoints[1])
lines(CanyonSprings[polypoints,], col="brown")

centerx<-mean(StockadeBeaver[,axisx])
centery<-mean(StockadeBeaver[,axisy])
text(centerx, centery, labels="SB", cex=1, col="blue")
polypoints<-chull(StockadeBeaver)
polypoints<-c(polypoints, polypoints[1])
lines(StockadeBeaver[polypoints,], col="blue")

text(Hulett$MDS1, Hulett$MDS2, labels="Hu", cex=1, col="hot pink")

centerx<-mean(RedwaterCamp[,axisx])
centery<-mean(RedwaterCamp[,axisy])
text(centerx, centery, labels="RA", cex=1, col="orange")
polypoints<-chull(RedwaterCamp)
polypoints<-c(polypoints, polypoints[1])
lines(RedwaterCamp[polypoints,], col="orange")

centerx<-mean(RedwaterMud[,axisx])
centery<-mean(RedwaterMud[,axisy])
text(centerx, centery, labels="RM", cex=1, col="red")
polypoints<-chull(RedwaterMud)
polypoints<-c(polypoints, polypoints[1])
lines(RedwaterMud[polypoints,], col="red")

centerx<-mean(RedwaterConc[,axisx])
centery<-mean(RedwaterConc[,axisy])
text(centerx, centery, labels="RN", cex=1, col="purple")
polypoints<-chull(RedwaterConc)
polypoints<-c(polypoints, polypoints[1])
lines(RedwaterConc[polypoints,], col="purple")

centerx<-mean(RedwaterOyster[,axisx])
centery<-mean(RedwaterOyster[,axisy])
text(centerx, centery, labels="RO", cex=1, col="grey")
polypoints<-chull(RedwaterOyster)
```

```
polypoints<-c(polypoints, polypoints[1])
lines(RedwaterOyster[polypoints,], col="grey")

centerx<-mean(WindyHill[,axisx])
centery<-mean(WindyHill[,axisy])
text(centerx, centery, labels="WH", cex=1, col="green")
polypoints<-chull(WindyHill)
polypoints<-c(polypoints, polypoints[1])
lines(WindyHill[polypoints,], col="green")

#Species Scores
windows()
plot(-AbundanceOver20.t1.MDS$species,type="n", xlab="MDS1",
ylab="MDS2", las=1, main="Species Scores")
text(-AbundanceOver20.t1.MDS$species,
labels=rownames(AbundanceOver20.t1.MDS$species), cex=0.75)


#Samples by facies
OpnShallowSub<-
AbundanceOver20.t1.MDS.dataframe[grep("Open",t(SampleOver20[,colname
s(SampleOver20)=="Facies"])),]
RestShallowSub<-
AbundanceOver20.t1.MDS.dataframe[grep("Restricted",t(SampleOver20[,col
names(SampleOver20)=="Facies"])),]
Offshore<-
AbundanceOver20.t1.MDS.dataframe[grep("Offshore",t(SampleOver20[,colna
mes(SampleOver20)=="Facies"])),]
Shell<-
AbundanceOver20.t1.MDS.dataframe[grep("Shell",t(SampleOver20[,colname
s(SampleOver20)=="Facies"])),]
Tidal<-
AbundanceOver20.t1.MDS.dataframe[grep("Tidal",t(SampleOver20[,colname
s(SampleOver20)=="Facies"])),]

windows()
plot(AbundanceOver20.t1.MDS.dataframe[,axisx],AbundanceOver20.t1.MDS.
dataframe[,axisy],type="n", las=1, main="Sample Scores by facies")
points(OpnShallowSub[,axisx], OpnShallowSub[,axisy], pch=16, col="red")
points(RestShallowSub[,axisx], RestShallowSub[,axisy], pch=16, col="blue")
points(Offshore[,axisx], Offshore[,axisy], pch=16, col="black")
points(Shell[,axisx], Shell[,axisy], pch=16, col="grey")
```

```
points(Tidal[,axisx], Tidal[,axisy], pch=16, col="green")

centerx<-mean(OpnShallowSub[,axisx])
centery<-mean(OpnShallowSub[,axisy])
text(centerx, centery, labels="OSS", col="red")
polypoints<-chull(OpnShallowSub)
polypoints<-c(polypoints, polypoints[1])
lines(OpnShallowSub[polypoints,], col="red")

centerx<-mean(RestShallowSub[,axisx])
centery<-mean(RestShallowSub[,axisy])
text(centerx, centery, labels="RSS", col="blue")
polypoints<-chull(RestShallowSub)
polypoints<-c(polypoints, polypoints[1])
lines(RestShallowSub[polypoints,], col="blue")

centerx<-mean(Offshore[,axisx])
centery<-mean(Offshore[,axisy])
text(centerx, centery, labels="Off", col="black")
polypoints<-chull(Offshore)
polypoints<-c(polypoints, polypoints[1])
lines(Offshore[polypoints,], col="black")

centerx<-mean(Shell[,axisx])
centery<-mean(Shell[,axisy])
text(centerx, centery, labels="Shell", col="grey")
polypoints<-chull(Shell)
polypoints<-c(polypoints, polypoints[1])
lines(Shell[polypoints,], col="grey")

centerx<-mean(Tidal[,axisx])
centery<-mean(Tidal[,axisy])
text(centerx, centery, labels="Tidal", col="green")
polypoints<-chull(Tidal)
polypoints<-c(polypoints, polypoints[1])
lines(Tidal[polypoints,], col="green")

#Species scores plotted by mobility
FacMobile<-
which(FaunaOver20[which(rownames(FaunaOver20)=="Mobility"),]=="Facul
tatively mobile")
```

```
Fast<-
which(FaunaOver20[which(rownames(FaunaOver20)=="Mobility"),]=="Fast
moving")
Stationary<-
which(FaunaOver20[which(rownames(FaunaOver20)=="Mobility"),]=="Stati
onary")
Slow<-
which(FaunaOver20[which(rownames(FaunaOver20)=="Mobility"),]=="Slow
moving")

windows()
plot(-AbundanceOver20.t1.MDS$species,type="n", las=1, main="Species
Scores by Mobility")
points(-AbundanceOver20.t1.MDS$species[FacMobile,], pch=16, col="blue")
points(-AbundanceOver20.t1.MDS$species[Fast,], pch=16, col="grey")
points(-AbundanceOver20.t1.MDS$species[Stationary,], pch=16, col="red")
points(-AbundanceOver20.t1.MDS$species[Slow,], pch=16, col="green")

centerx<- -mean(AbundanceOver20.t1.MDS$species[FacMobile,axisx])
centery<- -mean(AbundanceOver20.t1.MDS$species[FacMobile,axisy])
text(centerx, centery, labels="FacMob", cex=1, col="blue")

centerx<- -mean(AbundanceOver20.t1.MDS$species[Fast,axisx])
centery<- -mean(AbundanceOver20.t1.MDS$species[Fast,axisy])
text(centerx, centery, labels="Fast", cex=1, col="grey")

centerx<- -mean(AbundanceOver20.t1.MDS$species[Stationary,axisx])
centery<- -mean(AbundanceOver20.t1.MDS$species[Stationary,axisy])
text(centerx, centery, labels="Stationary", cex=1, col="red")

centerx<- -mean(AbundanceOver20.t1.MDS$species[Slow,axisx])
centery<- -mean(AbundanceOver20.t1.MDS$species[Slow,axisy])
text(centerx, centery, labels="Slow", cex=1, col="green")

#Species scores plotted by life habit
#LifeHabit
DeepIn<-which(FaunaOver20[which(rownames(FaunaOver20)=="Life
Habit"),]=="Deep infaunal")
In<-which(FaunaOver20[which(rownames(FaunaOver20)=="Life
Habit"),]=="Infaunal")
SemiIn<-which(FaunaOver20[which(rownames(FaunaOver20)=="Life
Habit"),]=="Semi-infaunal")
```

```
LowEpi<-which(FaunaOver20[which(rownames(FaunaOver20)=="Life Habit"),]=="Low-level epifaunal")
Epi<-which(FaunaOver20[which(rownames(FaunaOver20)=="Life Habit"),]=="Epifaunal")
UpEpi<-which(FaunaOver20[which(rownames(FaunaOver20)=="Life Habit"),]=="Upper-level epifaunal")
Nekt<-which(FaunaOver20[which(rownames(FaunaOver20)=="Life Habit"),]=="Nektonic")
Boring<-which(FaunaOver20[which(rownames(FaunaOver20)=="Life Habit"),]=="Boring")

windows()
plot(-AbundanceOver20.t1.MDS$species,type="n", las=1, main="Species Scores by Life Habit")
points(-AbundanceOver20.t1.MDS$species[DeepIn,], pch=16, col="black")
points(-AbundanceOver20.t1.MDS$species[In,], pch=16, col="brown")
points(-AbundanceOver20.t1.MDS$species[SemiIn,], pch=16, col="dark green")
points(-AbundanceOver20.t1.MDS$species[LowEpi,], pch=16, col="green")
points(-AbundanceOver20.t1.MDS$species[Epi,], pch=16, col="light blue")
points(-AbundanceOver20.t1.MDS$species[UpEpi,], pch=16, col="blue")
points(-AbundanceOver20.t1.MDS$species[Nekt,], pch=16, col="red")

centerx<- -mean(AbundanceOver20.t1.MDS$species[DeepIn,axisx])
centery<- -mean(AbundanceOver20.t1.MDS$species[DeepIn,axisy])
text(centerx, centery, labels="DeepIn", cex=1, col="black")

centerx<- -mean(AbundanceOver20.t1.MDS$species[In,axisx])
centery<- -mean(AbundanceOver20.t1.MDS$species[In,axisy])
text(centerx, centery, labels="In", cex=1, col="brown")

centerx<- -mean(AbundanceOver20.t1.MDS$species[SemiIn,axisx])
centery<- -mean(AbundanceOver20.t1.MDS$species[SemiIn,axisy])
text(centerx, centery, labels="SemiIn", cex=1, col="dark green")

centerx<- -mean(AbundanceOver20.t1.MDS$species[LowEpi,axisx])
centery<- -mean(AbundanceOver20.t1.MDS$species[LowEpi,axisy])
text(centerx, centery, labels="LowEpi", cex=1, col="green")

centerx<- -mean(AbundanceOver20.t1.MDS$species[Epi,axisx])
centery<- -mean(AbundanceOver20.t1.MDS$species[Epi,axisy])
text(centerx, centery, labels="Epi", cex=1, col="light blue")
```

```
centerx<- -mean(AbundanceOver20.t1.MDS$species[UpEpi,axisx])
centery<- -mean(AbundanceOver20.t1.MDS$species[UpEpi,axisy])
text(centerx, centery, labels="UpEpi", cex=1, col="blue")

centerx<- -mean(AbundanceOver20.t1.MDS$species[Nekt,axisx])
centery<- -mean(AbundanceOver20.t1.MDS$species[Nekt,axisy])
text(centerx, centery, labels="Nekt", cex=1, col="red")

#DCA Sample
GypsumSpring<-AbundanceOver20.t1.DCA$rproj[grep("GS-
*",rownames(AbundanceOver20.t1.MDS$points)),]
CanyonSprings<-AbundanceOver20.t1.DCA$rproj[grep("CS-
*",rownames(AbundanceOver20.t1.MDS$points)),]
StockadeBeaver<-AbundanceOver20.t1.DCA$rproj[grep("SB-
*",rownames(AbundanceOver20.t1.MDS$points)),]
Hulett<-AbundanceOver20.t1.DCA$rproj[grep("HU-
*",rownames(AbundanceOver20.t1.MDS$points)),]
RedConc<-AbundanceOver20.t1.DCA$rproj[grep("RN-
*",rownames(AbundanceOver20.t1.MDS$points)),]
RedMud<-AbundanceOver20.t1.DCA$rproj[grep("RM-
*",rownames(AbundanceOver20.t1.MDS$points)),]
RedOyster<-AbundanceOver20.t1.DCA$rproj[grep("RO-
*",rownames(AbundanceOver20.t1.MDS$points)),]
RedCamp<-AbundanceOver20.t1.DCA$rproj[grep("RA-
*",rownames(AbundanceOver20.t1.MDS$points)),]
WindyHill<-AbundanceOver20.t1.DCA$rproj[grep("WH-
*",rownames(AbundanceOver20.t1.MDS$points)),]

windows()
plot(AbundanceOver20.t1.DCA$rproj, type="n", las=1, main="DCA of all
samples by unit", asp=1)
points(GypsumSpring[,axisx],GypsumSpring[,axisy],pch=16, col="black")
points(CanyonSprings[,axisx],CanyonSprings[,axisy],pch=16, col="brown")
points(StockadeBeaver[,axisx],StockadeBeaver[,axisy],pch=16, col="blue")
points(Hulett[axisx],Hulett[axisy],pch=16, col="hotpink")
points(RedConc[,axisx],RedConc[,axisy],pch=16, col="purple")
points(RedMud[,axisx],RedMud[,axisy],pch=16, col="red")
points(RedOyster[,axisx],RedOyster[,axisy],pch=16, col="darkgrey")
points(RedCamp[,axisx],RedCamp[,axisy],pch=16, col="orange")
points(WindyHill[,axisx],WindyHill[,axisy],pch=16, col="green")
```

