1 Phylogeny, disparity, and mass extinction response in the trilobite order Harpetida by JAMES D. BEECH^{1,2} and JAMES C. LAMSDELL¹ 2 3 ¹Department of Geology and Geography, West Virginia University, Morgantown, West 4 Virginia 26505, USA; e-mails: james.lamsdell@mail.wvu.edu 5 ²Current address: Department of Earth Sciences, University of Southern California, Los 6 Angeles, California 90089, USA; e-mail: jdbeech@usc.edu 7 8 **Abstract:** The trilobite order Harpetida has long been easily recognized but many 9 unanswered evolutionary questions about the group remain. This work explores the 10 phylogenetic relationships within Harpetida and studies the harpetid response to the Late 11 Ordovician mass extinction to better understand the relationship between extinction

16 parsimony and Bayesian inference optimality criteria retrieve tree topologies that support

focusing on individual harpetid genera. Phylogenetic analyses under both maximum

attempt of its kind to characterize the overall morphology of Harpetida, rather than

events and disparity. A discrete morphological character matrix was assembled from

published descriptions and refined through first-hand observations. This matrix is the first

17 harpetid monophyly but throw doubt onto previous hypotheses of the internal

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18 relationships of the order. Harpetid disparity proves remarkably stable over time. A

19 modest peak in the Ordovician is followed by a slow decline throughout the Silurian and

20 Devonian. After the Ordovician period, harpetids demonstrate little or no ability to

- 21 colonize new areas of morphospace. This may represent a fundamental failure to recover,
- 22 where the lasting impacts of Late Ordovician mass extinction continue to suppress

- 23 morphological innovation. These findings demonstrate that mass extinction events may
- 24 have complex impacts that play out over many millions of years.
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- 27 Key words: mass extinction, disparity, end-Ordovician extinction, morphospace,
- 28 phylogeny, trilobites

29	THE Late Ordovician (end-Hirnantian) mass extinction was the first of the five major
30	extinction events to shape the evolutionary history of the Phanerozoic (Raup and
31	Sepkoski 1982) and was responsible for eliminating an estimated 85% of marine species
32	(Sheehan 2001). Of these five mass extinctions, the Late Ordovician event was the
33	second most severe in terms of proportion of genera and families that disappeared
34	(Sepkoski 1996). This mass extinction is generally attributed to a brief period of intense
35	glaciation at the South Pole, and is thought to have occurred in two discrete pulses
36	(Congreve 2013 <i>a</i> ; Harper <i>et al.</i> 2014). The first of these is ascribed to a sudden
37	temperature decrease, and the second to the retreating of the ice sheets and the
38	displacement of anoxic waters onto continental shelf habitats (Sheehan 1973; Sheehan
39	2001; Brenchley et al. 2003; Congreve 2008; Finnegan et al. 2011; Sclafani et al. 2019).
40	Whether the Late Ordovician mass extinction had a substantial, long term impact
41	on the subsequent evolution of biota has been called into question (Droser et al. 2000;
42	McGhee et al. 2004; McGhee et al. 2012). In particular, McGhee et al. (2004) stated that
43	the extinction failed to eliminate any ecologically dominant taxa or evolutionary
44	innovations and was of minimal ecological impact. However, recent work (Congreve et
45	al. 2019; Scalfani et al. 2019) has challenged this scenario, suggesting that many groups
46	that survived the Late Ordovician mass extinction in fact experienced significant changes
47	in their morphologies, which influenced their potential for subsequent evolutionary
48	success. We address this issue by exploring whether the trilobite order Harpetida
49	experienced major morphological changes following the Late Ordovician mass

