

Using GIS to Examine Biogeographic and Macroevolutionary patterns in Late Paleozoic Cephalopods from the North American Midcontinent Sea

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1 Abstract

2

3 Geographic range is an important macroevolutionary parameter frequently considered in

4 paleontological studies as species' distributions and range sizes determined by a variety of biotic

5 and abiotic factors well known to affect the differential birth and death of species. Thus,

6 considering how distributions and range sizes fluctuate over time can provide important insight

7 into evolutionary dynamics. This study uses Geographic Information Systems (GIS) and analyses

8 of evolutionary rates to examine how in the Cephalopoda, an important pelagic clade, geographic

9 range size and rates of speciation and extinction changed throughout the Pennsylvanian and early

10 Permian in the North American Midcontinent Sea. This period is particularly interesting for

11 biogeographic and evolutionary studies because it is characterized by repetitive interglacial-

12 glacial cycles, a global transition from an icehouse to a greenhouse climate during the Late

13 Paleozoic Ice Age, and decelerated macroevolutionary dynamics, i.e. low speciation and

14 extinction rates.

15 The analyses presented herein indicate that cephalopod species diversity was not completely

16 static and actually fluctuated throughout the Pennsylvanian and early Permian, matching findings

17 from other studies. However, contrary to some other studies, the mean geographic ranges of

18 cephalopod species did not change significantly through time, despite numerous climate

19 oscillations; further, geographic range size did not correlate with rates of speciation and

20 extinction. These results suggest that pelagic organisms may have responded differently to late

21 Paleozoic climate changes than benthic organisms, although additional consideration of this issue

22 is needed. Finally, these results indicate that, at least in the case of cephalopods, macroevolution

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24 during the late Paleozoic was more dynamic than previously characterized, and patterns may
25 have varied across different clades during this interval.

26 **Introduction**

27

28 Much work has focused on the relationship between geographic range size and rates of
29 speciation and extinction (e.g., Vrba, 1980; Jablonski, 1986; Eldredge, 1989; Stanley, 1990;
30 Lieberman, 2000; Jablonski & Roy, 2003; Rode & Lieberman, 2004, 2005; Kiessling &
31 Aberhan, 2007; Liow, 2007; Payne & Finnegan, 2007; Abe & Lieberman, 2009; Stigall, 2010;
32 Myers & Saupe, 2013; Myers, MacKenzie, & Lieberman, 2013; Dunhill & Wills, 2015;
33 Jablonski & Hunt, 2015; Orzechowski et al., 2015; Saupe et al., 2015; Castiglione et al., 2017;
34 Pie & Meyer, 2017; Simões et al., 2016; Lam, Stigall, & Matzke, 2018; Schneider, 2018).
35 Furthermore, the use of Geographic Information Systems (GIS) has greatly facilitated
36 investigations into this macroevolutionary relationship (Stigall & Lieberman, 2006; Hendricks,
37 Lieberman, & Stigall, 2008; Dunhill, 2012; Myers, MacKenzie, & Lieberman, 2013; Dunhill &
38 Wills, 2015; Lieberman & Kimmig, 2018). Here, we focus on how geographic range size and
39 rates of speciation and extinction changed throughout the Pennsylvanian and early Permian in
40 the North American Midcontinent Sea in the Cephalopoda, an important clade of pelagic
41 invertebrates (Landman, Tanabe, & Davis, 1996; Monnet, De Baets, & C. Klug, 2011; Korn et
42 al., 2015), using GIS. This time interval is particularly interesting for biogeographic and
43 evolutionary analysis because it is characterized by repetitive glacial-interglacial cycles, a global
44 transition from an icehouse to greenhouse climate during the Late Paleozoic Ice Age (LPIA)
45 (Montañez & Poulsen, 2013). Further, it is generally considered a time of sluggish
46 macroevolutionary dynamics, i.e. low speciation and extinction rates and low degrees of faunal

47 turnover, that have been demonstrated in studies of other marine invertebrate taxa (Sepkoski,
48 1998; Stanley & Powell, 2003; Bonelli & Patzkowsky, 2011). However, Balseiro (2016) did
49 document the existence of some profound evolutionary turnover in bivalves and brachiopods
50 over the course of this interval in regions closer to the ice sheets, such as present-day western
51 Argentina. Furthermore, recently Segessenman & Kammer (2018) showed that advanced cladid
52 crinoids do display elevated rates of evolution and turnover during this time interval (although
53 three other subclasses of crinoids do show subdued evolutionary rates), and fusulinid
54 foraminifera also fit the pattern shown in the advanced cladids (Groves & Lee, 2008; Groves &
55 Yue, 2009; Segessenman & Kammer, 2018).

56

57 There have been a variety of hypotheses proposed for the postulated decelerated
58 macroevolutionary dynamics of the LPPIA. Some studies contend that this pattern is a result of
59 environmental changes linked to glacial cycling while others point to tectonic activity (Stanley
60 and Powell, 2003; Powell, 2005; Fielding, Frank, & Isbell, 2008; DiMichele et al., 2009; Falcon-
61 Lang & DiMichele, 2010; Bonelli and Patzkowsky, 2011; Cecil, DiMichele, & Elrick, 2014;
62 Segessenman & Kammer, 2018). To date, many of the studies focusing on the
63 macroevolutionary dynamics of the LPPIA have concentrated on benthic marine invertebrates
64 (e.g., Stanley & Powell, 2003; Powell, 2007; Bonelli & Patzkowsky, 2011; Balseiro, 2016;
65 Segessenman & Kammer, 2018) as they are highly diverse and very abundant. However, it is
66 valuable to explicitly investigate evolutionary patterns in pelagic marine invertebrates as these
67 are also diverse and abundant organisms in late Paleozoic marine ecosystems (Landman, Tanabe,
68 & Davis, 1996; Monnet, De Baets, & Klug, 2011; Korn et al., 2015). In particular, given the
69 significant role that geographic factors play in speciation (Mayr, 1942; Eldredge & Gould, 1972;