```
centerx<-mean(GypsumSpring[,axisx])
centery<-mean(GypsumSpring[,axisy])
text(centerx, centery, labels="G.S.", cex=1, col="black")
polypoints<-chull(GypsumSpring)
polypoints<-c(polypoints, polypoints[1])
lines(GypsumSpring[polypoints,], col="black")

centerx<-mean(CanyonSprings[,axisx])
centery<-mean(CanyonSprings[,axisy])
text(centerx, centery, labels="C.S.", cex=1, col="brown")
polypoints<-chull(CanyonSprings)
polypoints<-c(polypoints, polypoints[1])
lines(CanyonSprings[polypoints,], col="brown")

centerx<-mean(StockadeBeaver[,axisx])
centery<-mean(StockadeBeaver[,axisy])
text(centerx, centery, labels="S.B.", cex=1, col="blue")
polypoints<-chull(StockadeBeaver)
polypoints<-c(polypoints, polypoints[1])
lines(StockadeBeaver[polypoints,], col="blue")

text(Hulett[axisx], Hulett[axisy], labels="Hu", cex=0.5, col="hot pink")

centerx<-mean(RedCamp[,axisx])
centery<-mean(RedCamp[,axisy])
text(centerx, centery, labels="R.W.-Camp", cex=1, col="orange")
polypoints<-chull(RedCamp)
polypoints<-c(polypoints, polypoints[1])
lines(RedCamp[polypoints,], col="orange")

centerx<-mean(RedMud[,axisx])
centery<-mean(RedMud[,axisy])
text(centerx, centery, labels="R.W.-Mud", cex=1, col="red")
polypoints<-chull(RedMud)
polypoints<-c(polypoints, polypoints[1])
lines(RedMud[polypoints,], col="red")

centerx<-mean(RedConc[,axisx])
centery<-mean(RedConc[,axisy])
text(centerx, centery, labels="R.W.-Conc", cex=1, col="purple")
polypoints<-chull(RedConc)
polypoints<-c(polypoints, polypoints[1])
```

```
lines(RedConc[polypoints,], col="purple")

centerx<-mean(RedOyster[,axisx])
centery<-mean(RedOyster[,axisy])
text(centerx, centery, labels="R.W.-Oyster", cex=1, col="darkgrey")
polypoints<-chull(RedOyster)
polypoints<-c(polypoints, polypoints[1])
lines(RedOyster[polypoints,], col="darkgrey")

centerx<-mean(WindyHill[,axisx])
centery<-mean(WindyHill[,axisy])
text(centerx, centery, labels="W.H.", cex=1, col="green")
polypoints<-chull(WindyHill)
polypoints<-c(polypoints, polypoints[1])
lines(WindyHill[polypoints,], col="green")

#DCA Species
windows()
plot(AbundanceOver20.t1.DCA$cproj, type="n", las=1, main="DCA of
species scores", asp=1)
text(AbundanceOver20.t1.DCA$cproj,
labels=rownames(AbundanceOver20.t1.DCA$cproj),cex=0.75)

#DCA Mobility
Stationary<-
AbundanceOver20.t1.DCA$cproj[grep("Stat",t(FaunaOver20[rownames(Faun
aOver20)=="Mobility",])),]
FacMob<-
AbundanceOver20.t1.DCA$cproj[grep("Facul",t(FaunaOver20[rownames(Fau
naOver20)=="Mobility",])),]
Fast<-
AbundanceOver20.t1.DCA$cproj[grep("Fast",t(FaunaOver20[rownames(Faun
aOver20)=="Mobility",])),]
Slow<-
AbundanceOver20.t1.DCA$cproj[grep("Slow",t(FaunaOver20[rownames(Faun
aOver20)=="Mobility",])),]

windows()
plot(AbundanceOver20.t1.DCA$cproj, type="n", las=1, main="DCA Species",
asp=1)
points(Stationary[,axisx],Stationary[,axisy],pch=16,col="red")
points(FacMob[,axisx],FacMob[,axisy],pch=16,col="blue")
```

```
points(Fast[,axisx],Fast[,axisy],pch=16,col="grey")
points(Slow[,axisx],Slow[,axisy],pch=16,col="green")

centerx<-mean(Stationary[,axisx])
centery<-mean(Stationary[,axisy])
text(centerx, centery, labels="Stationary", cex=1, col="red")

centerx<-mean(FacMob[,axisx])
centery<-mean(FacMob[,axisy])
text(centerx, centery, labels="FacMob", cex=1, col="blue")

centerx<-mean(Fast[,axisx])
centery<-mean(Fast[,axisy])
text(centerx, centery, labels="Fast", cex=1, col="grey")

centerx<-mean(Slow[,axisx])
centery<-mean(Slow[,axisy])
text(centerx, centery, labels="Slow", cex=1, col="green")

#DCA Life Habit
DeepIn<-AbundanceOver20.t1.DCA$cproj[grep("Deep",t(FaunaOver20[rownames(FaunaOver20)=="Life Habit",])),]
In<-AbundanceOver20.t1.DCA$cproj[grep("In",t(FaunaOver20[rownames(FaunaOver20)=="Life Habit",])),]
SemiIn<-AbundanceOver20.t1.DCA$cproj[grep("Semi",t(FaunaOver20[rownames(FaunaOver20)=="Life Habit",])),]
LowEpi<-AbundanceOver20.t1.DCA$cproj[grep("Low",t(FaunaOver20[rownames(FaunaOver20)=="Life Habit",])),]
Epi<-AbundanceOver20.t1.DCA$cproj[grep("Epi",t(FaunaOver20[rownames(FaunaOver20)=="Life Habit",])),]
UpEpi<-AbundanceOver20.t1.DCA$cproj[grep("Upper",t(FaunaOver20[rownames(FaunaOver20)=="Life Habit",])),]
Nekt<-AbundanceOver20.t1.DCA$cproj[grep("Nekt",t(FaunaOver20[rownames(FaunaOver20)=="Life Habit",])),]
```

```
Boring<-AbundanceOver20.t1.DCA$cproj[grep("Boring",t(FaunaOver20[rownames(FaunaOver20)=="Life Habit",])),]

windows()
plot(AbundanceOver20.t1.DCA$cproj, type="n", las=1, main="DCA Species", asp=1)
points(DeepIn[,axisx],DeepIn[,axisy],pch=16,col="black")
points(In[,axisx],In[,axisy],pch=16,col="brown")
points(SemiIn[,axisx],SemiIn[,axisy],pch=16,col="darkgreen")
points(LowEpi[,axisx],LowEpi[,axisy],pch=16,col="green")
points(Epi[,axisx],Epi[,axisy],pch=16,col="blue")
points(UpEpi[,axisx],UpEpi[,axisy],pch=16,col="lightblue")
points(Nekt[,axisx],Nekt[,axisy],pch=16,col="red")
points(Boring[axisx],Boring[axisy],pch=16,col="purple")

centerx<-mean(DeepIn[,axisx])
centery<-mean(DeepIn[,axisy])
text(centerx, centery, labels="DeepIn", cex=1, col="black")

centerx<-mean(In[,axisx])
centery<-mean(In[,axisy])
text(centerx, centery, labels="In", cex=1, col="brown")

centerx<-mean(SemiIn[,axisx])
centery<-mean(SemiIn[,axisy])
text(centerx, centery, labels="SemiIn", cex=1, col="darkgreen")

centerx<-mean(LowEpi[,axisx])
centery<-mean(LowEpi[,axisy])
text(centerx, centery, labels="LowEpi", cex=1, col="green")

centerx<-mean(Epi[,axisx])
centery<-mean(Epi[,axisy])
text(centerx, centery, labels="Epi", cex=1, col="blue")

centerx<-mean(UpEpi[,axisx])
centery<-mean(UpEpi[,axisy])
text(centerx, centery, labels="UpEpi", cex=1, col="lightblue")

centerx<-mean(Nekt[,axisx])
centery<-mean(Nekt[,axisy])
```

```
text(centerx, centery, labels="Nekt", cex=1, col="red")

centerx<-(Boring[axisx])
centery<-(Boring[axisy])
text(centerx, centery, labels="Boring", cex=0.5, col="purple")

#Feeding Type
Suspension<-
AbundanceOver20.t1.DCA$cproj[grep("Susp",t(FaunaOver20[rownames(Fau
naOver20)=="Feeding Type",])),]
Deposit<-
AbundanceOver20.t1.DCA$cproj[grep("Depos",t(FaunaOver20[rownames(Fa
unaOver20)=="Feeding Type",])),]
Graze<-
AbundanceOver20.t1.DCA$cproj[grep("Graze",t(FaunaOver20[rownames(Fau
naOver20)=="Feeding Type",])),]
Carnivore<-
AbundanceOver20.t1.DCA$cproj[grep("Carni",t(FaunaOver20[rownames(Fau
naOver20)=="Feeding Type",])),]
Chemo<-
AbundanceOver20.t1.DCA$cproj[grep("Chemo",t(FaunaOver20[rownames(Fa
unaOver20)=="Feeding Type",])),]

windows()
plot(AbundanceOver20.t1.DCA$cproj, type="n", las=1, main="DCA Species",
asp=1)
points(Suspension[,axisx],Suspension[,axisy],pch=16,col="black")
points(Deposit[,axisx],Deposit[,axisy],pch=16,col="brown")
points(Graze[,axisx],Graze[,axisy],pch=16,col="green")
points(Carnivore[,axisx],Carnivore[,axisy],pch=16,col="red")
points(Chemo[axisx],Chemo[axisy],pch=16,col="orange")

centerx<-mean(Suspension[,axisx])
centery<-mean(Suspension[,axisy])
text(centerx, centery, labels="Suspension", cex=1, col="black")

centerx<-mean(Deposit[,axisx])
centery<-mean(Deposit[,axisy])
text(centerx, centery, labels="Deposit", cex=1, col="brown")

centerx<-mean(Graze[,axisx])
centery<-mean(Graze[,axisy])
```

```
text(centerx, centery, labels="Grazer", cex=1, col="green")

centerx<-mean(Carnivore[,axisx])
centery<-mean(Carnivore[,axisy])
text(centerx, centery, labels="Carnivore", cex=1, col="red")

centerx<-(Chemo[axisx])
centery<-(Chemo[axisy])
text(centerx, centery, labels="Chemo", cex=0.5, col="orange")

#Bubble plot
SpeciesDCA<-AbundanceOver20.t1.DCA$cproj
FaunaRotate<-t(FaunaOver20)
FaunaDCA<-as.data.frame(cbind(FaunaRotate,SpeciesDCA))

DCA1.Order<-order(FaunaDCA$DCA1)
FaunaDCA.by.DCA1.Rank<-FaunaDCA[DCA1.Order,]
AbundanceOver20.t1.by.DCA1.Rank<-AbundanceOver20.t1[,DCA1.Order]

BubbleMatrix<-matrix(nrow=0,ncol=3)
Sample=2
Taxa=1
bubbleweight=3

for(i in 1:nrow(AbundanceOver20.t1.by.DCA1.Rank)) {
        for(j in 1:ncol(AbundanceOver20.t1.by.DCA1.Rank)) {
                temprow<-matrix(nrow=1,ncol=3)
                temprow[1,Taxa]=j
                temprow[1,Sample]=i

        temprow[1,bubbleweight]=AbundanceOver20.t1.by.DCA1.Rank[i,j]
                BubbleMatrix<-rbind (BubbleMatrix,temprow)
        }
}

ListOfTaxa<-
FaunaDCA.by.DCA1.Rank[,colnames(FaunaDCA.by.DCA1.Rank)=="Genus"]
ListOfSamples<-rownames(AbundanceOver20.t1.by.DCA1.Rank)

windows()
```

```
plot(BubbleMatrix[,Taxa],BubbleMatrix[,Sample],type="n",las=1,
main="Abundances of taxa in samples", xlab="Taxa", ylab="Samples",
xaxt="n", yaxt="n")
axis(side=1,at=1:length(ListOfTaxa),labels=ListOfTaxa, cex.axis=0.5, las=3)
axis(side=2,at=1:length(ListOfSamples),labels=ListOfSamples,cex.axis=0.5,
las=1)
points(BubbleMatrix[,Taxa],BubbleMatrix[,Sample],pch=16,cex=2*BubbleMa
trix[,bubbleweight])
abline(h=max(grep("GS",rownames(AbundanceOver20.t1)))+0.5)
abline(h=max(grep("CS",rownames(AbundanceOver20.t1)))+0.5)
abline(h=max(grep("SB",rownames(AbundanceOver20.t1)))+0.5)
abline(h=max(grep("HU",rownames(AbundanceOver20.t1)))+0.5)
abline(h=max(grep("RN",rownames(AbundanceOver20.t1)))+0.5)
abline(h=max(grep("RM",rownames(AbundanceOver20.t1)))+0.5)
abline(h=max(grep("RO",rownames(AbundanceOver20.t1)))+0.5)
abline(h=max(grep("RA",rownames(AbundanceOver20.t1)))+0.5)

text(x=30,y=median(grep("GS",rownames(AbundanceOver20.t1))),labels="
GS")
text(x=30,y=median(grep("CS",rownames(AbundanceOver20.t1))),labels="C
S")
text(x=30,y=median(grep("SB",rownames(AbundanceOver20.t1))),labels="S
B")
text(x=30,y=median(grep("HU",rownames(AbundanceOver20.t1))),labels="
HU")
text(x=30,y=median(grep("RN",rownames(AbundanceOver20.t1))),labels="
RN")
text(x=30,y=median(grep("RM",rownames(AbundanceOver20.t1))),labels="
RM")
text(x=30,y=median(grep("RO",rownames(AbundanceOver20.t1))),labels="
RO")
text(x=30,y=median(grep("RA",rownames(AbundanceOver20.t1))),labels="R
A")
text(x=30,y=median(grep("WH",rownames(AbundanceOver20.t1))),labels="
WH")