51	Mass extinction events are responsible for macroecological turnovers and,
52	ultimately, impose constraints on the long-term evolutionary success of clades (Harper et
53	al. 2014). While much work has explored the effects of these events on taxonomic
54	diversity, their impact on morphological disparity remains poorly understood (e.g.
55	Dommergues et al. 1996; Lupia 1999; Thorne et al. 2011; Bapst et al. 2012; Korn et al.
56	2013; Ruta et al. 2013; Lamsdell and Selden 2017; Sclafani et al. 2019). Why do some
57	extinction events remove morphologies at random, while others are highly selective
58	(Raup 1992; Jablonski and Raup 1995; Jablonski 2001; Korn et al. 2013)? Why do some
59	clades survive extinctions but fail to occupy new areas of morphospace (Thorne et al.
60	2011), while others seem primed for morphological innovation (Bapst et al. 2012)?
61	Addressing these questions is important for understanding the patterns of evolution and
62	extinction in the fossil record and for predicting how modern ecosystems may respond to
63	future mass extinctions (Dirzo et al. 2014).
64	Previous studies have suggested that trilobites in particular exhibited unique
65	patterns of survivorship following the Late Ordovician mass extinction. Chatterton and
66	Speyer (1989) focused primarily on trilobite developmental strategy during the Late
67	Ordovician and demonstrated that species with planktonic larvae were more prone to
68	extinction. Congreve and Lieberman (2011) showed that sphaerexochine trilobites, which
69	are thought to have had benthic larvae, were largely unaffected by the Late Ordovician
70	mass extinction. However, the closely related deiphonine trilobites seem to have been
71	much more strongly affected by this event, despite having a similar developmental
72	strategy, lifestyle, and distribution (Congreve 2013b), suggesting a more complex

73 scenario may have been at work. Additionally, the Late Ordovician mass extinction

eliminated all trilobites with a presumed pelagic adult lifestyle (Chatterton and Speyer1989).

76 Cold-water adaptations are thought to have been key to the survival and recovery 77 of various trilobites. This idea was examined in homalonotid trilobites by Congreve 78 (2013a), who concluded that a cold-water-adapted lineage was driven to evolve into a 79 warm-water-adapted lineage following the end-Ordovician mass extinction. Finnegan et 80 al. (2012) found that the maximum palaeolatitude at which a genus had been previously 81 sampled, a macroecological trait linked to thermal tolerance, strongly influenced 82 extinction risk during the Late Ordovician; specifically, they observed an unexpectedly 83 high extinction rate of low-paleolatitude genera. Finnegan et al. (2016) examined both 84 biogeographic and bathymetric factors and found that the extinction event preferentially 85 affected genera restricted to deeper waters or to relatively narrow palaeolatitudinal 86 ranges. All of this seems indicative of a strong ecological component to the mass 87 extinction event. At family level, Adrain et al. (1998) confirmed that extinction patterns 88 in Late Ordovician trilobites were related to clade size; families that survive the mass 89 extinction are more diverse than families that do not. 90 The present contribution examines the phylogeny and morphology of harpetid 91 trilobites. Harpetida Whittington, 1959 was an order of trilobites first recorded 500

92 million years ago during the Late Cambrian (Hughes 2007) and went extinct during the

93 Late Devonian at the base of the Upper Kellwasser Event (McNamara *et al.* 2009).

94 Harpetids are identified by the horseshoe-shaped "harpetid brim"; long genal

95 prolongations (broader and flatter than typical genal spines); reduced eyes, often with

96 strong ridges; a small pygidium; and an anteriorly narrowing glabella (Fortey and Owens

97 1997). Because harpetid trilobites are morphologically distinctive (Fig. 1, Fig. 2), they 98 are an ideal group for the discovery of informative phylogenetic characters. In addition, 99 harpetids were one of a handful of trilobite orders to survive the Late Ordovician mass 100 extinction (Hughes 2007). As such, harpetids are also an ideal model group for exploring 101 models of post-extinction recovery, specifically linking patterns of disparity change with 102 fluctuations in taxic richness.

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HISTORY OF THE HARPETIDA CONCEPT

105 Harpetida was raised to ordinal status by Ebach and McNamara (2002). The 106 group was previously placed within Ptychopariida, but harpetids are distinguished from 107 true ptychopariids by their marginal facial sutures and lack of a rostral plate (Ebach and 108 McNamara 2002). Ebach and McNamara (2002) recognized three harpetid families, 109 Harpetidae, Harpididae, and Entomaspididae, and approximately 30 genera. Although the 110 monophyly of the group is generally accepted, Adrain (2011) did not positively identify a 111 unified Harpetida. Instead, he placed the family Harpetidae (including those species 112 previously assigned to Entomaspididae) within the order Harpida, while regarding the 113 family Harpididae as incertae sedis.