70 Jablonski, 1986; Brooks & McLennan, 1991; Wiley & Lieberman, 2011; Jablonski & Hunt,
71 2015; Pie & Meyer, 2017), we might expect that pelagic organisms, because of their innately
72 greater dispersal ability (at least as adults), might show different patterns relative to taxa that
73 were benthic (Rojas et al., 2017; Yacobucci, 2017). This greater dispersal ability might allow
74 pelagic organisms to more fully occupy potentially available habitats than benthic organisms,
75 which could lead to larger geographic ranges and also less change in geographic ranges through
76 time. It also could potentially influence patterns of speciation and extinction by dampening
77 opportunities for geographic isolation and creating larger effective population sizes.

78

79 This study focuses on cephalopods from the Pennsylvanian-early Permian (Morrowan, Atokan,
80 Desmoinesian, Missourian, Virgilian, and Wolfcampian) in the Midcontinent Sea of the United
81 States as knowledge of the systematic affinities, geographic distribution and overall diversity of
82 cephalopods during this interval is relatively well understood (Miller, Dunbar, & Condra, 1933;
83 Newell, 1936; Plummer & Scott, 1937; Miller & Youngquist, 1949; Nassichuk, 1975; Landman,
84 Tanabe, & Davis, 1996; Kröger, 2005; Korn et al., 2015), the stratigraphy of the region is well
85 constrained (Heckel, 2008, 2013), and there are extensive exposures of fossiliferous units in the
86 region. Moreover, at this time the Midcontinent Sea was bordered by the Antler Orogeny to the
87 north, the Ancestral Rocky Mountain Orogeny to the west/northwest and the Ouachita Mountain
88 belt to the south/southeast (as well as various structural arches), such that it constituted a distinct
89 biogeographic region for marine invertebrates (Wells et al., 2007; Nelson & Lucas, 2011;
90 Joachimski & Lambert, 2015).

91

92 The Late Paleozoic Ice Age (LPIA) was the longest lived glacial period of the Phanerozoic and is
93 relatively well understood due to numerous stratigraphic, sedimentologic, paleontologic, and
94 isotopic studies (e.g., Mii, Grossman, & Yancey, 1999; Isbell, 2003; Stanley & Powell, 2003;
95 Raymond & Metz, 2004; Montañez, 2007; Powell, 2007; Tabor & Poulsen, 2007; Fielding,
96 Frank, & Isbell, 2008; Heckel, 2008; DiMichele et al., 2009; Bonelli & Patzkowsky, 2011;
97 Montañez & Poulsen, 2013; Balseiro, 2016; Roark et al., 2017; Segessenman & Kammer, 2018).
98 Glacial cycling in the midcontinent region has received much study (e.g., Isbell, 2003; Heckel,
99 2008, 2013). Modern synthesis of the glacial history indicates that the Morrowan to early
100 Desmoinesian represented a localized glacial period, the late Desmoinesian to early Virgilian
101 represented a widespread interglacial period with minor glaciation, and the late Virgilian to early
102 Wolfcampian represented the apex of widespread glaciation (Montañez & Poulsen, 2013).
103 Modeling predicts that sea-level oscillations in the late Pennsylvanian were between 50-100
104 meters depending upon the number and volume of melting ice sheets, and that water
105 temperatures are estimated to have been between 4-7°C cooler during glacial maxima than inter-
106 glacial periods (Heckel, 1986; Isbell, 2003; Montañez, 2007; Tabor, 2007; Heckel, 2008; Cecil,
107 DiMichele, & Elrick, 2014). The sea-level and temperature changes were likely to have had an
108 important influence on species distribution and geographic range size during this time
109 (Waterhouse & Shi, 2010). Though perhaps pelagic taxa would be less influenced by glacial
110 sea-level cycles than benthic taxa, as these cycles are also known to cause variation in seafloor
111 ventilation, with concomitant dysoxia/anoxia that is more severe for benthic taxa (A. Dunhill,
112 pers. comm., 2018).

113 **Materials and methods**

114
115

Comentario [GP1]: Yes, maybe, dysoxia-anoxia can be verified in hypersaline stratified estuarine or delta conditions, where soft body organisms predominate but have a lower preservational potential. So, you must be specific here and leave clear that you are talking just for cephalopods, do you? If not, you may have a taphonomic bias affecting the real stability of the benthic communities that is not being taken into account.