#Evenness and Diversity calculations
SimpsonsD<-matrix(ncol=3,nrow=0)

for(i in 1:nrow(AbundanceOver20)){
        RowSum<-sum(AbundanceOver20[i,])
        SampleProportions<-matrix(ncol=1,nrow=0)
```

```
        for(j in 1:ncol(AbundanceOver20)){
                TaxaProportion<-AbundanceOver20[i,j]/RowSum
                TaxaProportion.sqrd<-TaxaProportion^2
                SampleProportions<-
rbind(SampleProportions,TaxaProportion.sqrd)
        }
        D<-colSums(SampleProportions)
        D.1<-(1-D)
        DiversityRow<-AbundanceOver20[i,]
        DiversityRow[which(DiversityRow[]>0)]<-1
        DiversityRowSum<-sum(DiversityRow)
        SampleName<-rownames(AbundanceOver20[i,])
        temprow<-c(SampleName,D.1,DiversityRowSum)
        SimpsonsD<-rbind(SimpsonsD,temprow)
}
SamplesList<-c(SimpsonsD[,1])
rownames(SimpsonsD)<-c(SamplesList)
SimpsonsD<-SimpsonsD[,-1]
SimpsonsD<-as.data.frame(SimpsonsD)
SimpsonsD

#Abundance and Occupancy Plot
SeawayEntranceSouth=54
#Edit PBDB Matrix
#Replace abundances of all crinoid columnals (Isocrinus & Chariocrinus) with
1 individual
PBDBwithFieldAbundances$Isocrinus[PBDBwithFieldAbundances$Isocrinus>0
]<-1
PBDBwithFieldAbundances$Chariocrinus[PBDBwithFieldAbundances$Chariocri
nus>0]<-1

#Remove samples under abundances of 20, remove corresponding samples
from sample matrix
PBDB.AbundanceOver20<-
PBDBwithFieldAbundances[rowSums(PBDBwithFieldAbundances)>20,]

#PercentAbundance transformation
PBDB.AbundanceOver20.t1<-decostand(PBDB.AbundanceOver20,
method="total")

NorthLatitude<-vector()
for(i in 1:length(PBDB.AbundanceOver20.t1)){
```

```
        Latitude<-
PBDBresults[which(PBDBresults$NorthernMostOccurrenceRank==i),which(col
names(PBDBresults)=="paleolat")]
        Latitude<-Latitude[!is.na(Latitude)]
        NorthLatitude[i]<-max(Latitude)
}
NorthLatitude<-NorthLatitude[!is.infinite(NorthLatitude)]
NorthLatitude

SouthLatitude<-vector()
for(counter in 1:length(PBDB.AbundanceOver20.t1)){
        Latitude<-
PBDBresults[which(PBDBresults$NorthernMostOccurrenceRank==counter),w
hich(colnames(PBDBresults)=="paleolat")]
        Latitude<-Latitude[!is.na(Latitude)]
        SouthLatitude[counter]<-min(Latitude)
}
SouthLatitude<-SouthLatitude[!is.infinite(SouthLatitude)]
SouthLatitude

LatitudeRange<-matrix(ncol=3,nrow=length(NorthLatitude))
for(rangelength in 1:length(PBDB.AbundanceOver20.t1)){
        LatitudeRange[rangelength,1]<-SouthLatitude[rangelength]
        LatitudeRange[rangelength,2]<-NorthLatitude[rangelength]
        LatitudeRange[rangelength,3]<-NorthLatitude[rangelength]-
SouthLatitude[rangelength]
}
LatitudeRange

NorthernTaxaAvgRange<-median(LatitudeRange[1:39,3])
NorthernTaxaAvgRange
SouthernTaxaAvgRange<-
median(LatitudeRange[39:nrow(LatitudeRange),3])
SouthernTaxaAvgRange

TaxaNames<-colnames(PBDB.AbundanceOver20.t1)

NorthernTaxa<-which(NorthLatitude>=SeawayEntranceSouth)
NorthernTaxaNames<-TaxaNames[NorthernTaxa]
SouthernTaxa<-which(NorthLatitude<SeawayEntranceSouth)
SouthernTaxaNames<-TaxaNames[SouthernTaxa]
```

```
MedianTaxaAbundance<-vector()
TaxaOccurrences<-vector()

for(TaxaCounter in 1:ncol(PBDB.AbundanceOver20.t1)){
        TaxaAbundance<-PBDB.AbundanceOver20.t1[,TaxaCounter]
        zeros<-which(TaxaAbundance<=0)
        TaxaAbundance<-TaxaAbundance[-zeros]
        if(length(TaxaAbundance>0)){
                MedianAbundance<-median(TaxaAbundance)
        }
        else{
                MedianAbundance<-0
        }
        MedianTaxaAbundance[TaxaCounter]<-MedianAbundance
        TaxaOccurrences[TaxaCounter]<-
length(TaxaAbundance)/nrow(PBDB.AbundanceOver20.t1)
}

windows()
plot(MedianTaxaAbundance,TaxaOccurrences,type="n",xlab="Median Percent
Abundance",ylab="Percent Occupancy", las=1)
points(MedianTaxaAbundance[NorthernTaxa],TaxaOccurrences[NorthernTaxa
],pch=16,col="blue")
points(MedianTaxaAbundance[SouthernTaxa],TaxaOccurrences[SouthernTax
a],pch=16,col="red")
text(MedianTaxaAbundance[NorthernTaxa],TaxaOccurrences[NorthernTaxa],l
abels=NorthernTaxaNames, cex=0.5, col="blue")
text(MedianTaxaAbundance[SouthernTaxa],TaxaOccurrences[SouthernTaxa],
labels=SouthernTaxaNames, cex=0.5, col="red")

#BioGeography Plot
PBDBnames<-as.vector(PBDBtaxalist[,1])
GenusOccurrences<-
table(PBDBresults[,colnames(PBDBresults)=="NorthernMostOccurrenceRank"
])
TaxaAndOccurrences<-matrix(ncol=1,nrow=length(GenusOccurrences))
TaxaAndOccurrences<-as.data.frame(cbind(PBDBnames,GenusOccurrences))

SouthernTaxaOccurrences<-
TaxaAndOccurrences[40:nrow(TaxaAndOccurrences),]
MedianSouthOccurrences<-
median(GenusOccurrences[40:length(GenusOccurrences)])
```

```
MedianAbundance<-median(GenusOccurrences)
MedianAbundance<-round(MedianAbundance)
TaxaResamples<-MedianSouthOccurrences
Resamples<-10000
Lower25<-(Resamples*25)/100
Upper75<-(Resamples*75)/100

LowerConfidence<-vector(length=length(GenusOccurrences))
UpperConfidence<-vector(length=length(GenusOccurrences))

for(taxon in 1:length(GenusOccurrences)){
	Latitude<-
PBDBresults[which(PBDBresults$NorthernMostOccurrenceRank==taxon),whic
h(colnames(PBDBresults)=="paleolat")]
	Latitude<-Latitude[!is.na(Latitude)]
	if(length(Latitude)>TaxaResamples){
		NorthernMosts<-vector()
		for(i in 1:Resamples){
			subsample<-
sample(Latitude,TaxaResamples,replace=TRUE)
			MaxNorth<-max(subsample)
			NorthernMosts[i]<-MaxNorth
		}
		SortedNorths<-sort(NorthernMosts,decreasing=FALSE)
		LowerConfidence[taxon]<-SortedNorths[Lower25]
		UpperConfidence[taxon]<-SortedNorths[Upper75]
	}
	else{
	LowerConfidence[taxon]<--99999
	UpperConfidence[taxon]<--99999
	}
}

windows()
plot(PBDBresults$NorthernMostOccurrenceRank,PBDBresults$paleolat,type="
n",las=1, main="PBDB Paleolatitude Occurrences",xlab="",ylab="Jurassic
Paleolatitude", xaxt="n")
axis(side=1,at=1:length(PBDBnames),labels=PBDBnames,cex.axis=0.5,las=
3)
rect(xleft=-5,ybottom=30,xright=95,ytop=60,col="grey",border="grey")
```

```
rect(xleft=-
5,ybottom=55,xright=95,ytop=60,col="lightgrey",border="lightgrey")
points(PBDBresults$NorthernMostOccurrenceRank,
PBDBresults$paleolat,pch=16,col=rgb(red=0.2,green=0.2,blue=1.0,alpha=0
.2,))
box()

for(j in 1:length(LowerConfidence)){
segments(x0=j,y0=LowerConfidence[j],x1=j,y1=UpperConfidence[j],
col="red", lwd=2)
}