114 Drawing on the conclusions of Fortey and Owens (1999), Adrain et al. (2004) 115 described members of the family Harpetidae as belonging to a morpho-functional group 116 of small, filter-feeding trilobites, characterized by a vaulted cephalic chamber flanked by 117 genal prolongations, a thorax suspended above the sediment surface, weak axial 118 musculature, a hypostome held above the level of the cephalic margin, and (usually) 119 reduced eyes. While highly generalized, this description offers a basis for understanding

the harpetid morphotype. Early work in experimental biomechanics (Pearson 2017) has
suggested that other members of this morpho-functional group are unlikely to have been
genuine filter feeders, casting uncertainty onto harpetids' ecological adaptations. Much of
the debate hinges upon the function of the harpetid brim, which has been variously
suggested to act as a plough, a sieve, a hydrostatic device, a sensory or respiratory organ,
or a structure for strengthening and lightening the exoskeleton (Ebach and McNamara
2002; McNamara et al. 2009).

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128 THE STUDY OF DISPARITY

129 While taxonomic diversity measures the number of taxa within a clade, disparity, 130 or morphological diversity, measures the range of forms (Foote 1991a; Foote 1992b; 131 Foote 1993; Foote 1994; Wills et al. 1994; Foote 1995; Foote 1997; Roy and Foote 132 1997). There are essentially two ways to quantify disparity (Briggs et al. 1992, Villier 133 and Eble 2004; Hetherington et al. 2015; Deline et al. 2018). The first is through 134 morphometrics, which can be further broken down into those techniques that use 135 continuous measurements (traditional morphometrics) and those that use landmarks 136 (geometric morphometrics). However, reliable morphometric data can be problematic to 137 collect when working with taxa with highly variable or divergent morphologies. The 138 alternative approach is to use discrete characters (which can be combined with 139 continuous data), often derived from cladistic data (Foote 1992b; Wills et al. 1994; 140 Wanger 1995; Lloyd 2016; Hopkins and Gerber 2017; Guillerme et al. 2020). Character-141 based disparity analyses overcome some of the challenges associated with divergent 142 morphology and multiple comparative studies have used discrete characters successfully

to study shifts in disparity over time and across multiple mass extinctions (Foote 1994,
144 1999; Wills 1998; Lofgren *et al.* 2003; Wesley-Hunt 2005; Young *et al.* 2010; Thorne *et al.* 2011; Bapst *et al.* 2012; Hughes *et al.* 2013; Ruta *et al.* 2013; Lamsdell and Selden
146 2017).

147 Notably, character-based disparity analyses appear to yield findings comparable 148 to more conventional, morphometric approaches (Villier and Eble 2004; Hetherington et 149 al. 2015). Hetheirngton et al. (2015), looking at caecilian amphibians, found that 150 disparity measurements based on skull morphometrics correlated well with disparity 151 measurements based on discrete neuroanatomical characters. This supports the earlier 152 findings of Villier and Eble (2004), saw patterns of high early disparity in both landmark 153 and character-based analyses of spatangoid echinoids. However, assessments of disparity 154 from traditional morphometrics may diverge from the other methods when very different 155 aspects of morphology are being measured; Villier and Eble (2004) cite the example of 156 quantifying an echinoid's overall shape, as opposed to its tuberculation and plate 157 architecture.