Taxa considered, stratigraphic correlation, specimens examined, and georeferencing: 79
 species belonging to 26 genera (13 nautiloids and 13 ammonoids) of cephalopods in the
 Pennsylvanian-Permian North American Midcontinent Sea were considered (Table S1). These
 represent the most abundant, well preserved, and taxonomically well understood species. Range
 reconstructions relied on the occurrence records of specimens derived from a comprehensive
 consideration of the entire taxonomic literature on the taxa studied. In particular, the following
 publications were utilized: Cox (1857), Swallow (1858), McChesney (1860), Meek & Worthen
 (1860, 1870), White & St. John (1867), White (1889), Hyatt (1891, 1893), Keyes (1894), Miller
 (1892), Smith (1896, 1903), Girty (1911, 1915), Mather (1915) Böse (1919, 1920), Miller
 (1930), Sayre (1930), Miller, Dunbar, & Condra (1933), Miller & Cline (1934), Miller & Owen
 (1934, 1937, 1939), Foerste (1936), Miller & Thomas (1936), Newell (1936), Plummer & Scott
 (1937), Elias (1938a, b), Miller & Moore (1938), Smith (1938), Miller & Furnish (1940a, b,
 1957), Teichert (1940), Clifton (1942), Miller & Unklesbay (1942), Young (1942), Sturgeon
 (1946), Miller, Lane, & Unklesbay (1947), Miller & Downs (1948, 1950), Miller & Youngquist
 (1947, 1949), Miller, Youngquist, & Nielsen (1952), Kummel (1953, 1963), Ruzhentsev &
 Shimanskiy (1954), Unklesbay (1954), Arkell et al. (1957), Unklesbay & Palmer (1958), Hoare
 (1961), Furnish, Glenister, & Hansman (1962), McCaleb (1963), Gordon (1964), Miller & Breed
 (1964), Teichert et al. (1964), Furnish & Glennister (1971), Ruzhentsev & Bogoslovskaya
 (1971), Nassichuk (1975), Sturgeon et al. (1982), Hewitt et al. (1989), Boardman et al. (1994),
 Kues (1995), White & Skorina (1999), Kröger & Mapes (2005), Furnish et al. (2009), and Niko
 & Mapes (2009) as well as from examination of all specimens, including types, housed in: the
 Division of Invertebrate Paleontology, Biodiversity Institute, University of Kansas (KUMIP); the
 University of Iowa Paleontology Repository (UI); and the Yale University Peabody Museum of

139 Natural History (YPM). These institutions house the most complete repository of cephalopod
140 diversity from this region and time as well as contain many of the type specimens of the species
141 examined. Moreover, all specimens used in the analysis were personally examined and
142 taxonomically-vetted via consideration of the literature, relevant type specimens, and other
143 material, with species assignments and determinations made by the first author. Over 1,100
144 specimens were identified to species level in this study (Kolis, 2017). We chose to focus on the
145 particular species considered, rather than downloading data from the Paleobiology Data Base
146 (PBDB), as we wanted to be able to personally validate the taxonomic identity of specimens
147 using collections data in conjunction with the literature in order to present more rigorously
148 corroborated hypotheses about the geographic distributions of species. We consider this
149 approach to be complementary to those approaches that utilize the PBDB in paleobiogeographic
150 studies. On the one hand, our approach did limit the number of species we were able to consider.
151 On the other hand, we believe it is quite important to evaluate hypotheses about systematic
152 affinities of fossil specimens, the actual data of the fossil record themselves, in detail and thereby
153 accurately define the taxonomic units considered. Given that species represent key
154 macroevolutionary units in nature (Eldredge, 1989; Wiley & Lieberman, 2011; Hendricks et al.,
155 2014), correctly characterizing them taxonomically, and thus validating the scope of their
156 geographic distributions, is critical. Moreover, it has recently been shown by Marshall et al.
157 (2018) that incorporating museum specimen data in the manner that our study has can greatly
158 expand, enhance, and improve knowledge of geographic distributions of fossil species, relative
159 to studies that only utilize data from the PBDB.

160

Specimens were assigned to the Virgilian, Missourian, Desmoinesian, Atokan, Morrowan, or Wolfcampian stages using the USGS National Geologic Map Database (U.S. Geological Survey, 2017), Sawin et al. (2006, 2008, 2009), Zeller (1968), Pope (2012), and Heckel (2013). The temporal boundaries of stages were derived from Davydov, Korn, & Schmitz (2012) (Table S2). All specimen localities were georeferenced during the course of the study. *GEOLocate* (Rios and Bart, 2018) and the *MaNIS Georeferencing Calculator* (Wieczorek, 2015) were used to obtain coordinates and uncertainty radii. All points were calculated in decimal degrees within the WGS84 model in the *GEOLocate* (Rios & Bart, 2018) world topo layer to ensure consistency and accuracy in determinations. Most uncertainty radii were less than 10 kms. Any specimens with questionable locality information were excluded from analyses, as were specimens with an uncertainty radius larger than the county they were contained within. This left 950 specimens (Table S1) to use in range reconstruction and statistical analysis of geographic range through geologic time. All statistical analyses were performed using Minitab® Statistical Software *Minitab v. 17* (Minitab, 2016) and *R-Studio Version 3.4.0* (2017).

Range reconstruction using GIS: Methods for range reconstruction follow Rode & Lieberman (2004, 2005), Stigall & Lieberman (2006), Hendricks, Lieberman, & Stigall (2008), Myers & Lieberman (2011), Myers, MacKenzie, and Lieberman (2013), and Dunhill & Wills (2015). In particular, after specimen occurrence data were georeferenced and assigned to temporal bins, *Excel* CSV files were compiled for the occurrence points for all specimens within species. CSV files were imported into *ArcGIS v. 10.3* (ESRI, 2014) and layers were created using geographic coordinate system ‘WGS 1984’ and projected coordinate system ‘WGS 1984 World Mercator’ (Fig. 1). These layers were input into *PaleoWeb* (The Rothwell Group LP, 2016) to rotate coordinates into continental configuration and geographic position of the midcontinent region

185 during the Pennsylvanian-early Permian (Fig. 2). These paleo-coordinate layers were then re-
186 projected into *ArcMap* (ESRI, 2014).