#Comparison of MDS and DCA Scores
MultivariateScores<-cbind(1-
AbundanceOver20.t1.MDS$points,AbundanceOver20.t1.DCA$rproj)
round(cor(MultivariateScores), digits=2)
```

APPENDIX D

FIELD SAMPLES

Sample	Field Sample	Unit	Latitude	Longitude
GS01	CHMNY-2	Gypsum Spring	44.56146	-107.74734
GS02	CR1138-1	Gypsum Spring	44.58117	-108.12869
GS03	CR1138-6	Gypsum Spring	44.58117	-108.12869
GS04	GSR-01	Gypsum Spring	45.00826	-108.42319
GS05	GSR-02	Gypsum Spring	45.00826	-108.42319
GS06	GSR-03	Gypsum Spring	45.00826	-108.42319
GS07	GSR-04	Gypsum Spring	45.00826	-108.42319
GS08	GSR-05	Gypsum Spring	45.00826	-108.42319
GS09	GSR-19	Gypsum Spring	45.01901	-108.42322
GS10	HYATT-1	Gypsum Spring	44.36499	-107.65196
GS11	LSM-N-1	Gypsum Spring	44.81867	-108.30419
GS12	SM-E-6	Gypsum Spring	44.56423	-108.04270
GS14	THERMO-1	Gypsum Spring	43.67262	-108.18438
GS15	TPCK-1	Gypsum Spring	44.52795	-107.74025
GS16	TPCK-5	Gypsum Spring	44.52795	-107.74025
CS01	CODY-2	Canyon Springs	44.44756	-109.04082
CS02	CODY-3	Canyon Springs	44.44756	-109.04082
CS03	CODY-4	Canyon Springs	44.44913	-109.04228
CS04	CODY-6	Canyon Springs	44.44913	-109.04228
CS05	GSR-16	Canyon Springs	45.00842	-108.42234
CS06	GSR-17	Canyon Springs	45.00842	-108.42234
CS07	LSM-N-2	Canyon Springs	44.81951	-108.30491
CS08	LSM-N-3	Canyon Springs	44.81951	-108.30491
CS09	LSM-SOR-5	Canyon Springs	44.67836	-108.19253
CS10	RED-1	Canyon Springs	44.46211	-107.81023
CS11	RED-2	Canyon Springs	44.46211	-107.81023
CS12	RED-3	Canyon Springs	44.46211	-107.81023
CS13	RED-4	Canyon Springs	44.46211	-107.81023
CS14	SM-E-7	Canyon Springs	44.56638	-108.04331
CS15	SM-PANTO-1	Canyon Springs	44.53882	-108.02953
CS16	TPCK-2	Canyon Springs	44.52770	-107.74104
CS17	TPCK-3	Canyon Springs	44.52770	-107.74104
SB01	CHMNY-1	Stockade Beaver	44.55315	-107.75612
SB02	CHMNY-3	Stockade Beaver	44.56166	-107.75818
SB03	CODY-5	Stockade Beaver	44.44913	-109.04228
SB04	CR1138-2	Stockade Beaver	44.58009	-108.12888
SB05	GSR-06	Stockade Beaver	45.00826	-108.42319
SB06	GSR-18	Stockade Beaver	45.00797	-108.42221

SB07	HYATT-2	Stockade Beaver	44.36456	-107.65244
SB08	LSM-N-4	Stockade Beaver	44.81951	-108.30491
SB09	RED-7	Stockade Beaver	44.46296	-107.81620
SB10	RED-8	Stockade Beaver	44.46296	-107.81620
SB11	RED-9	Stockade Beaver	44.46296	-107.81620
SB12	SM-E-8	Stockade Beaver	44.56680	-108.04309
SB13	SM-PANTO-2	Stockade Beaver	44.53844	-108.02959
SB14	SM-PANTO-6	Stockade Beaver	44.53645	-108.02458
SB15	TPCK-4	Stockade Beaver	44.52770	-107.74104
HU01	SM-E-1	Hulett	44.56695	-108.04254
RN01	HYATT-4	Redwater-Concretions	44.36401	-107.65249
RN02	LSM-N-5	Redwater-Concretions	44.81951	-108.30491
RN03	LSM-SOR-1	Redwater-Concretions	44.69410	-108.25164
RN04	SM-PANTO-3	Redwater-Concretions	44.53645	-108.02458
RN05	THERMO-2	Redwater-Concretions	43.67376	-108.17846
RM01	CR1138-5	Redwater-Mud	44.58043	-108.13307
RM02	CR49-1	Redwater-Mud	44.21010	-107.56345
RM03	GSR-09	Redwater-Mud	45.00901	-108.42181
RM04	GSR-15	Redwater-Mud	45.00996	-108.42143
RM05	SM-E-4	Redwater-Mud	44.56747	-108.04163
RM06	SM-PANTO-5	Redwater-Mud	44.53645	-108.02458
RO01	CR1138-3	Redwater-Oyster	44.58043	-108.13307
RO02	HYATT-3	Redwater-Oyster	44.36437	-107.65246
RO03	LSM-SOR-2	Redwater-Oyster	44.69340	-108.25160
RO04	RED-5	Redwater-Oyster	44.46949	-107.80939
RO05	SM-E-3	Redwater-Oyster	44.56747	-108.04163
RO06	SM-PANTO-4	Redwater-Oyster	44.53645	-108.02458
RA01	CR1138-4	Redwater-*Camptonectes*	44.58043	-108.13307
RA02	GSR-11	Redwater-*Camptonectes*	45.00996	-108.42143
RA03	LSM-N-6	Redwater-*Camptonectes*	44.81951	-108.30491
RA04	LSM-SOR-3	Redwater-*Camptonectes*	44.69381	-108.25183
RA05	THERMO-3	Redwater-*Camptonectes*	43.67376	-108.17846
WH01	CODY-1	Windy Hill	44.44627	-109.03716
WH02	GSR-10	Windy Hill	45.00901	-108.42181
WH03	GSR-12	Windy Hill	45.00735	-108.42149
WH04	GSR-13	Windy Hill	45.00735	-108.42149
WH05	GSR-14	Windy Hill	45.00735	-108.42149
WH06	HYATT-5	Windy Hill	44.36401	-107.65249
WH07	LSM-N-7	Windy Hill	44.81951	-108.30491
WH08	LSM-SOR-4	Windy Hill	44.69381	-108.25183
WH09	RED-6	Windy Hill	44.47002	-107.80939
WH10	SM-E-5	Windy Hill	44.56747	-108.04163
WH11	SM-E-9	Windy Hill	44.57014	-108.04238

WH12	THERMO-4	Windy Hill	43.67376	-108.17846

Sample	Sample Type	Collector
GS01	Pieces	Kris, Courtney
GS02	Pieces	Kris, Courtney
GS03	Pieces	Kris, Courtney
GS04	Pieces	Kris, Courtney, Silvia, Steve, Annaka, Jason
GS05	Pieces	Silvia
GS06	Pieces	Courtney
GS07	Pieces	Courtney
GS08	Pieces	Silvia
GS09	Slab	Annaka, Jason
GS10	Pieces	Kris, Courtney
GS11	Pieces	Kris, Courtney, Silvia
GS12	PIeces	Kris, Courtney, Annaka, Jason
GS14	Pieces	Kris
GS15	Pieces	Courtney, Silvia
GS16	PIeces	Courtney, Silvia
CS01	Slab	Kris, Courtney
CS02	Bulk	Courtney
CS03	Slab	Kris, Courtney
CS04	Slab	Jason
CS05	Pieces	Kris, Courtney, Silvia
CS06	Pieces	Kris, Courtney, Silvia
CS07	Pieces	Kris, Courtney, Silvia, Steve
CS08	Slab	Kris, Steve
CS09	Pieces	Kris, Courtney, Silvia, Steve, Annaka, Jason
CS10	Pieces	Kris, Courtney, Silvia
CS11	Pieces	Kris, Courtney, Silvia
CS12	Pieces	Silvia
CS13	Pieces	Kris, Courtney, Silvia
CS14	Pieces	Kris, Courtney, Steve
CS15	Pieces	Kris, Courtney
CS16	Pieces	Courtney, Silvia
CS17	Pieces	Kris
SB01	Pieces	Kris, Courtney, Jason
SB02	Bulk	Courtney
SB03	Surface	Kris, Courtney
SB04	Bulk	Kris, Courtney
SB05	Bulk	Kris, Courtney, Silvia

SB06	Surface	Kris, Courtney, Silvia, Annaka, Jason
SB07	Bulk	Kris, Courtney
SB08	PIeces	Kris, Courtney, Silvia, Steve
SB09	Bulk	Kris, Courtney
SB10	Bulk	Kris, Courtney
SB11	Bulk	Kris, Courtney
SB12	Bulk	Kris, Courtney
SB13	Bulk	Kris, Courtney
SB14	Pieces	Kris, Courtney
SB15	Bulk	Kris, Courtney, Silvia
HU01	Surface	Kris, Courtney
RN01	Pieces	Kris, Courtney
RN02	Concretions	Kris, Courtney, Steve
RN03	Concretions	Kris, Courtney, Silvia, Steve, Annaka, Jason
RN04	Concretions	Kris, Courtney
RN05	Concretions	Kris
RM01	Bulk	Kris, Courtney
RM02	Bulk	Kris, Courtney
RM03	Bulk	Courtney
RM04	Surface	Kris, Courtney, Silvia, Steve
RM05	Surface	Courtney
RM06	Bulk	Kris, Courtney
RO01	Bulk	Kris
RO02	Bulk	Kris, Courtney
RO03	Surface	Kris, Courtney, Silvia, Annaka, Jason
RO04	Bulk	Courtney, Silvia
RO05	Bulk	Kris
RO06	Bulk	Kris, Courtney
RA01	Pieces	Kris, Courtney
RA02	Pieces	Kris, Courtney, Silvia, Steve
RA03	Pieces	Kris, Courtney