158 Brusatte et al. (2011) built on the idea of character-based disparity and presented 159 a method for phylogenetically correcting for missing data in such studies. The method 160 infers hypothetical ancestors at every node of the phylogenetic tree, reconstructs their 161 character states, and includes them in the disparity analysis as if they were sampled taxa. 162 Halliday and Goswami (2015) expanded on this approach by introducing the "extended 163 punctuational" method, which gives reconstructed ancestors a temporal range, rather than 164 having them appear only in a single time bin. This technique better enables direct 165 comparisons between disparity measures and taxonomic diversity measures, which are

166 often phylogenetically corrected, and is especially useful for groups with periods of low 167 sampled diversity, such as harpetids. However, this method must be applied cautiously, as the reconsticuted ancestors are not truly independent data points and may introduce 168 169 problematic side effects (e.g. smoothing bias) (Lloyd 2016; Guillerme et al. 2020). 170 Using a wide variety of approaches to study disparity, Foote (1997) concluded 171 that the evolution of morphological disparity is typically non-uniform, often expanding 172 early in clade history while taxonomic diversity remains comparatively low. Hughes et 173 al. (2013) likewise found that clades tend to reach their highest morphological disparity 174 early in their evolutionary history. However, this pattern can be truncated by mass 175 extinction events (Hughes et al. 2013), which is consistent with findings suggesting that a 176 wide variety of environmental factors contribute to patterns of disparity, including global 177 sea level (Dommerrgues et al. 1996), bathymetry (McClain 2005; Hopkins 2014), 178 substrate (Hopkins 2014), temperature (Hopkins 2014), and salinity (Lamsdell and 179 Selden 2017). 180 Whatever the contributing factors, it has long been recognized that taxonomic 181 diversity and disparity are frequently decoupled (Foote 1993; Lupia 1999; Thorne et al. 182 2011; Hopkins 2013; Ruta et al. 2013; Congreve et al. 2018). Hopkins (2013) studied this 183 phenomenon in Cambrian trilobites and concluded that signals of high disparity with low 184 taxonomic diversity are more likely the results of random or mean-targeted extinction, 185 rather than increased rates of morphological diversification. This finding is of particular relevance to this study, given its focus on the harpetid response to mass extinction. 186 187

188 DISPARITY AND MASS EXTINCTION

189 Mass extinctions can impact disparity in various ways. Korn et al. (2013), 190 studying the Devonian and Permian extinction events, suggested that disparity could be 191 affected during periods of widespread extinction in accordance with one of three general 192 modes. The first mode is essentially random, where available morphologies are removed 193 in a nonselective fashion. In this mode, overall morphospace occupation is not affected. 194 Possible examples of this are seen in ammonoids during the Toarcian–Aalenian transition 195 (Simon et al. 2010) and end-Permian mass extinction (Korn et al. 2013), and in blastoid 196 echinoderms (Foote 1991b). The second characteristic mode is marginal, where the edges 197 of morphospace are selectively and symmetrical trimmed. In this mode, overall variation 198 is reduced. Possible examples of this are seen in phacopid and proetid trilobites (Foote 199 1993). Finally, the mode of extinction may be lateral, with asymmetric selection 200 eliminating a particular region of previously occupied morphospace. In this mode, the 201 centroid of occupied morphospace shifts position. Possible examples of this are seen in 202 the response of ammonoids to the Kellwaser and Hangenberg events (Korn et al. 2013). 203 Additionally, Lamsdell and Selden (2017) examined the disparity of eurypterids 204 and suggested that even when mass extinctions remove morphologies with a high degree 205 of apparent randomness, recovery (i.e. re-expansion following a morphological 206 bottleneck) is often limited to those taxa that share a limited range of morphologies. This 207 finding is consistent with the work of Thorne et al. (2011), Congreve et al. (2018), and 208 Sclafani et al. (2019).