187 Geographic range values were calculated for each species (Table S3), using minimum bounding
188 geometry. This method has been shown to provide the most accurate procedure for
189 reconstructing changes in geographic range, especially for fossil taxa (Darroch & Saupe, 2018).
190 Convex hulls or buffers were given to every specimen occurrence point in each species and these
191 shapefiles were re-projected in 'South America-Albers Equal Area Conic'. This model was used
192 to accommodate the rotation of species occurrence coordinates into the southern hemisphere
193 during the Late Paleozoic. Species with three or more occurrence points were given a convex
194 hull that spanned the entire area between occurrences. In this way, multiple occurrence points
195 were combined to recreate the geographic range of a single species. Species with only one
196 occurrence point were given a 10km² buffer; species with just two occurrence points were given
197 a 10km² wide buffer which was used, in conjunction with their distance, to derive an area value
198 (following Rode & Lieberman [2004, 2005], Hendricks, Lieberman, & Stigall [2008], Myers &
199 Lieberman [2011], and Myers, MacKenzie, and Lieberman [2013]).

Eliminado: method

Comentario [GP2]: Why you use
Late here and "late" in other parts of
the text?

Con formato: Resaltar

200
201 **Assessing fossil record bias:** A common concern when studying the fossil record is that there
202 might be biases that could lead to inaccurate or artifactual findings. This concern can be
203 manifold, but the two most pertinent issues here involve incomplete sampling and/or issues of
204 stratigraphic bias. While it is important to be aware of the fact that the fossil record is
205 incomplete, it is worth recognizing that there is a large body of research that demonstrates that
206 many of the biogeographic patterns preserved in the fossil record, particularly in marine settings,
207 represent real biological phenomena, rather than taphonomic artifacts (Myers & Lieberman,

209 2011; Rook, Heim, & Marcot, 2013; Dunhill & Wills, 2015). Further, it is also prudent to realize
210 that sampling bias is a common issue in studies of extant biodiversity and species distribution,
211 and much work needs to be done in this area to alleviate the biases of the extant biota
212 (Lieberman, 2002; Carrasco, 2003).

213 The possibility that biases in the fossil record might lead to artifactual results was assessed in a
214 few different ways. First, the relationship between outcrop availability and the geographic range
215 of Pennsylvanian and Permian cephalopods was determined (see Myers & Lieberman, 2011). A
216 percent coverage table of the range size of species overlaid against temporal outcrop availability
217 was created using *ArcGIS* v. 10.3 (ESRI, 2014). A low percentage of overlap between range size
218 and outcrop area would suggest species distributions are more likely to reflect ‘real’
219 biogeographic patterns while a high percentage of overlap would suggest the presence or absence
220 of outcrops was significantly influencing results (Myers & Lieberman, 2011; Myers, MacKenzie,
221 & Lieberman, 2013; however, see also Dunhill, 2012 for an alternative viewpoint). The second
222 test used was an “n-1” jackknifing analysis. This procedure sub-sampled species range size
223 within each temporal bin to test the resilience of data to outliers. Mean range size estimations
224 were generated for each temporal bin; these were input into a one-way ANOVA to compare
225 jackknife estimates with the initial geographic range size estimates (Myers & Lieberman, 2011;
226 Myers, MacKenzie, & Lieberman, 2013). Finally, a Pearson rank correlation test was performed
227 to test the association of occurrence points and geographic range size; a close correlation would
228 indicate that reconstructed ranges were very much dependent on sampling and suggest that
229 reconstructed biogeographic patterns might be an artifact of a biased fossil record (Myers,
230 MacKenzie, & Lieberman, 2013).

232

Comentario [GP3]: Yes, it is possible, but see my previous comment for this particular study.

Comentario [GP4]: Sampling bias is a problem when part of the original community was not preserved, but you are right that the problem exists even in studies of recent biotas.

Con formato: Resaltar

Comentario [GP5]: It is as 2013 in the references list. Please check

233 **Speciation and extinction rate calculations:** Speciation and extinction rates were calculated in
 234 order to consider macroevolutionary dynamics in cephalopods from the Late Paleozoic
 235 Midcontinent Sea. Macroevolutionary rates were calculated using the following equation,
 236 presented in Foote (2000) and Rode & Lieberman (2005):

$$N_f = N_0 e^{rt}$$

237
 238
 239
 240 where N_0 is the species richness at the beginning of a temporal bin, N_f is the species richness at
 241 the end of a temporal bin, t is the duration of a temporal bin, and r is the total rate of diversity
 242 change. The temporal bins used were North American stages (Table S2). Species richness values
 243 (N_f) were determined for each temporal bin and were parsed into ‘carry-over’ (N_0) and ‘new’
 244 species richness values to ensure the accuracy of speciation and extinction rate calculation. In
 245 this way, it was possible to calculate the rate of diversity change between bins. For example, r
 246 $_{Atokan} = (\ln N_{0-Desmoinesian} - \ln N_{0-Atokan}) / t_{Atokan}$. Speciation rate within each temporal bin was
 247 calculated using the equation $S_{Atokan} = (\ln N_{f-Atokan} - \ln N_{0-Atokan}) / t_{Atokan}$, and extinction rate within
 248 each temporal bin was calculated using the equation $E_{Atokan} = S_{Atokan} - r_{Atokan}$ for each temporal
 249 stage (Foote, 2000; Rode & Lieberman, 2005).

251 **Results**

252
 253 **Paleobiogeographic patterns:** Geographic range data were analyzed separately across all
 254 cephalopods and individually for both nautiloids and ammonoids. Species geographic range size
 255 data were tested for normality within each temporal stage using the Anderson-Darling normality
 256 test. Range size data within each temporal stage were not normally distributed for any data

257 combination ($P < 0.005$). Instead, distributions were left skewed across all temporal stages for
258 every data grouping. Data were subsequently log-transformed to normalize data, and statistical
259 analyses were performed on both original and transformed data.