RA04	Pieces	Kris, Courtney, Silvia, Annaka, Jason
RA05	Pieces	Kris
WH01	Pieces	Kris, Courtney, Silvia, Steve, Annaka, Jason
WH02	Pieces	Silvia
WH03	Slab	Kris, Courtney, Silvia, Steve
WH04	Slab	Kris, Steve
WH05	Slab	Steve
WH06	Slab	Kris, Courtney
WH07	Pieces	Kris, Courtney
WH08	Pieces	Kris

WH09	Slab	Kris, Steve
WH10	Pieces	Kris, Courtney
WH11	Pieces	Kris, Courtney
WH12	Slab	Kris

Sample	**Field Noted Fossils**	**Notes**
GS01	bivalve, disarticulated, whole	odd weathering, some turns green when esposed to air, both green layer and more typical orange iron coloration
GS02	disarticulated bivalve, whole, butterflied	lime mudstone blocks
GS03	bivalve, articulated and disarticulated, whole and mostly whole, *Camptonectes*	at same location as CR1138-1
GS04	Bivalves: bufferflied articulated, most disarticulated, whole shell and casts	Fossils found in orange iron oxidation (liminite)
GS05	Bivalves: bufferflied articulated, most disarticulated, whole shell and casts	Fossils found in orange iron oxidation (liminite)
GS06	*Camptonectes*: disarticulated with ornamentation	
GS07	Bivalves: bufferflied articulated, most disarticulated, whole shell and casts	Fossils found in orange iron oxidation (liminite)
GS08	Bivalves: preserved on surface, disarticulated shell, abundant	Oolitic carbonate
GS09	bivalves, disarticulated whole	
GS10	disarticulated bivalve, whole shell	grey lime mudstone, extremely fossilferous and orange iron coloration
GS11	disarticulated whole bivalves, butterflied	very thinly bedded lime mudstone, fossils in orange iron coloration

GS12	oyster/ *Camptonectes*	grey/light grey lime mudstone, on resistant layer holding up ridge
GS14	*Modiolus*, bivalve, whole, disarticulated	sparsely fossilferous lime mudstone
GS15	disarticulated bivalve, whole valve	lime mudstone, light grey coloration, fossils in orange iron coloration
GS16	disarticulated bivalve, whole valve	lime mudstone, light grey coloration, fossils in orange iron coloration, similar to TPCK-1
CS01	*Camptonectes*, bivalve, crinoid	
CS02	crinoid	bulk sample of sediment underlying and dislodged by removal of CODY-2 slab
CS03	crinoid, bivalve	oolitic, up section from CODY-2 & CODY-3
CS04	*Camptonectes*, *Gryphaea*, belemnite, crinoid, oyster	
CS05	Bivalve: disarticulated, mostly whole, convex up	
CS06	Bivalve: disarticulated, mostly whole, convex up	up the gully about 4m from GSR-16
CS07	heavily weathered bivalves, small (~3 cm) gastropods	poorly preserved, weathered sandy mudstone
CS08	disarticulated bivalves, whole shell, crinoid	stratigraphically above LSM-N-2, shelly slab, sandy slab
CS09		oolitic packstone-ooid skeletal packstone to grainstone
CS10	large snails, *Modiolus*, oyster, disarticulated, whole, and fragments	
CS11	large snail, some Modiolus, shark tooth	lower resistant ledge
CS12	oyster disarticulated fragments, crinoid, gastropod	lower white resistant layer, below RED-1
CS13	disarticulated	upper grey/white resistant layer

	bivalve, small gastropod	
CS14	bivalve, whole, 2-3 articulated, urchin	face of resistant ridge
CS15	disarticulated oyster fragments, gastropods	white sandy or oolitic
CS16	disarticulated whole and fragment bivalve, 2-3 large gastropods, oyster	white/light tan sandy layer, bed ~10-15 cm thick
CS17	oyster, whole, disarticulated, fragments	oyster stone, below TPCK-2 horizon by about 20-30 cm, 2 outcrops on knob
SB01	belemnites, *Gryphaea*	Stockade Beaver or Canyon Springs, unclear, some *Gryphaea* in rock, also *Gryphaea* present if weathered outer layer dug past
SB02	*Gryphaea,* disarticulated whole and fragment, crinoid	
SB03	*Gryphaea,* belemnite, crinoid	1x1 m
SB04	disarticulated *Gryphaea*, crinoid	
SB05	*Gryphaea:* disarticulated, whole and fragments	
SB06	*Gryphaea*	
SB07	*Gryphaea*, whole and fragment, belemnite	
SB08	disarticulated *Gryphaea*, 1 articulated *Gryphaea*, *Isocrinus*	exposed gully cut, ~30-40 cm exposed at bottom of gully cut, shaley
SB09	*Gryphaea*	0.5-1.0 m up from contact
SB10	*Gryphaea*	0.0-0.5 m up from contact
SB11	*Gryphaea*	1.0-1.5 m up from contact
SB12	*Gryphaea*, oyster	
SB13	disarticulated *Gryphaea*, whole and fragment	
SB14	*Gryphaea*	Gryphaea stone cobble, found near contact with Hulett, found at 2 sites, one sampled

SB15	*Gryphaea*, disarticulated	
HU01	*Gryphaea*, disarticulated, whole and fragments	shelly horizon, below eolian horizon, above Stockade Beaver contact
RN01	*Camptonectes*, crinoid	White concretions
RN02	ammonites, belemnite, bivalves-*Astarte*	rusty concretions in lower 1/2 of unit, exploded concretions
RN03	Bivalve: mold, most disarticulated, few articulated; Ammonite	
RN04	disarticulated bivalves, belemnites, crinoid	6-8 concretions on knob below oyster horizon
RN05	bivalve, whole, disarticulated	
RM01	belemnite, oyster, echinoid fragments, bivalve fragments	
RM02	belemnite, oyster, fragments, disarticulated	
RM03	Oyster, belemnite	
RM04		
RM05	belemnite fragment, bivalve fragment	1x1 m
RM06	oyster, crinoid, belemnite	
RO01	disarticulated oyster, belemnites	
RO02	Oyster, belemnite	
RO03	Oyster	2x2m plot
RO04	disarticulated oyster fragment, belemnites, crinoid	oyster heavy knob
RO05	disarticulated oyster fragments, belemnite fragments	shell hash
RO06	disarticulated oyster, belemnite	above SM-PANTO-3
RA01	*Camptonectes*	poorly exposed *Camptonectes* bed
RA02	*Camptonectes*	

RA03	1 articulated *Camptonectes*	white exploded concretions
RA04	*Camptonectes*	
RA05	*Camptonectes*	
WH01	serpulid, bivalve disarticulated fragments, brachiopod, oyster	shelly sandstone, ~25 cm above sandy bed with herring-bone cross stratification
WH02		
WH03		
WH04	Shell and sand	
WH05		Underside of GSR-12
WH06	bivalve, disarticulated	
WH07	fragments, disarticulated	
WH08	fragments, disarticulated	sandstone and shell hash
WH09	disarticulated shell, whole and fragment	top of shelly horizon
WH10	disarticulated whole and fragment, mold, original shell	sandstone above contact with Readwater
WH11	disarticulated shell and fragments, bivalve, oyster	shelly horizon at top of Windy Hill, crumbly sandstone
WH12	fragmented bivalve, *Camptonectes*	

APPENDIX E

FAUNAL ABUNDANCES

	Asta	Camp	Card	Cera	Cerc	Char	Clio	Corbi	Corbu	echi
GS01	19	0	0	0	0	0	0	12	0	0
GS02	0	4	0	0	0	0	0	42	2	0