The disparity of phylogenetic groups tends to decrease over time, particularly during the interval immediately before or after a mass extinction (Zelditch *et al.* 2003). Valentine (1995) suggested that this may be due to a decrease in available ecological

212	habitats, while Gould (1991) suggested it may result from an increase in developmental
213	constraints. Crônier expanded on this idea of developmental constraint in her work on
214	phacopid trilobites (Crônier and Courville 2003; Crônier et al. 2005, 2011; Crônier and
215	Fortey 2006; Crônier 2007, 2010, 2013). Her findings demonstrated that changes in the
216	timing of development (i.e. heterochrony) were an important source of disparity in
217	trilobites. In times of ecological stress, such as sea level rise, trilobites tended to revert to
218	more juvenile (paedomorphic), presumably less specialized forms (Crônier 2013). This
219	reduced overall disparity by encouraging generalist morphologies.
220	Extinction events can also have a variety secondary or indirect effects on disparity
221	and diversity. These can include adaptive radiations (Sunberg 1996; Bapst et al. 2012),
222	where disparity and diversity both increase rapidly after a period of sharp decrease.
223	Alternatively, disparity may fail to recover despite modest gains in diversity (Thorne et
224	al. 2011; Ruta et al. 2013).
225	To understand the various responses to mass extinctions, further case studies are
226	needed. No previous study has explicitly explored the disparity of Harpetida and many
227	fundamental questions about harpetid morphology and phylogeny remain unanswered
228	(Ebach and McNamara 2002). Moreover, the question of selectivity in the Late
229	Ordovician mass extinction remains open (Adrain et al. 1998; McGhee et al. 2004;
230	Finnegan et al. 2012, 2016; Sclafani et al. 2019), especially with regard to trilobites
231	(Chatterton and Speyer 1989; Congreve and Lieberman 2011; Congreve 2013a, b). In
232	using harpetid disparity to explore selectivity during the Late Ordovician mass extinction,
233	this work seeks to shed light on both of these issues.
234	

235 METHODS

236 Phylogenetic Methods

We summarized harpetid morphology in the form of a discrete character matrix 237 238 (Supplemental Table 1), drawing upon the published trilobite literature. We drew many 239 characters in this matrix from the *Treatise on Invertebrate Paleontology* (Fortey and 240 Owens 1997) and from Ebach and McNamara (2002), which was a review of harpetid 241 systematics that presented a number of discrete morphological characters (between 3 and 242 26 for each genus, exclusively concerning the cephalon and related structures) that were 243 incorporated into several genus-level character matrices. Our study elevated this work to the ordinal level by synthesizing the relevant characters from these genus-level matrices 244 245 together with characters drawn from the *Treatise* and direct observations of specimens 246 housed at the Yale Peabody Museum of Natural History. 247 We coded 76 discrete morphological characters (Appendix 1; Supplemental Figure 1; the 248 data matrix is also available in the onlineMorphoBank database [O'Leary and Kaufman 249 2012] under the project code p2804, accessible at 250 http://morphobank.org/permalink/?P2804), including 69 cephalic characters, three 251 thoracic characters, and four pygidial characters. We included data coded from 47 252 species, using 35 museum specimens observed firsthand, 14 museum specimens observed 253 digitally, and c. 160 published figures. The coded taxa included 21 of the 29 recognized 254 harpetid genera, and included multiple representatives of each of the three previously 255 recognized harpetid families: Entomaspididae, Harpididae, and Harpetidae. The 256 remaining 8 genera, Chencunia Qiu, 1984; Kathrynia Westrop, 1986; Palaeoharpes Lu 257 and Qian in Zhou et al., 1977; Dictyocephalites Bergeron, 1895; Kitatella Petrunia in

Khalfin, 1960; *Metaharpides* Pillet and Courtessole, 1981; *Paraharpides* Pillet and
Courtessole, 1981; and *Pscemiaspis* Abdullaev and Khaletskaya, 1970 were excluded due
to the difficulty of procuring adequate fossil material or figures from which to code
character states (Table 1); the harpidid genus *Chencunia*, for example, is currently known
only from a few partial pygidia from the Upper Cambrian of China (Qiu 1984). Six
ptychopariid trilobites were included as outgroup taxa, with the analysis rooted on a
seventh outgroup, the redlichiid *Eoredlichia intermedia* Lu, 1940.