260

261 In general, geographic range size (either mean of transformed data or median of original) of
262 ammonoids and nautiloids increases during the Missourian and Virgilian stages (Fig. 3), which
263 was a time of sea-level rise due to warming during an interglacial (Isbell, 2003; Montañez &
264 Poulsen, 2013), such that there may be an association between the sea-level rise and the increase
265 in geographic range. Another possibility is that there was some change in taphonomic conditions
266 that occurred during the Virgilian that made it easier to discern the actual biogeographic
267 distributions of species at this time, relative to other time intervals (G. Piñeiro, pers. comm.,
268 2018). However, none of the changes in geographic range were statistically significant, so it is
269 not possible to infer strong correlation between the sea-level rise, or possible taphonomic factors,
270 and the range expansion. For instance, Mann-Whitney U tests found no statistically significant
271 changes (at $P \leq 0.05$) in median geographic range size for any temporal stages separately across
272 all cephalopods, as well as individually for nautiloids and ammonoids, even prior to correction
273 for multiple comparisons. This is because with the Mann-Whitney U test median range values

274 are considered, and for all cephalopods the median range values are constant through time
275 (79km²).

276

277 The same was true for two-sample t-tests performed on log-transformed data which again found
278 no statistically significant changes (at $P \leq 0.05$) in mean geographic range size though time, even
279 prior to correction for multiple comparisons. Again, recall that mean range size data are shown

Con formato: Resaltar

Comentario [GP6]: This is confusing to me, sorry. You applied the Mann-Whitney U test in your cephalopod sample to test the median range value, right? On the other hand you calculated the median of range size for all cephalopods and according to your figure 3 it is not constant through time. Please, explain a little better the results shown in figure 3.

Con formato: Resaltar

Comentario [GP7]: Do you have any figure to refer here?

Con formato: Fuente: Cursiva

280 in Figure 3, and the differences among log-transformed data through time are far less substantial
281 (and ultimately not significant). Furthermore, a one-way ANOVA, either with or without the
282 assumption of equal variance, failed to find any significant differences (at $P \leq 0.05$) between
283 stages for log-transformed mean geographic range size across all cephalopods as well as
284 individually for nautiloids and ammonoids.

Comentario [GP8]: But the peak shown in figure 3 corresponding to the Virgilian period should mean something!

285
286 **Analysis of macroevolutionary rates:** Speciation rate (S) and extinction rate (E) were
287 calculated for the Atokan, Desmoinesian, Missourian, and Virgilian stages across all
288 cephalopods and within nautiloids and ammonoids, respectively. The S and E presented across
289 all cephalopods are comprised of two calculations; one calculation included taxa that only
290 occurred in a single temporal stage (Table 1; Fig. 4), while the other calculation excluded taxa
291 that occurred in a single temporal stage (Table S4). S and E was also calculated for ammonoids
292 and for nautiloids including (Tables S5, S6) and excluding taxa that occurred in a single stage
293 (Tables S7, S8). Note, due to the dependence of calculations on diversity metrics from both
294 adjacent stages, it is not possible to accurately calculate the rate of biodiversity change (R), or S
295 and E for the first stage considered, the Morrowan, nor R or E for the last stage considered, the
296 Wolfcampian (these are thus left blank in Table 1 and Tables S4-S8). While it might have been
297 possible to infer S and E using other methods, to do so would exaggerate the significance of edge
298 effects and thus be problematic (Foote, 2000).

Comentario [GP9]: Ok again, but the peak shown in figure 3 corresponding to the Virgilian period should mean something! Maybe it would be good to say that even though the lack of any significant differences suggested by the tests used, there is a peak in the Virgilian that could suggest that a change existed but it is not as relevant as to be detected statistically. Because the peak exists and casually you have the highest extinction rate also in the Virgilian and continued so in the Wolfcampian (your figure 4)!

299
300 Across all cephalopods, S was high in the Atokan and Desmoinesian, fell in the Missourian, and
301 reached very low levels in the Virgilian and Wolfcampian (Fig. 4). By contrast, E was low in the
302 Atokan and Desmoinesian, began to rise in the Missourian, and reached even higher levels in the

303 Virgilian (Fig. 4). Essentially, across all cephalopods examined, when S is high, E is low, and
304 when S is low, E is high. This is potentially contrary to the pattern expected with an ecological
305 opportunity model of speciation (Simões et al., 2016), although the specific processes driving the
306 diversification could not be determined at this time. However, it is possible that when S was
307 high there may have been many short-lived species that could not be sampled that were actually
308 going extinct, and this phenomenon would artificially depress E.

309

310 As expected, S and E are lower when singletons are excluded (see Tables 1, S4). (See
311 Segesseman & Kammer [2018] for a recent discussion of how singletons can affect manifest
312 patterns in these types of studies.) Notably though, S and E patterns diverge somewhat between
313 ammonoids and nautiloids when considered individually. For instance, in nautiloids S is high in
314 the Atokan and Desmoinesian, then declines to moderate in the Missourian, and is at its lowest in
315 the Missourian and Wolfcampian (Table S6), whereas in ammonoids S is only high in the
316 Atokan, declines to moderate in the Desmoinesian, declines somewhat more in the Missourian
317 and then remains essentially constant through the Wolfcampian (Table S5). In addition, E is low
318 in ammonoids during the Desmoinesian and Missourian but high in the Atokan and
319 Wolfcampian (Table S5), whereas in nautiloids there are no observed extinctions during the
320 Atokan; values remain quite low for nautiloids in the Desmoinesian, rise somewhat in the
321 Missourian, and then rise again in the Virgilian (Table S6).