GS03	0	6	0	0	1	0	0	30	2	0
GS04	9	0	0	0	0	0	0	0	0	0
GS05	5	0	0	0	0	0	0	0	3	0
GS06	4	49	0	0	0	0	0	0	0	0
GS07	14	2	0	0	0	0	0	0	3	0
GS08	4	0	0	0	0	0	0	0	0	0
GS09	2	0	0	0	0	0	0	0	0	0
GS10	3	0	0	0	2	0	0	0	4	0
GS11	11	1	0	0	0	0	0	0	4	0
GS12	3	15	0	0	0	0	0	0	0	0
GS14	0	0	0	0	0	0	0	0	1	0
GS15	4	0	0	0	1	0	0	0	0	0
GS16	2	0	0	0	0	0	0	0	0	0
CS01	1	88	0	0	0	0	0	0	0	0
CS02	13	4	0	0	0	0	1	0	0	0
CS03	0	0	0	0	0	0	0	0	0	0
CS04	8	61	0	0	0	0	0	0	0	0
CS05	37	58	0	0	0	0	0	0	0	0
CS06	2	3	0	0	0	0	0	0	0	0
CS07	9	0	0	0	0	0	0	0	0	0
CS08	0	63	0	0	0	26	0	0	0	0
CS09	1	0	0	0	0	0	0	0	0	0
CS10	8	0	0	1	0	0	0	0	0	0
CS11	26	4	0	0	0	0	0	0	0	0
CS12	1	21	0	0	0	0	0	0	0	1
CS13	1	0	0	0	0	0	0	0	0	0
CS14	7	0	0	0	0	0	0	0	0	0
CS15	5	0	0	0	0	0	0	0	0	0
CS16	4	7	0	3	0	0	0	0	0	0
CS17	0	0	0	0	0	0	0	0	0	0
SB01	1	0	0	0	0	0	0	0	0	0
SB02	0	1	0	0	0	0	0	0	0	0
SB03	0	0	0	0	0	0	0	0	0	0
SB04	0	0	0	0	0	0	0	0	0	0
SB05	0	0	0	0	0	0	0	0	0	0
SB06	0	0	0	0	0	0	0	0	0	0
SB07	0	0	0	0	0	0	0	0	0	0
SB08	0	0	0	0	0	0	0	0	0	0
SB09	0	0	0	0	0	0	0	0	0	0

SB10	0	0	0	0	0	0	0	0	0	0
SB11	0	1	0	0	0	0	0	0	0	0
SB12	0	1	0	0	0	0	0	0	0	0
SB13	1	0	0	0	0	0	0	0	0	0
SB14	0	2	0	0	0	0	0	0	0	0
SB15	0	0	0	0	0	0	0	0	0	0
HU01	0	0	0	0	0	0	0	0	0	0
RN01	23	65	0	0	0	0	0	0	0	0
RN02	60	7	0	0	0	0	0	0	0	0
RN03	159	0	5	0	1	0	0	0	0	0
RN04	5	3	0	0	0	2	0	0	0	0
RN05	1	0	0	0	0	0	0	0	0	0
RM01	0	0	0	0	0	0	0	0	0	0
RM02	0	0	0	0	0	0	0	0	0	0
RM03	2	1	0	0	0	0	0	0	0	0
RM04	0	0	0	0	0	0	0	0	0	0
RM05	1	0	0	0	0	0	0	0	0	1
RM06	1	0	0	0	0	0	0	0	0	0
RO01	0	1	0	0	0	0	0	0	0	0
RO02	0	1	0	0	0	0	0	0	0	0
RO03	0	1	0	0	0	0	0	0	0	0
RO04	0	1	0	0	0	0	0	0	0	0
RO05	0	1	0	0	0	0	0	0	0	0
RO06	2	1	0	0	0	3	1	0	0	0
RA01	0	17	0	0	0	0	0	0	0	1
RA02	0	54	0	0	0	0	0	0	0	1
RA03	2	35	0	0	0	0	0	0	0	0
RA04	0	67	0	0	0	0	0	0	0	1
RA05	1	51	0	0	0	0	0	0	0	0
WH01	0	4	0	0	0	0	0	0	0	0
WH02	0	5	0	0	0	0	0	0	0	0
WH03	0	5	0	0	0	0	0	0	0	0
WH04	0	0	0	0	0	0	0	0	0	0
WH05	0	7	0	0	0	0	0	0	0	0
WH06	0	4	0	0	0	0	0	0	0	0
WH07	0	1	0	0	0	0	0	0	0	0
WH08	0	3	0	0	0	0	0	0	0	0
WH09	0	32	0	0	0	0	0	0	0	0
WH10	0	4	0	0	0	0	0	0	0	0
WH11	0	13	0	0	0	0	0	0	0	0
WH12	0	5	0	0	0	0	0	0	0	0

	Erym	Gram	Gryp	Hamu	Homo	Hybo	Idon	Isoc	Isog	Kall
GS01	0	0	0	0	0	0	0	0	0	0
GS02	0	0	0	0	0	0	0	0	0	0
GS03	0	0	0	0	0	0	0	0	0	0
GS04	0	0	0	0	1	0	0	0	0	0
GS05	0	0	0	0	0	0	0	0	0	0
GS06	0	0	0	0	0	0	0	0	0	0
GS07	0	0	0	0	2	0	0	0	0	0
GS08	0	0	15	0	0	0	0	0	0	0
GS09	0	0	0	0	0	0	0	0	0	0
GS10	0	0	0	0	0	0	0	0	0	0
GS11	0	0	0	0	0	0	0	0	0	0
GS12	0	0	0	0	0	0	0	0	0	0
GS14	0	0	0	0	0	0	0	0	0	0
GS15	0	1	0	0	1	0	0	0	1	0
GS16	0	0	0	0	0	0	0	0	0	0
CS01	0	0	0	0	0	0	0	16	0	0
CS02	0	0	3	0	0	0	0	1543	0	0
CS03	0	0	0	0	0	0	0	80	0	0
CS04	0	0	58	0	0	0	0	192	0	0
CS05	0	0	4	0	0	0	0	0	0	0
CS06	0	0	0	0	0	0	0	0	0	0
CS07	0	0	10	0	0	0	0	0	0	0
CS08	0	0	0	0	0	0	0	144	0	0
CS09	0	0	2	0	0	0	0	0	0	0
CS10	0	0	0	0	0	0	0	0	0	0
CS11	0	0	11	0	0	1	0	0	0	0
CS12	0	0	0	0	0	0	0	0	0	0
CS13	0	0	0	0	0	0	0	0	0	0
CS14	0	0	0	0	0	0	0	0	0	0
CS15	0	0	5	0	0	0	0	0	0	0
CS16	0	0	8	0	0	0	0	0	0	0
CS17	0	0	0	0	0	0	0	0	0	0
SB01	0	0	48	0	0	0	0	0	0	0
SB02	0	0	76	0	0	0	0	2	0	0
SB03	0	0	105	0	0	0	0	0	0	0
SB04	0	0	310	0	0	0	0	127	0	0
SB05	0	0	102	0	0	0	0	0	0	0
SB06	0	0	380	0	0	0	0	19	0	0
SB07	0	0	72	0	0	0	0	0	0	0
SB08	0	0	136	0	0	0	0	5	0	0
SB09	0	0	11	0	0	0	0	0	0	0

SB10	0	0	50	0	0	0	0	0	0	0
SB11	0	0	12	0	0	0	0	0	0	0
SB12	0	0	377	0	0	0	0	140	0	0
SB13	0	0	597	0	0	0	0	2	0	0
SB14	0	0	68	0	0	0	0	0	0	0
SB15	0	0	335	0	0	0	0	20	0	0
HU01	0	0	56	0	0	0	0	0	0	0
RN01	0	0	0	1	0	0	0	0	0	0
RN02	1	0	0	0	0	0	0	0	0	4
RN03	0	0	0	0	0	0	1	0	0	2
RN04	0	0	8	0	0	0	0	5	0	33
RN05	0	2	0	0	0	0	0	0	0	0
RM01	0	0	2	0	0	0	0	0	0	0
RM02	0	0	0	0	0	0	0	3	0	0
RM03	0	0	0	0	0	0	0	0	0	0
RM04	0	0	3	0	0	0	0	0	0	0
RM05	0	0	0	0	0	0	0	0	0	0
RM06	0	0	8	0	0	0	0	49	0	0
RO01	0	0	0	0	0	0	0	2	0	0
RO02	0	0	0	0	0	0	0	0	0	0
RO03	0	0	0	0	0	0	0	21	0	0
RO04	0	0	0	0	0	0	0	7	0	0
RO05	0	0	4	0	0	0	0	0	0	0
RO06	0	0	0	0	0	0	0	21	0	0
RA01	0	0	0	0	0	0	0	1	0	0
RA02	0	0	0	0	0	0	0	0	0	0
RA03	0	0	0	0	0	0	0	0	0	0
RA04	0	0	0	0	0	0	0	0	0	0
RA05	0	0	0	0	0	0	0	16	0	0
WH01	0	0	0	0	0	0	0	0	0	51
WH02	0	0	0	0	0	0	0	0	0	0
WH03	0	0	0	0	0	0	0	0	0	0
WH04	0	0	0	0	0	0	0	0	0	2
WH05	0	0	0	0	0	0	0	0	0	0
WH06	0	0	0	0	0	0	0	0	0	0
WH07	0	0	0	0	0	0	1	0	0	0
WH08	0	0	0	0	0	0	0	0	0	0
WH09	0	0	0	0	0	0	2	0	0	0
WH10	0	0	0	0	0	0	4	0	0	0
WH11	0	0	0	0	0	0	0	0	0	0
WH12	0	0	0	0	0	0	0	0	0	0

	Lima	Lios	Loph	Lyos	Mact	Mele	Micr	Modi	Myop	nati
GS01	0	3	0	0	0	0	0	1	0	0
GS02	0	0	0	0	0	0	0	0	0	0
GS03	0	0	0	0	0	0	0	0	0	0
GS04	0	0	0	0	0	0	0	0	0	0
GS05	0	0	0	0	0	0	0	7	0	0
GS06	0	6	0	0	0	0	0	0	0	0
GS07	0	0	0	0	0	0	0	4	0	0
GS08	0	10	0	0	0	0	0	1	0	0
GS09	0	0	0	0	0	0	0	0	0	0
GS10	0	0	0	0	0	0	0	0	0	0
GS11	0	0	0	0	2	0	0	2	0	0
GS12	0	0	0	0	0	0	0	0	0	0
GS14	0	3	0	0	0	0	0	1	0	0
GS15	0	0	0	0	0	0	0	1	0	0
GS16	0	0	0	0	0	0	0	1	0	0
CS01	0	11	0	0	0	0	0	0	1	0
CS02	0	16	0	0	0	0	0	4	0	0
CS03	0	10	0	0	0	0	1	0	0	0
CS04	0	13	0	0	0	0	0	2	0	0
CS05	0	0	0	0	0	0	0	6	0	0
CS06	1	2	0	0	0	0	0	0	0	0
CS07	0	3	0	0	0	0	0	4	0	0
CS08	0	5	0	0	0	0	0	0	0	0
CS09	0	6	0	0	0	0	0	0	0	1
CS10	0	0	0	0	0	0	0	3	0	4
CS11	0	29	0	0	0	0	0	21	0	6
CS12	0	5	0	1	0	0	0	0	0	0
CS13	0	0	0	0	0	0	0	2	0	0
CS14	2	0	0	0	0	0	0	0	0	0
CS15	0	46	0	0	0	1	0	4	0	0
CS16	0	0	0	0	0	0	0	6	0	2
CS17	0	1135	0	0	0	0	0	0	0	0
SB01	0	0	0	0	0	0	0	0	0	0
SB02	0	0	0	0	0	0	0	0	0	0
SB03	0	0	0	0	0	0	0	0	0	0
SB04	0	0	0	0	0	0	0	0	0	0
SB05	0	0	0	0	0	0	0	0	0	0
SB06	0	0	0	0	0	0	0	0	0	0
SB07	0	0	0	0	0	0	0	0	0	0
SB08	0	0	0	0	0	0	0	0	0	0
SB09	0	0	0	0	0	0	0	0	0	0

SB10	0	0	0	0	0	0	0	0	0	0
SB11	0	0	0	0	0	1	0	0	0	0
SB12	0	0	0	0	0	0	0	0	0	0
SB13	0	0	0	0	0	0	0	0	0	0
SB14	0	0	0	0	0	0	0	0	0	0
SB15	0	0	0	0	0	0	0	0	0	0
HU01	0	0	0	0	0	0	0	0	0	0
RN01	0	4	0	0	0	0	0	1	0	0
RN02	0	0	0	0	0	0	0	0	0	0
RN03	0	7	0	0	0	0	0	6	0	0
RN04	0	6	0	0	0	0	0	0	0	0
RN05	0	0	0	0	0	0	0	0	0	0
RM01	0	4	1	0	0	2	0	0	0	0
RM02	0	1	0	0	0	0	0	1	0	0
RM03	0	15	0	0	0	0	0	0	0	0
RM04	0	1	0	0	0	0	0	0	0	0
RM05	0	0	5	0	0	1	0	0	0	0
RM06	0	5	0	0	0	1	0	0	0	0
RO01	0	38	0	0	0	0	0	0	0	0
RO02	0	36	0	0	0	1	0	0	0	0
RO03	1	24	0	0	0	0	0	0	0	0
RO04	0	64	0	0	0	1	0	0	0	0
RO05	0	50	0	0	0	1	0	0	0	0
RO06	0	88	0	0	0	1	0	0	0	0
RA01	0	1	0	0	0	0	0	0	0	0
RA02	0	0	0	0	0	0	0	0	0	0
RA03	0	1	0	0	0	0	0	0	0	0
RA04	0	1	0	0	0	0	0	0	0	0
RA05	1	0	0	0	0	0	0	0	0	0
WH01	0	5	0	0	0	0	0	0	0	0
WH02	0	2	0	0	0	0	0	0	0	0
WH03	0	18	0	0	9	0	0	0	0	0
WH04	0	2	0	0	0	0	0	0	0	0
WH05	0	2	0	0	0	0	0	0	0	0
WH06	0	10	0	0	0	0	0	1	0	0
WH07	0	18	0	0	97	0	0	0	0	0
WH08	0	3	0	0	0	0	0	1	0	0