265 To test harpetid monophyly, we need to include several ptychopariids in our data 266 matrix, as it could not be known which ptychopariid taxa would prove most closely related to Harpetida. Lamsdell and Selden (2014) included both ptychopariids and 267 268 harpetids in a data matrix designed to robustly test the monophyly of proetid trilobites. 269 The work suggested several ptychopariid genera as viable candidates for inclusion in our 270 new matrix, including Modocia, Coosella, Crepicephalus, and Tricrepicephalus. These 271 four taxa represent a broad sampling of Ptychopariida, capturing much of the disparity of 272 the group. In addition, we chose to include representatives of the ptychopariid genera 273 *Cedaria* and *Ptychoparia*. The similarity between these trilobites and the members of 274 Harpetida has been noted by Rasetti (1945) in his work on the more basal members of the 275 order (i.e. the entomaspidids). The notion of including a trinucleid trilobite (order 276 Asaphida) was considered and eventually discarded on the basis of the high degree of 277 morphological convergence currently assumed between trinucleid and harpetid trilobites (Adrain et al. 2004). To provide structure, the outgroup was rooted on Eoredlichia 278 279 *intermedia*, from the paraphyletic order Redlichiida, thought to be the group that gave 280 rise to Ptychopariida during the Early to Middle Cambrian (Hughes 2007).

281	We performed parsimony analysis in TNT ((Tree analysis using New
282	Technology) (Goloboff et al. 2008). The data matrix was subjected to cladistic analysis,
283	employing random addition sequences followed by tree bisection-reconnection (TBR)
284	branch swapping with 100,000 repetitions with all characters unordered and of equal
285	weight; for more on the subject of differential character weighting see Congreve and
286	Lamsdell (2016). We also conducted Bayesian inference analyses in MrBayes 3.2.6
287	(Huelsenbeck and Ronquist 2001) with four independent runs of 100,000,000 generations
288	and four chains each under the maximum likelihood model for discrete morphological
289	character data (Mkv + Γ : Lewis 2001), with gamma-distributed rate variation among
290	sites. All characters were treated as unordered and equally weighted (Congreve and
291	Lamsdell 2016). Trees were sampled with a frequency of every 100 generations, resulting
292	in 1,000,000 trees per run. The first 25,000,000 generations (250,000 sampled trees) of
293	each run were discarded as burn-in, and the 50% majority rule consensus tree calculated
294	from the remaining 750,000 sampled trees across all four runs. Posterior probabilities
295	were calculated from the frequency at which a clade occurred among the sampled trees
296	included in the consensus tree.

297 Disparity Methods

The disparity analysis relied on scripts written in R, adapted from the work of Hughes *et al.* (2013). Discrete morphological characters from the character matrix were converted to generalized pairwise Euclidean distances (GED). These distances differ from the other most commonly used distance metric, Gower's coefficient (GC) (Gower 1971), primarily in the ways they handle missing data. The GED metric inserts a weighted mean fractional univariate distance based on those distances that are calculable,

304 while the GC metric simply rescales calculable distances based on the amount of 305 information available. Our GED distances were then combined with the known age 306 ranges of harpetid taxa to track changes in disparity over geological time. Disparity was 307 quantified based on the sums of ranges (measuring amount of morphospace occupied) 308 and of variances (measuring dispersion of taxa around group centroids) (Foote 1992a; 309 Wills et al. 1994; Ruta et al. 2013). We binned taxa from the matrix by geological age 310 and produced morphospace plots, each representing the suite of available morphologies at 311 a different point in the history of Harpetida. Multivariate statistical tests (PERMANOVA 312 - permutational multivariate analysis of variance using the Euclidean distance measure) 313 were performed in the software package PAST (Hammer et al. 2001) to test the 314 significance of overlap and separation of groups of taxa across all axes between time bins 315 at the period, stage, and epoch levels (Anderson 2017). Significance was estimated by 316 permutation and resampling of the taxa across groups with 9999 replicates. Statistical 317 analysis was performed with and without Bonferroni correction to control the familywise 318 error rate (Dunn 1961; Armstrong 2014). Particular attention was devoted to changes 319 across the Late Ordovician mass extinction boundary. Bonferroni corrections have been 320 criticized as overly conservative (Sokal and Rohlf 1995; Moran 2003; Nakagawa 2004; 321 Garamszegi 2006) but for this study we found it appropriate to skew against false 322 positives. 323 We inferred the habitat affinities of harpetid genera by adapting the methods of 324 Kiessling and Aberhan (2007). Harpetid occurrence data were taken from the 325 Paleobiology Database. For a few recently described genera (Eskoharpes, Globoharpes,