322

323 An important caveat regarding the calculation of S is that many of the species analyzed belong to
324 genera that were widely distributed beyond the Midcontinent Sea during the Late Paleozoic.
325 Thus, although none of the species considered in these analyses occurred outside of the

Comentario [GP10]: Interesting that in ammonoids S and E are high in the Atokan, a pattern that is not seen in the study for all cephalopods. It seems that the pattern for nautiloids is prevalent.

326 Midcontinent Sea, their close relatives did. It is conceivable that while speciation events and
327 rates by necessity are **herein** treated as occurring *in situ*, this might not always have been the
328 case. Instead, some speciation events could have occurred outside of the Midcontinent Sea with
329 subsequent invasion events into that region. These invasions would appear as *in situ* speciation
330 events in this analysis, although they actually were not. In the absence of phylogenetic
331 hypotheses for the genera considered it is not currently possible to consider how much of the
332 pattern pertaining to speciation rate shown in Fig. 4 is due to invasion instead of **speciation**.
333 Further, a related phenomenon could affect the calculation of E: at times what were treated as
334 extinction events might have simply been local extinctions in the Midcontinent Sea which could
335 have included emigration to other regions. As mentioned previously, it does not appear that any
336 of the species considered occur outside of the Midcontinent Sea, but a phylogenetic hypothesis
337 for these groups would be valuable for considering this issue in greater detail.

Eliminado: herein

Comentario [GP11]: Perhaps it is what the individual patterns are suggesting?

338
339 **Relationship between biogeography and macroevolutionary rates:** Mean geographic range
340 size increased during the Missourian and Virgilian and declined in the Wolfcampian (Fig. 3);
341 speciation rates were high in the Atokan and Desmoinesian and fell in the Virgilian (Fig. 4);
342 extinction rates were low in the **Atokan** and Desmoinesian and rose in the Virgilian (Fig. 4). The
343 Pearson correlation test in *Minitab 17* (Minitab, 2016) was used to examine the association
344 between geographic range and either speciation rate extinction rate in greater detail. No
345 significant (at $P \leq 0.05$) correlation between speciation or extinction rate and range size was
346 found across all cephalopods or within ammonoids or nautiloids individually (Table 2).

Eliminado: ¶

Comentario [GP12]: Except for ammonoids?

347 **However, in cases the values approach $P = 0.05$, for instance, the association between**

Eliminado: :

351 decreasing geographic range size and increasing extinction for all cephalopods and for
352 ammonoids alone. Notably, an association between decreasing geographic range size and
353 increasing extinction has been documented by numerous studies (e.g. Vrba, 1980; Jablonski,
354 1986; Eldredge, 1989; Stanley, 1990; Jablonski & Roy, 2003; Rode & Lieberman, 2004, 2005;
355 Kiessling & Aberhan, 2007; Payne & Finnegan, 2007; Stigall, 2010; Dunhill & Wills, 2015;
356 Jablonski & Hunt, 2015; Orzechowski et al., 2015; Saupe et al., 2015; Castiglione et al., 2017;
357 Pie & Meyer, 2017; Lam, Stigall, & Matzke, 2018; Schneider, 2018) and thus is a very robust
358 phenomenon in general and likely to be operating to some extent herein. However, over this time
359 interval and for this particular group of species the association is not statistically significant
360 (Table 2), probably because sample sizes are not large, and further this is likely because many
361 taxa were culled by the late Mississippian extinction (M. Powell, pers. comm., 2018).

Comentario [GP13]: Sentence needs revision. It seems something is missing or maybe it is wrong formulated or it is closely related to the following sentence?

Con formato: Resaltar

Comentario [GP14]: Thus, this same problem can be affecting the results that suggest a constant geographic range size for cephalopods through time

363 **Analysis of fossil record bias:** The low percentage of overlap between cephalopod species
364 geographic ranges and available outcrops, less than 1% in 29 out of 30 species (Table S9; the one
365 species with a larger percentage value, *Orthoceras kansasense*, occurs throughout the
366 Midcontinent Sea), suggests the results are not simply an artifact of an incomplete fossil record,
367 at least pertaining to outcrop availability. The “n-1” jackknifing analysis also supports the
368 robustness of the reconstructed ranges, as no statistically significant differences were found
369 between the mean of the reconstructed and subsampled range values for any time interval (all P-
370 values > 0.9), suggesting that one or a few occurrence records are not having a major influence
371 on biogeographic patterns. Similar results were found in other taxa and time periods by Hunt,
372 Roy, & Jablonski (2005), Myers & Lieberman (2011), and Myers, MacKenzie, & Lieberman
373 (2013), although Dunhill, Hannisdal, & Be dysoxia/anoxia is more severe for benthic taxa

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nton (2014) did find some association between outcrop area and diversity in the case of the marine fossil record of Great Britain. Finally, the Pearson correlation test shows no correlation (-0.055, P-Value = 0.789) between the number of occurrence points and geographic range size; this provides further evidence that the biogeographic signatures of Late Paleozoic cephalopods are unlikely to be simply an artifact of the fossil record.