WH09	0	110	0	0	0	0	0	3	0	0
WH10	0	4	0	0	20	0	0	0	0	0
WH11	0	5	0	0	1	1	0	0	0	0
WH12	0	19	0	0	0	0	0	0	0	0

	Nodo	**Nucu**	**Pach**	**Para**	**Pros**	**Phol**	**Pinn**	**Plat**	**Pleu**	**Proc**
GS01	0	0	0	0	0	0	0	0	369	0
GS02	0	0	0	0	0	0	0	0	1	0
GS03	0	0	0	0	0	0	0	0	0	0
GS04	0	0	0	0	0	0	0	0	535	0
GS05	0	0	0	0	0	0	0	1	1160	0
GS06	0	0	0	0	0	0	5	0	15	0
GS07	0	0	0	0	0	0	0	0	75	0
GS08	1	0	0	0	0	0	0	0	76	0
GS09	0	0	0	0	0	0	0	0	5	0
GS10	0	0	0	0	0	0	0	0	608	0
GS11	0	0	0	0	0	0	0	0	125	0
GS12	0	0	0	0	0	0	0	0	1	0
GS14	0	1	0	0	0	0	0	0	15	0
GS15	0	0	0	0	0	0	0	0	805	0
GS16	0	0	0	0	0	0	0	0	243	0
CS01	0	0	0	0	0	0	0	0	0	0
CS02	0	0	0	0	0	0	0	0	0	0
CS03	0	0	0	0	0	0	0	0	0	0
CS04	0	0	0	0	0	0	0	0	0	0
CS05	0	0	0	0	0	0	0	0	17	0
CS06	0	0	0	0	0	0	0	0	40	0
CS07	0	2	0	0	0	0	0	0	4	0
CS08	0	0	0	0	0	0	0	0	1	0
CS09	0	0	0	0	0	0	0	0	2	0
CS10	0	1	0	0	0	0	0	0	5	0
CS11	0	0	0	0	0	0	0	0	15	0
CS12	0	0	0	0	0	0	0	0	2	109
CS13	0	0	0	0	0	0	0	0	15	16
CS14	0	0	0	0	0	0	0	0	21	0
CS15	0	0	0	0	0	0	0	0	0	0
CS16	0	0	0	0	0	0	0	0	15	0
CS17	0	0	0	0	0	0	0	0	0	0
SB01	0	0	1	0	0	0	0	0	0	0
SB02	0	1	0	0	0	0	0	0	0	0
SB03	0	0	1	0	0	0	0	0	0	0
SB04	0	0	0	0	0	0	0	0	0	0
SB05	0	0	0	0	0	0	0	0	0	0
SB06	0	0	1	0	0	0	0	0	0	0
SB07	0	0	1	0	0	0	0	0	0	0
SB08	0	0	0	0	0	0	0	0	0	0
SB09	0	0	0	0	0	0	0	0	0	0

SB10	0	0	0	0	0	0	0	0	0	0
SB11	0	0	0	0	0	0	0	0	0	0
SB12	0	0	0	0	0	0	0	0	0	0
SB13	0	0	0	0	0	0	0	0	0	0
SB14	0	0	0	0	0	0	0	0	0	0
SB15	0	0	0	0	0	0	0	0	0	0
HU01	0	0	1	0	0	0	0	0	0	0
RN01	0	0	5	0	0	5	0	0	0	0
RN02	0	0	2	0	3	0	0	0	0	0
RN03	0	0	1	0	0	1	0	0	0	0
RN04	0	0	3	0	0	0	0	0	13	0
RN05	0	0	0	0	0	22	0	0	19	0
RM01	0	0	70	1	0	0	0	0	0	0
RM02	0	0	7	0	0	0	0	0	0	0
RM03	0	0	19	0	0	0	0	0	0	0
RM04	0	0	21	0	0	0	0	0	0	0
RM05	0	0	58	0	0	0	0	0	0	0
RM06	0	0	26	0	0	0	0	0	8	0
RO01	0	0	84	0	0	0	0	0	0	0
RO02	0	0	15	0	0	0	0	0	0	0
RO03	0	0	10	0	0	0	0	0	0	0
RO04	0	1	3	0	0	0	0	0	0	0
RO05	0	0	1	0	0	0	0	0	0	0
RO06	0	0	81	0	0	0	0	0	0	0
RA01	0	0	1	0	0	0	0	0	0	0
RA02	0	0	3	0	0	0	0	0	0	0
RA03	0	0	3	0	0	0	0	0	1	0
RA04	0	0	0	0	0	0	0	0	0	0
RA05	0	0	3	0	0	0	0	0	0	0
WH01	0	0	0	0	0	0	0	0	3	0
WH02	0	0	0	0	0	0	0	0	5	0
WH03	0	0	0	0	0	0	0	0	1	0
WH04	0	0	1	0	0	0	0	0	0	0
WH05	0	0	0	0	0	0	0	0	0	0
WH06	0	0	0	0	0	0	0	0	2	0
WH07	0	0	0	0	0	0	0	0	0	0
WH08	0	0	0	0	0	0	0	0	0	0
WH09	0	0	0	0	0	0	0	0	6	0
WH10	0	0	0	0	0	0	0	0	0	0
WH11	0	0	0	0	0	0	0	0	4	0
WH12	0	0	1	0	0	0	0	0	0	0

	Pron	Quen	rou	serp	Stom	Tanc	Trig	Tylo	Vaug
GS01	0	0	0	0	0	0	32	0	0
GS02	0	0	0	0	0	0	1	0	0
GS03	0	0	0	0	0	0	0	0	0
GS04	0	0	0	0	0	4	41	0	0
GS05	0	0	0	0	0	0	33	0	0
GS06	0	0	0	0	0	0	1	3	0
GS07	0	0	0	0	0	0	185	0	0
GS08	0	0	0	0	0	0	0	0	0
GS09	0	0	0	0	0	0	199	0	0
GS10	0	0	0	0	0	0	72	0	0
GS11	1	0	0	0	0	0	38	0	0
GS12	0	0	0	0	0	0	0	0	0
GS14	0	0	0	0	0	0	0	0	0
GS15	0	0	0	0	0	0	6	0	0
GS16	0	0	0	0	0	0	10	0	0
CS01	0	0	0	0	0	0	0	0	0
CS02	0	0	1	1	0	0	0	0	0
CS03	0	0	0	0	0	0	0	0	0
CS04	0	0	0	0	0	0	0	2	0
CS05	0	1	0	0	0	0	5	0	0
CS06	0	4	0	0	0	0	14	0	0
CS07	0	0	0	0	0	0	7	0	0
CS08	0	0	0	0	0	0	0	0	0
CS09	0	0	0	0	0	0	0	0	0
CS10	0	0	0	0	0	0	1	0	0
CS11	0	0	0	0	0	0	5	0	0
CS12	0	0	0	0	0	0	0	0	0
CS13	0	0	0	0	0	2	0	2	0
CS14	0	0	0	0	1	0	12	0	0
CS15	0	0	0	0	0	0	0	0	0
CS16	0	0	0	0	0	0	8	0	0
CS17	0	0	0	0	0	0	0	0	0
SB01	0	0	0	0	0	0	0	0	0
SB02	0	0	1	0	0	0	0	0	0
SB03	0	0	1	0	0	0	0	0	0
SB04	0	0	3	0	0	0	0	0	0
SB05	0	0	2	0	0	0	0	0	0
SB06	0	0	0	0	0	0	0	0	0
SB07	0	0	3	0	0	0	0	0	0
SB08	0	0	6	0	0	0	0	0	0
SB09	0	0	15	0	0	0	0	0	0

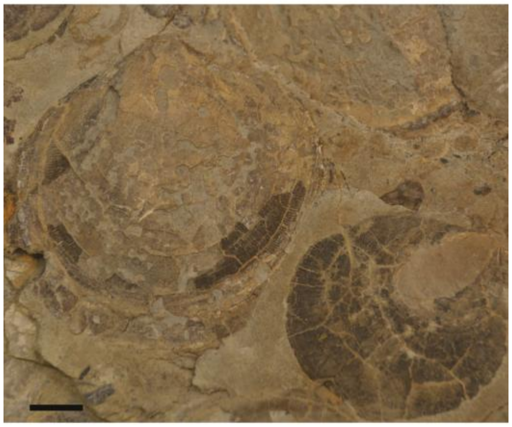
SB10	0	0	1	0	0	0	0	0	0
SB11	0	0	0	0	0	0	0	0	0
SB12	0	0	8	0	0	0	0	0	0
SB13	0	0	2	0	0	0	0	0	0
SB14	0	0	0	0	0	0	0	0	0
SB15	0	0	3	0	0	0	0	0	0
HU01	0	0	0	0	0	0	0	0	0
RN01	0	0	0	0	0	1	0	0	0
RN02	0	0	0	0	0	0	0	0	0
RN03	0	0	0	1	0	0	0	0	0
RN04	0	0	1	0	0	1	0	0	0
RN05	0	0	0	0	0	46	0	0	2
RM01	0	0	1	0	0	0	0	0	1
RM02	0	0	0	0	0	0	0	0	1
RM03	0	0	1	0	0	0	0	0	0
RM04	0	0	0	0	0	0	0	0	0
RM05	0	0	0	0	0	0	0	0	0
RM06	0	0	0	0	0	0	0	0	0
RO01	0	0	5	1	0	0	0	0	0
RO02	0	0	1	0	0	0	0	0	0
RO03	0	0	0	0	0	0	0	0	0
RO04	0	0	2	0	0	0	0	0	0
RO05	0	0	0	0	0	0	0	0	0
RO06	0	0	1	0	0	0	0	0	0
RA01	0	0	0	0	0	0	0	0	0
RA02	0	0	0	1	0	0	0	0	0
RA03	0	0	0	0	0	0	0	0	0
RA04	0	0	3	0	0	0	0	0	0
RA05	0	0	0	0	0	0	0	0	0
WH01	0	0	0	1	0	0	0	0	0
WH02	0	0	0	0	0	0	0	0	1
WH03	0	0	0	0	0	6	0	0	0
WH04	0	0	0	0	0	0	0	0	0
WH05	0	0	0	0	0	0	0	0	0
WH06	0	0	0	0	0	0	0	0	0
WH07	0	0	0	1	0	8	0	0	0
WH08	0	0	0	0	0	0	0	0	0
WH09	0	0	0	0	0	0	0	0	0
WH10	0	0	0	0	0	0	0	0	0
WH11	0	0	0	0	0	3	0	0	1
WH12	0	0	0	0	0	1	0	0	0

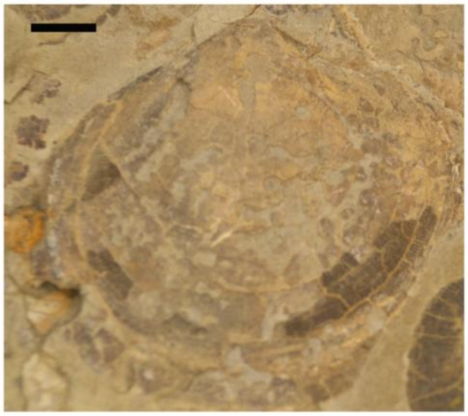
APPENDIX F

TAXON PHOTOGRAPHS (Unless otherwise stated, scale bar: 1 cm)

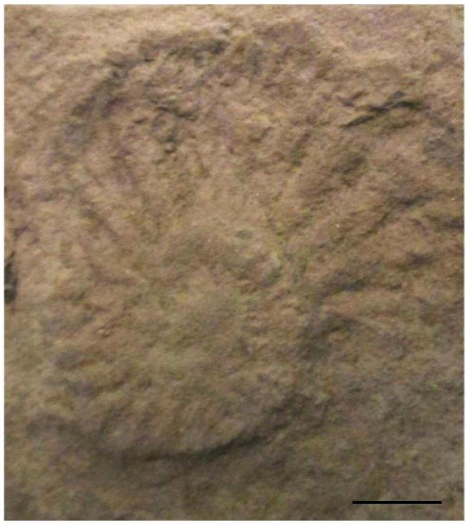
Astarte

Camptonectes

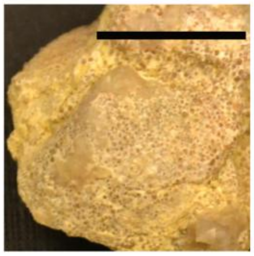




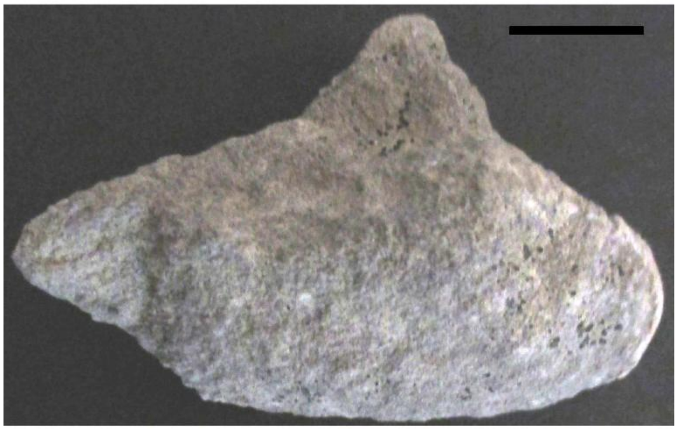
Cardioceras



Ceratomya



Cercomya

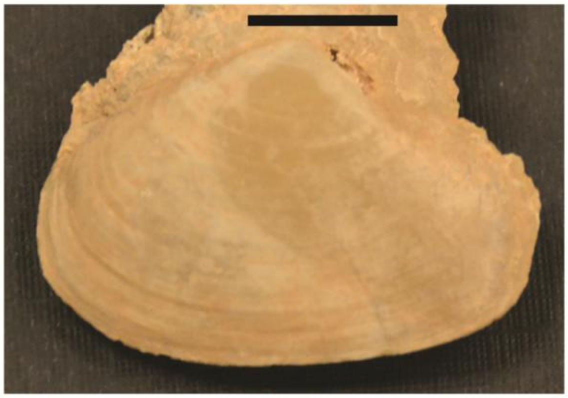


Chariocrinus (scale: 1 mm)

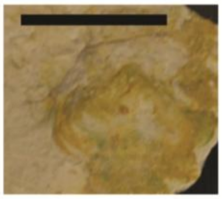
Cliona

coral

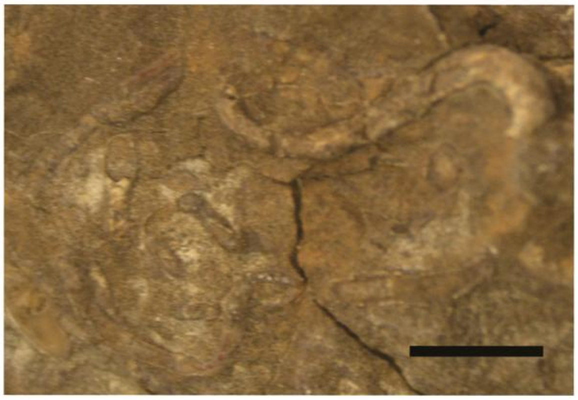
Corbicellopsis



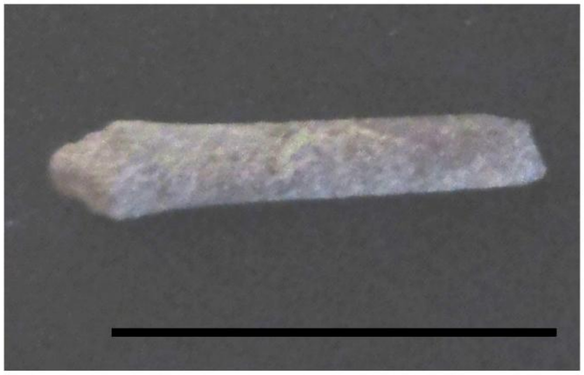
Corbula



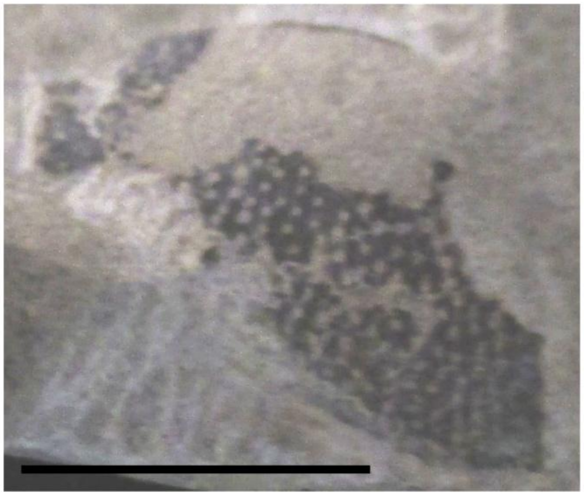
curving serpulid tubes



echinoid



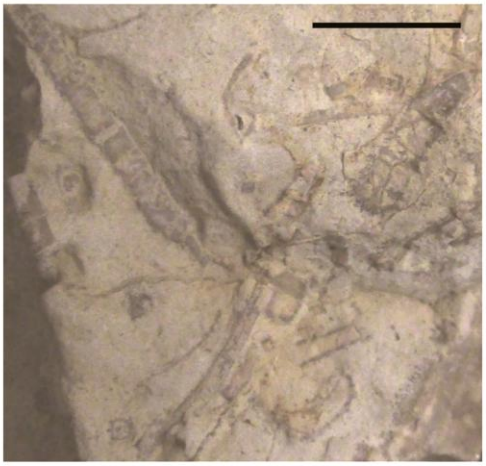
Eryma



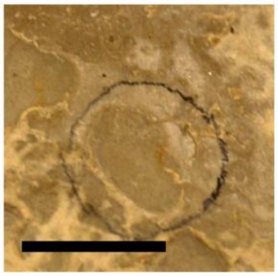
Grammatodon

Gryphaea

Hamulus

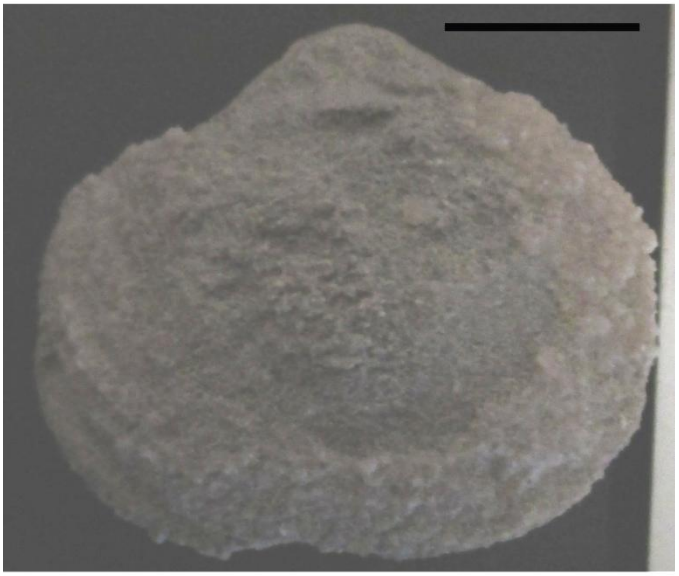


Homomya



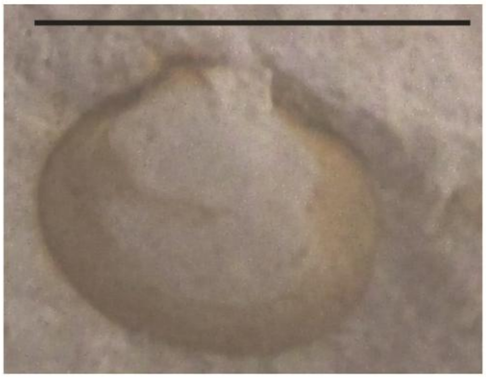
Hybodus

Idonearca



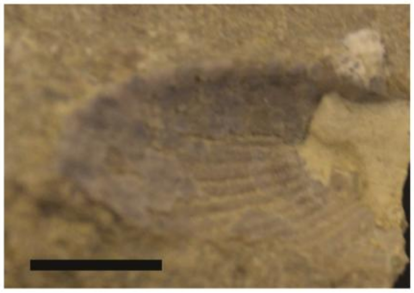
Isocrinus

Isognomon



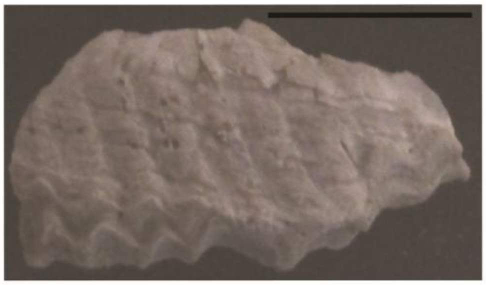
Kallirhynchia

Lima

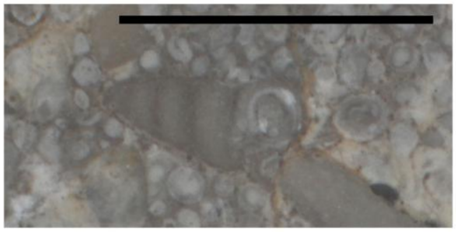


Liostrea

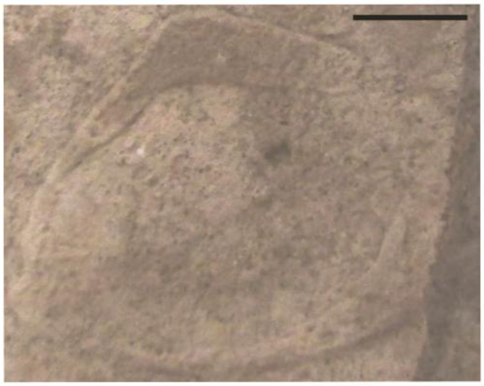
Lopha



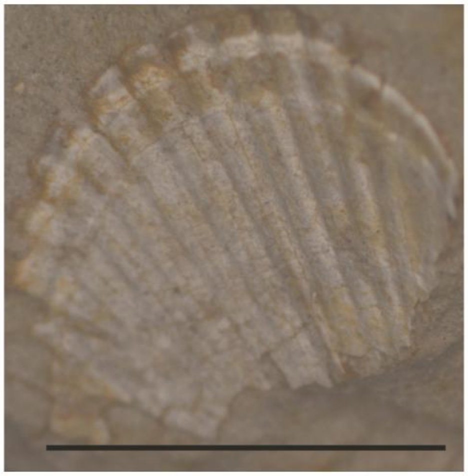
Lyosoma (scale: 2.5 mm)



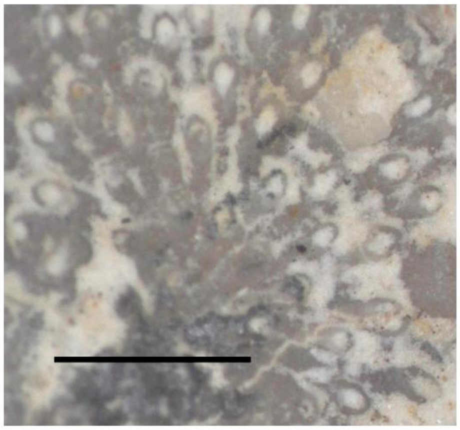
Mactromya



Meleagrinella (scale: 5 mm)

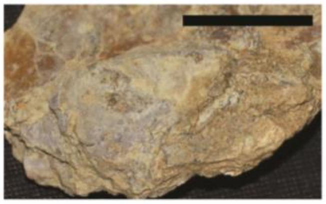


Microeciella (scale: 2.5 mm)

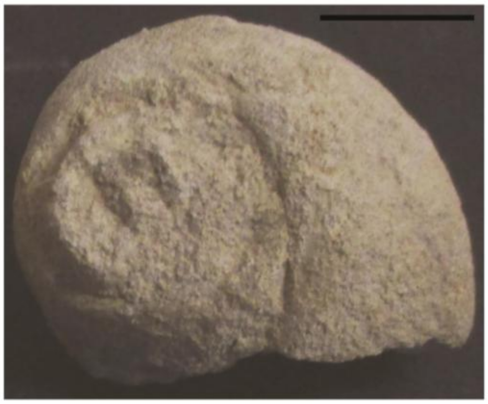


Modiolus

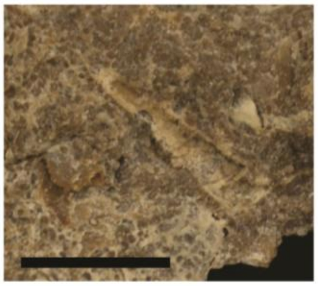
Myophorella



naticiform gastropod



Nododelphinula

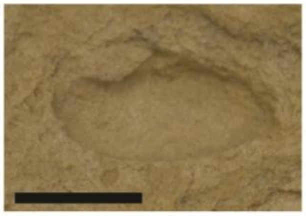


Nucula

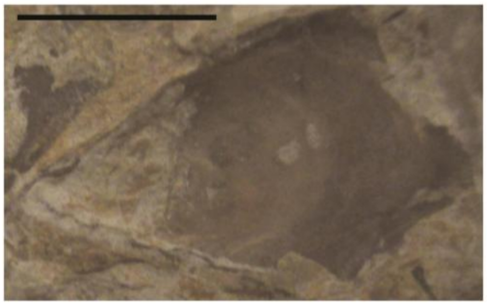
Pachyteuthis

Parastomechinus

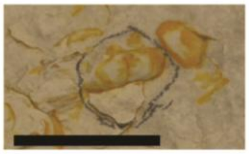
Pholadomya



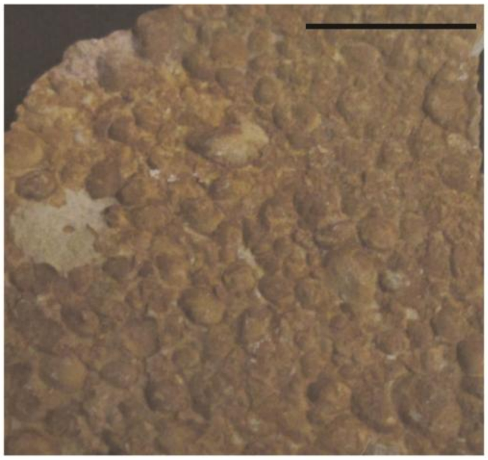
Pinna



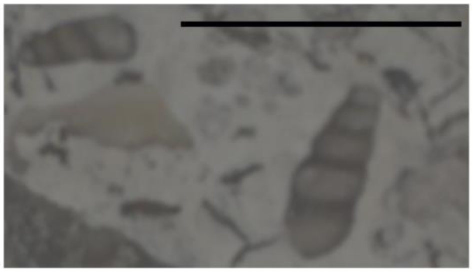
Platymyoidea



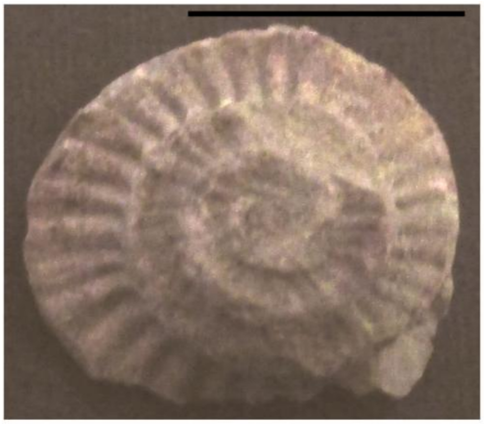
Pleuromya



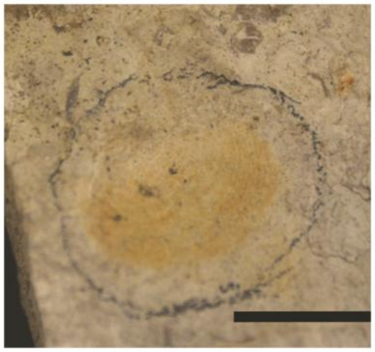
Procerithium (scale: 5 mm)



Prososphinctes

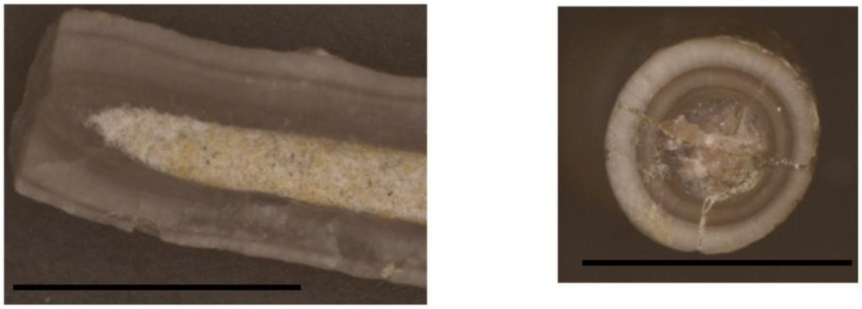