326 Notchpeakia) occurrence data were instead taken from the primary literature. We chose

to classify occurrences either deep water (deep subtidal to abyssal) or shallow water
 (marginal marine to shallow subtidal, including reefs) based on the reported depositional

329 environments. The apparent affinity of each genus (A_g) was calculated as

$$A_g = \frac{g_h}{Total_h} / \frac{g_i}{Total_i}$$

331 where g_h was the number occurrences of genus g in habitat h, g_i was the number of 332 occurrences of genus g in habitat i, Total_h was the total number of PBDB collections over 333 genus g's stratigraphic range collected from habitat h, and Totali was the total number of 334 PBDB collections over genus g's stratigraphic range collected from habitat i. An A_g greater than one indicates an apparent affinity for habitat h, while an A_g less than one 335 336 indicates an apparent affinity for habitat *i*. Whether A_g is significant was determined by 337 an exact one-sided binomial test (Kiessling and Aberhan 2007). As the absence of strictly 338 significant affinities is primarily due to low sample sizes, we assigned affinities based on 339 marginal significance ($p \le 0.1$) (Kiessling and Aberhan 2007). Taxa that could have 340 reached marginal significance given their abundance, but whose actual probability of 341 having an affinity for a particular habitat was not significant were classified as 342 generalists. PERMANOVA testing was used determine whether harpetids with differing 343 habitat affinities occupied significantly different areas of morphospace. 344 Additionally, PERMANOVA tests were used to verify that harpetids belonging to 345 different taxonomic families occupied significantly different areas of morphospace. This 346 method explored the possibility of correlation between harpetid distribution in 347 morphospace and phylogenetic clade membership. 348 We included reconstructed ancestors in addition to the sampled taxa to 349 phylogenetically correct for intervals of low sampling. We generated these according the

350 methods described by Brusatte et al. (2011) and Halliday and Goswami (2015). We 351 mapped reconstructed characters onto the nodes of the parsimony consensus tree using 352 Mesquite (Maddison and Maddison 2018) and coded each node as if it were a sampled 353 taxon. Thirty-six reconstructed harpetids were generated in all. These reconstructed taxa 354 were assigned age ranges using the "extended punctuational" method (Halliday and 355 Goswami 2015). This method treats the ancestral morphology as occurring along the 356 entire phylogenetic branch so that the total morphological disparity of each time bin can 357 be accurately assessed (Halliday and Goswami 2015).

358

359 **RESULTS**

360 Phylogenetic Analysis

361 The parsimony analysis yielded 18 most parsimonious trees with an ensemble 362 Consistency Index of 0.456, an ensemble Retention Index of 0.815, a Rescaled 363 Consistency Index of 0.572, and a tree length of 189. A strict consensus of these trees is 364 shown in Figure 3. Bayesian inference analysis retrieved a broadly similar set of 365 relationships, also shown in Figure 3. The parsimony strict consensus tree showed a 366 monophyletic Harpetida preceded by a paraphyletic grade of ptychopariid trilobites. In 367 the Bayesian analysis *Ptychoparia striata* appeared as the sister to group to Harpetida 368 (Fig. 3).

Two of the three previously recognized harpetid families—Harpetidae and Harpididae—were retrieved as monophyletic groups in both Bayesian and parsimony analyses. By contrast, Entomaspididae consistently appeared as a polyphyletic grade of basal harpetids, with Harpididae clustered within Entomaspididae. The entomaspidid

Baikadimapsis jikdongensis appeared as the sister to all other harpetids in both Bayesianand parsimony analyses.