379

Diversity patterns: Across all cephalopods, species richness increased from the Morrowan to the Atokan, peaked in the Desmoinesian, and decreased through the Wolfcampian (Fig. S1). A similar pattern is seen in the nautiloids (Fig. S2). However, the ammonoids (Fig. S3) demonstrate an earlier peak in the Atokan, followed by a Desmoinesian to Virgilian plateau, with a decrease in the Wolfcampian. Notably, previous studies of Late Paleozoic brachiopod communities in Bolivia showed a consistent trend between diversity and glacial cycling with increased diversity during glacial periods and decreased diversity during inter-glacial periods (Badyrka, Clapham, & Lopez, 2013). However, there seems to be less consistency between species richness trends and glacial cycling in the Midcontinent Sea. For instance, there is an increase in cephalopod species richness throughout the Morrowan to Desmoinesian associated with localized glaciation, and an interglacial period with generally minor glaciation is associated with a decrease in cephalopod species richness from the Desmoinesian to Virgilian, yet by contrast widespread glaciation is associated with a decrease in species richness from the Virgilian to the Wolfcampian. An important point, however, is that these are just raw diversity patterns and sample standardized diversity patterns show a different result (M. Powell, pers. comm., 2018).

Discussion

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397

Comentario [GP15]: Yes, it is clear that the pattern for all cephalopods is influenced by nautiloids.

Comentario [GP16]: You have not selected lower case for this? Why?

Con formato: Resaltar

Comentario [GP17]: Also, it should be taken into account that brachiopods and cephalopods can show different behavior in response to climatic changes and the conditions associated to them.

398 Geographic range shifts through time are one of the pervasive phenomena in the history of
399 life; these are manifest both within species and higher-level clades, occur at a number of
400 different time scales, and are frequently linked to climatic change (Wiley & Lieberman, 2011).
401 Specific examples do come from the Late Paleozoic, a time of extensive climate change
402 including profound glaciation along with numerous glacial and interglacial cycles (Montañez and
403 Poulsen, 2013). Those changes impacted patterns of geographic range in both terrestrial plant
404 (e.g., DiMichele et al., 2009; Falcon-Lang & DiMichele, 2010) and marine invertebrate
405 ecosystems (e.g., Leighton, 2005; Powell, 2007; Waterhouse & Shi, 2010). When it comes to
406 marine invertebrates from this time interval, most of the focus has been on the highly diverse
407 benthic faunas (e.g., Stanley & Powell, 2003; Powell, 2007; Bonelli & Patzkowsky, 2011;
408 Balseiro, 2016; Segessenman & Kammer, 2018); however, taxa that have a pelagic life style (as
409 adults) are also worth examining. Herein, 79 pelagic species of cephalopods were examined for
410 patterns of range size change using GIS and although in general these species exhibit some
411 evidence for changes in geographic range size (Fig. 3), those changes were not statistically
412 significant nor can they be directly tied to climate change. In a similar vein, many
413 paleontological studies have demonstrated that species with larger geographic ranges tend to
414 have lower extinction rates than species with narrower geographic range sizes (e.g., Vrba, 1980;
415 Jablonski, 1986; Eldredge, 1989; Stanley, 1990; Rode & Lieberman, 2004; Stigall & Lieberman,
416 2006; Payne & Finnegan, 2007; Stigall, 2010; Hopkins, 2011; Dunhill & Wills, 2015). Again,
417 this phenomenon was not found to be statistically significant in the case of the Late Paleozoic
418 cephalopod species considered herein (Table 2).

Con formato: Resaltar

Comentario [GP18]: However, the peak in figure 3 for an increased geographic range is associated to a widespread glaciation.

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Comentario [GP19]: To be consistent with all the results you got, I would say that the same phenomenon can be detected in the Late Paleozoic cephalopod species considered herein, but it resulted statistically not significant, probably because the small samples size.

420 There may be a few different explanations for these findings. First, it may be that cephalopod
421 species were not significantly affected by the glacial-interglacial climatic cycles transpiring
422 within the Late Paleozoic Midcontinent Sea. A second possible explanation, perhaps coupled to
423 the first, is that since cephalopods are highly mobile relative to benthic marine invertebrates such
424 as gastropods, bivalves, brachiopods, etc., they can more easily occupy a greater portion of their
425 potential range (at least as adults). Further, perhaps the available potential range of cephalopod
426 species does not change much in glacial relative to interglacial regimes. This may seem unlikely
427 given the vast fluctuations in sea level occurring at the time, but pelagic marine organisms,
428 because of their ease of dispersal, may more easily maintain consistent geographic ranges
429 relative to benthic counterparts. Another possible explanation for the pattern retrieved is that,
430 given the limits of stratigraphic correlation, sample size, and the completeness of the fossil
431 record, it was necessary for the analyses of species distribution conducted herein to focus on the
432 time scale of geological stages, whereas in actuality there were climatic changes occurring within
433 stages (Heckel, 2008, 2013); these probably did cause fluctuations in species' geographic ranges
434 within stages, but simply could not be observed in the present study. A final set of explanations
435 are related to the issue of sampling. For instance, it was more difficult for the analyses presented
436 herein to detect a relationship between geographic range size and macroevolutionary rate
437 because speciation and extinction rates could only be calculated for four stages. Further, a
438 common concern when studying the fossil record is that there might be biases that can lead to
439 inaccurate findings. This concern can be manifold, and although it is not entirely obviated by the
440 results presented regarding the apparent quality of the fossil record suggested by the various tests
441 presented, it does become harder to invoke as a specific, primary reason for results retrieved.