Quenstedtia

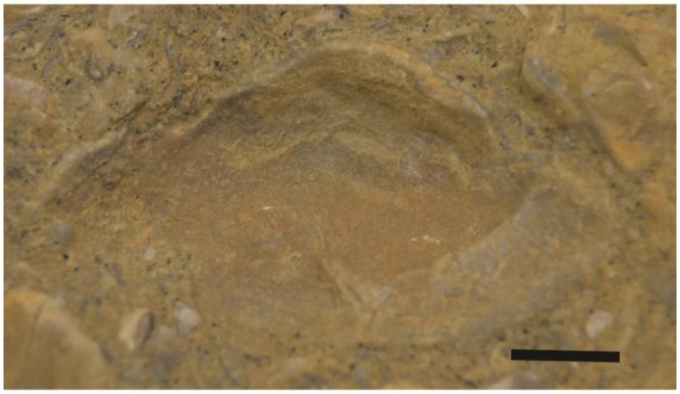


round, straight serpulid tubes

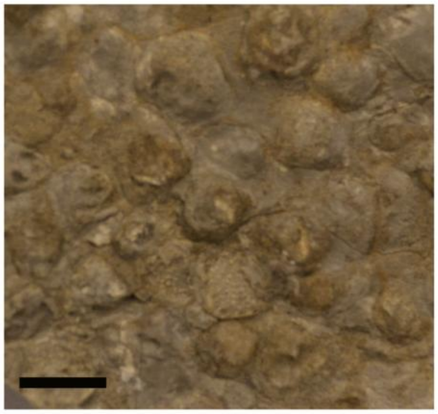
round, straight serpulid tubes, polished cross-section (scale: 5 mm)

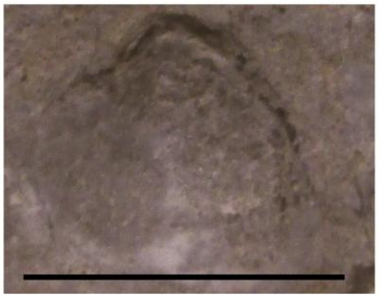


Tancredia

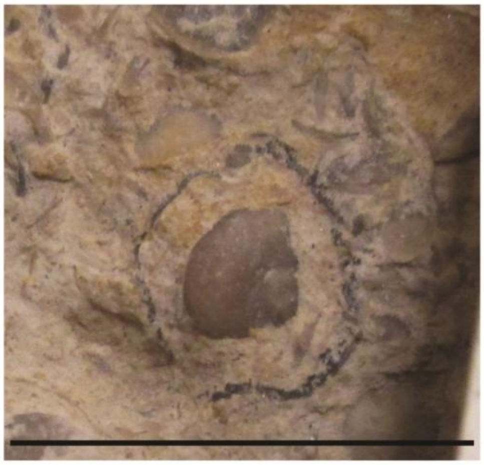


Trigonia

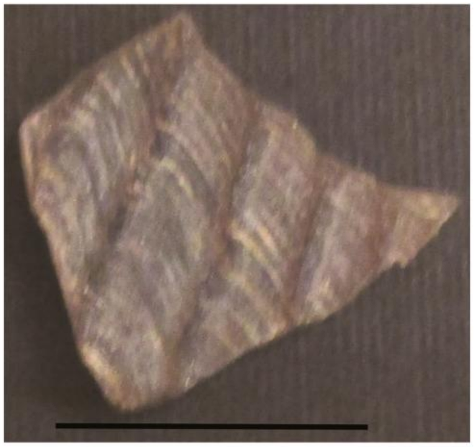




Tylostoma



Vaugonia



APPENDIX G

FAUNAL TAXONOMIC AND ECOLOGICAL DATA

	Asta	**Camp**	**Card**	**Cera**
Genus	*Astarte*	*Camptonectes*	*Cardioceras*	*Ceratomya*
Family	*Astartidae*	*Pectinoidae*	*Cardioceratidae*	*Ceratomyidae*
Order	*Carditida*	*Pectinida*	*Ammonitida*	*Pholadida*
Class	*Bivalvia*	*Bivalvia*	*Cephalopoda*	*Bivalvia*
Mobility	Facultatively mobile	Facultatively mobile	Fast moving	Facultatively mobile
Life Habit	Infaunal	Low-level epifaunal	Nektonic	Infaunal
Feeding Type	Suspension feeder	Suspension feeder	Carnivore	Suspension feeder

	Cerc	**Char**	**Clio**	**Corbi**
Genus	*Cercomya*	*Chariocrinus*	*Cliona*	*Corbicellopsis*
Family	*Laternulidae*	*Isocrinidae*	*Clionaidae*	*Tancrediidae*
Order	*Pandorida*	*Isocrinida*	*Clavulina*	*Cardiida*
Class	*Bivalvia*	*Crinoidea*	*Demospongea*	*Bivalvia*
Mobility	Facultatively mobile	Stationary	Stationary	Facultatively mobile
Life Habit	Deep infaunal	Upper-level epifaunal	Boring	Deep infaunal
Feeding Type	Suspension feeder	Suspension feeder	Suspension feeder	Deposit feeder

	Corbu	**echi**	**Erym**	**Gram**
Genus	*Corbula*	unknown	*Eryma*	*Grammatodon*
Family	*Corbulidae*	unknown	*Erymidae*	*Parallelodontidae*
Order	*Pholadida*	unknown	*Decapoda*	*Arcida*
Class	*Bivalvia*	*Echinoidea*	*Malacostraca*	*Bivalvia*
Mobility	Stationary	Slow moving	Fast moving	Facultatively mobile
Life Habit	Infaunal	Epifaunal	Epifaunal	Low-level epifaunal
Feeding Type	Suspension feeder	Grazer/Deposit feeder	Carnivore	Suspension feeder

	Gryp	**Hamu**	**Homo**	**Hybo**
Genus	*Gryphaea*	*Hamulus*	*Homomya*	*Hybodus*
Family	*Gryphaeidae*	unknown	*Pholadomyidae*	*Hybodontidae*
Order	*Ostreida*	*Serpulimorpha*	*Pholadomyida*	*Hybodontiformes*
Class	*Bivalvia*	*Polychaeta*	*Bivalvia*	*Chondrichthyes*
Mobility	Stationary	Stationary	Facultatively mobile	Fast moving
Life Habit	Epifaunal	Epifaunal	Deep infaunal	Nektonic
Feeding Type	Suspension feeder	Suspension feeder	Suspension feeder	Carnivore

	Idon	**Isoc**	**Isog**	**Kall**
Genus	*Idonearca*	*Isocrinus*	*Isognomon*	*Kallirhynchia*
Family	*Cucullaeidae*	*Isocrinidae*	*Malleidae*	*Tetrarhynchiidae*
Order	*Arcida*	*Isocrinida*	*Ostreida*	*Rhynchonellida*
Class	*Bivalvia*	*Crinoidea*	*Bivalvia*	*Rhynchonellata*
Mobility	Facultatively mobile	Stationary	Stationary	Stationary
Life Habit	Infaunal	Upper-level epifaunal	Epifaunal	Epifaunal
Feeding Type	Suspension Feeder	Suspension feeder	Suspension feeder	Suspension feeder

	Lima	**Lios**	**Loph**	**Lyos**
Genus	*Lima*	*Liostrea*	*Lopha*	Lyosoma
Family	*Limidae*	*Gryphaeidae*	*Ostreidae*	unknown
Order	*Pectinida*	*Ostreida*	*Ostreida*	*Archaeogastropoda*
Class	*Bivalvia*	*Bivalvia*	*Bivalvia*	*Gastropoda*
Mobility	Facultatively mobile	Stationary	Stationary	Slow moving
Life Habit	Epifaunal	Epifaunal	Epifaunal	Epifaunal
Feeding Type	Suspension feeder	Suspension feeder	Suspension feeder	unknown

	Mact	**Mele**	**Micr**	**Modi**
Genus	*Mactromya*	*Meleagrinella*	*Microeciella*	*Modiolus*
Family	*Mactromyidae*	*Oxytomidae*	*Oncousoeciidae*	*Mytilidae*
Order	*Lucinida*	*Pectinida*	*Cyclostomata*	*Mytilida*
Class	*Bivalvia*	*Bivalvia*	*Stenolaemata*	*Bivalvia*
Mobility	Facultatively mobile	Stationary	Stationary	Stationary
Life Habit	Infaunal	Epifaunal	Epifaunal	Semi-infaunal
Feeding Type	Chemosymbiotic	Suspension feeder	Suspension feeder	Suspension feeder

	Myop	**nati**	**Nodo**	**Nucu**
Genus	*Myophorella*	naticiform gastropod	*Nododelphinula*	*Nucula*
Family	*Myophorelloidae*	unknown	*Nododelphinulidae*	*Nuculidae*
Order	*Trigoniida*	unknown	*Amberleyoidea*	*Nuculida*
Class	*Bivalvia*	*Gastropoda*	*Gastropoda*	*Bivalvia*
Mobility	Facultatively mobile	Slow moving	Slow moving	Facultatively mobile
Life Habit	Infaunal	Epifaunal	Epifaunal	Infaunal
Feeding Type	Suspension feeder	Carnivore	Grazer	Deposit feeder/ Suspension feeder

	Pach	**Para**	**Phol**	**Pinn**
Genus	*Pachyteuthis*	*Parastomechinus*	*Pholadomya*	*Pinna*
Family	unknown	unknown	*Pholadomyidae*	*Pinnidae*
Order	*Belemnitida*	*Stomopneustoida*	*Pholadomyida*	*Ostreida*
Class	*Cephalopoda*	*Echinoidea*	*Bivalvia*	*Bivalvia*
Mobility	Fast moving	Slow moving	Facultatively mobile	Stationary
Life Habit	Nektonic	Epifaunal	Deep infaunal	Semi-infaunal
Feeding Type	Carnivore	Grazer/Deposit feeder	Suspension feeder	Suspension feeder

	Plat	**Pleu**	**Proc**	**Pron**
Genus	*Playtmyoidea*	*Pleuromya*	*Procerithium*	*Pronoella*
Family	*Laternulidae*	*Pleuromyidae*	*Procerithiidae*	*Arcticidae*
Order	*Pandorida*	*Pholadida*	*Sorbeoconcha*	*Cardiida*
Class	*Bivalvia*	*Bivalvia*	*Gastropoda*	*Bivalvia*
Mobility	Facultatively mobile	Facultatively mobile	Slow moving	Facultatively mobile
Life Habit	Deep infaunal	Infaunal	Epifaunal	Infaunal
Feeding Type	Suspension feeder	Suspension feeder	Grazer	Suspension feeder

	Pros	**Quen**	**rou**	**serp**
Genus	*Prososphinctes*	*Quenstedtia*	round tube	unknown
Family	unknown	*Quenstedtiidae*	*Serpulidae*	*Serpulidae*
Order	*Ammonitida*	*Cardiida*	*Canalipalpata*	*Canalipalpata*
Class	*Cephalopoda*	*Bivalvia*	*Polychaeta*	*Polychaeta*
Mobility	Fast moving	Facultatively mobile	Stationary	Stationary
Life Habit	Nektonic	Infaunal	Epifaunal	Epifaunal
Feeding Type	Carnivore	Deposit feeder	Suspension feeder	Suspension feeder

	Stom	**Tanc**	**Trig**
Genus	*Stomechinus*	*Tancredia*	*Trigonia*
Family	*Stomechinidae*	*Tancrediidae*	*Trigoniidae*
Order	*Stomopneustoida*	*Cardiida*	*Trigoniida*
Class	*Echinoidea*	*Bivalvia*	*Bivalvia*
Mobility	Slow moving	Facultatively mobile	Facultatively mobile
Life Habit	Epifaunal	Deep infaunal	Infaunal
Feeding Type	Grazer	Deposit feeder	Suspension feeder

	Tylo	**Vaug**
Genus	*Tylostoma*	*Vaugonia*
Family	*Tylostomatidae*	*Myophorelloidae*
Order	*Stromboidea*	*Trigoniida*
Class	*Gastropoda*	*Bivalvia*
Mobility	Slow moving	Facultatively mobile
Life Habit	Epifaunal	Infaunal
Feeding Type	Grazer	Suspension feeder