Comentario [GP20]: Removed
redundant text

Eliminado: relative to taxa that are
benthic

Eliminado:), such as brachiopods

446 | Another finding perhaps contrary to what might typically be expected for the Late Paleozoic is
 447 | that there was at least some evolutionary diversification and turnover within cephalopods, such
 448 | that species diversity did fluctuate throughout the Pennsylvanian and Early Permian.
 449 | Pennsylvanian rates of macroevolution are typically classified as ‘sluggish’ or ‘stolid’ across all
 450 | marine animals, and Sepkoski (1998) formalized the notion that there was a marked decline in
 451 | evolutionary rates of Carboniferous and Permian marine faunas. Stanley & Powell (2003)
 452 | reiterated this result and identified low mean macroevolutionary rates for marine invertebrate
 453 | taxa. Bonelli & Patzkowsky (2011) also documented a pattern of low turnover in the face of
 454 | major episodes of sea-level rise and fall due to climatic change. The results from the analyses
 455 | presented herein could indicate that macroevolutionary rate, at least in the case of Late Paleozoic
 456 | cephalopods, was more dynamic than often thought. One possible reason for this result is that
 457 | cephalopods are a fairly evolutionarily volatile group (Lieberman & Melott, 2013) relative to
 458 | many other marine invertebrate groups and have relatively high rates of diversification (Stanley,
 459 | 1979; Jacobs et al., 1994; Landman, Tanabe, & Davis, 1996; Monnet, De Baets, & Klug, 2011;
 460 | Korn, Klug, & Walton, 2015; Korn et al., 2015); thus, they would generally be expected to have
 461 | higher rates of speciation and extinction than typical. However, this may not be the entire
 462 | explanation, as other groups also seem to show elevated rates of speciation and extinction during
 463 | this time interval. For instance, Balseiro (2016) did document evolutionary turnover at high
 464 | latitudes, and elevated evolutionary rates have also been found in fusulinid foraminifera (Groves
 465 | & Lee, 2008; Groves & Yue, 2009) and advanced cladid crinoids (Segessenman & Kammer,
 466 | 2018). Ultimately, we support the contention raised by Segessenman & Kammer (2018) that
 467 | patterns from a few individual groups do not refute the general pattern of sluggish
 468 | macroevolution postulated for this time period in the history of life. The results may lend

Comentario [GP21]: I do not understand. If you use “late” instead “Late” you should be consistent.

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Comentario [GP22]: Both are benthic taxa

471 credence to the notion that macroevolutionary patterns across all marine animals are rarely
472 unitary for any one time period in the history of life, and instead often tend to be variegated.

473

474 **Conclusions**

475

476 Patterns of range size change in **late** Paleozoic cephalopods from the North American
477 Midcontinent Sea were investigated using GIS. These species do exhibit some evidence for
478 changes in geographic range size through time, but the changes were not statistically significant
479 nor could they be directly tied to climate change. Further, in contradistinction to what is usually
480 found in the fossil record, cephalopod species with larger geographic ranges were not found to
481 have lower extinction rates than species with narrower geographic ranges. These distinctive
482 patterns may perhaps be related to the fact that cephalopods are pelagic and highly mobile, at
483 least relative to many benthic marine invertebrates. Finally, the group shows more evolutionary
484 diversification and turnover during the Pennsylvanian and **early** Permian than is typical of other
485 marine invertebrate groups and this could be related to the fact that cephalopods are an
486 evolutionarily volatile group.

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487

488 **Acknowledgements**

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490

491 Thanks to Chris Beard, Kirsten Jensen, Julien Kimmig, and Luke Strotz for very helpful
492 discussions on this work and thanks to them and Matthew Powell, Alexander Dunhill, Dieter
493 Korn, Graciela Piñeiro, Thomas Algeo, and Wolfgang Kiessling for comments on previous

versions of the manuscript. Thanks to Julien Kimmig for assistance with collections related matters and for providing access to specimens in the KUMIP; thanks to Tiffany Adrain for assistance with collections related matters and for providing access to specimens in the UI; and thanks to Susan Butts for assistance with collections related matters and for providing access to specimens in the YPM. Thanks to Michelle Casey and Erin Saupe for assistance with stratigraphic correlations and use of GIS.

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Figure Captions

Figure 1: Distribution of Pennsylvanian and early Permian cephalopods.

A) Distribution of Pennsylvanian nautiloid and ammonoid data points (red) and B) early Permian
nautiloid and ammonoid data points (blue) across the midcontinent region of North America.
Plotted using *ArcGIS v. 10.3* (ESRI, 2014) software at 1: 20,000,000.

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Figure 2: Occurrence points of *Metacoceras* sp. and *Mooreoceras* sp.
For the Virgilian, shown on possible paleogeography of that stage, at 1:1,000,000,000 scale;
plotted using *PaleoWeb* (The Rothwell Group LP, 2016).

924 **Figure 3: Mean geographic range size in km² of cephalopods through time.**

925 Nautiloid species (A) and ammonoid species (B) range changes occur but are not statistically
926 significant when analyzed using non-parametric tests (note, median range size data not graphed
927 but for all cephalopods they are 79km² for all time intervals, for ammonoids they are 78.5km² for
928 the Desmoinesian and Wolfcampian and 79km² for all other time intervals, and for nautiloids
929 they are 79km² for all time intervals) or when log transformed data are analyzed using
930 parametric tests (note log transformed data not graphed but mean transformed values for all
931 cephalopods are 5.51 [standard error 0.75] for the Morrowan, 4.05 [standard error 1.02] for the
932 Atokan, 4.36 [standard error 0.49] for the Desmoinesian, 5.65 [standard error 0.49] for the
933 Missourian, 5.96 [standard error 0.79] for the Virgilian, and 4.31 [standard error 0.52] for the
934 Wolfcampian).

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Con formato: Superíndice

936 **Figure 4: Speciation and extinction rates through time.**

937 Values given in per Myr and derived from Table 1.