375 Three taxa previously assigned to Harpetidae (Conococheaguea ovata, Bowmania 376 lassieae, and Heterocaryon vargum) also fell within the entomaspidid grade. In both 377 Bayesian and parsimony analyses, these three taxa formed a clade within the 378 entomaspidid grade, which may indicate support for a monophyletic Heterocaryonidae. 379 The remaining harpetidids formed a large clade. This group included 380 representatives of many recognized harpetid genera. Of these, *Eoharpes, Dubhglasina*, 381 Brachyhipposiderus, Bohemoharpes, Kielania, Globoharpes, Eskoharpes, and 382 Dolichoharpes appeared as monophyletic in both Bayesian and parsimony analyses. In 383 the parsimony analysis *Hibbertia* appeared as a paraphyletic grade, while *Scotoharpes* 384 was found to be polyphyletic. Bayesian analysis retrieved a monophyletic *Hibbertia* but a 385 paraphyletic Scotoharpes. Both analyses found Lioharpes to be polyphyletic and Harpes 386 to be either polyphyletic or paraphyletic. Collectively this group corresponded well with 387 the established harpetid family Harpetidae and is defined by a wide bilamellar brim, 388 marginal sutures, and small, tuberculate eyes. The entomaspidid trilobite *Entomaspis* 389 *radiatus* was retrieved as the sister group to Harpetidae in both analyses. 390 Disparity Analysis

391 Disparity levels remained largely stable within Harpetida over time. Analyses at 392 the stage and epoch level failed to show statistically significant changes in the sum of 393 variances over time (Fig. 4), but analysis at the period level suggested that harpetid 394 disparity reached a modest maximum in the Ordovician and then declined steadily until 395 the group's extinction in the Late Devonian (Fig. 5). At all levels of analysis, the sum of

ranges likewise showed a slow overall decline following a modest peak in the Ordovician(Fig. 4; Fig. 5).

398 Harpetid morphospace occupation remained statistically significantly different for 399 all four time periods (Table 2; Fig. 6). From their initial occupied region of morphospace, 400 early harpetids initially expanded their overall morphospace occupation as the group 401 diversified and then underwent a migration in occupied morphospace via a vacation 402 through extinction of their ancestral morphospace region and preferential radiation within 403 the newly occupied area of morphospace, so that from the Middle Ordovician onward 404 morphospace occupation has largely inverted, with overall morphospace occupation 405 decreasing on slightly as the group transitioned into the Silurian. Originations continue 406 across this newly defined region of morphospace until the Late Devonian, where another 407 shift occurs with the centroid migrated toward what had previously been the margins of 408 occupied morphospace, again driven by preferential extinction within specific sub-409 regions of morphospace.

410 As expected, harpetid distribution in morphospace is largely correlated with 411 phylogenetic clade membership. PERMANOVA testing of family level partitions showed 412 highly significant statistical differences in the morphospace occupied by each putative 413 harpetid family, with the lowest levels of significance seen between Entomaspididae and 414 Harpididae (Table 3). The most populous family, Harpetidae, occupied a distinct region 415 of morphospace encompassing about half of the total occupied morphospace, including 416 the regions occupied in the Middle Ordovician and Late Devonian. Harpididae, 417 Heterocaryonidae and entomaspidids occupy overlapping regions of morphospace 418 incorporating the regions occupied in the Cambrian and Early Ordovician (Fig. 7).

419	PERMANOVA testing showed that inferred shallow water harpetids occupied
420	significantly different areas of morphospace than inferred deep water harpetids (Table 4).
421	Shallow water taxa also occupied significantly different areas of morphospace than
422	generalist taxa. However, generalist taxa did not occupy significantly different areas than
423	deep water taxa (Table 4). Specifically, shallow water taxa occupy areas of harpetid
424	morphospace including the Cambrian and Early Ordovician region as well as region
425	colonized during the Middle Devonian. Deep water taxa are predominantly located in the
426	region of morphospace occupied in the Late Devonian (Fig. 8).

428 **DISCUSSION**

429 Harpetid Phylogeny

430 Harpetid Monophyly. Both our Bayesian and parsimony trees show strong support for the 431 monophyly of harpetids. They group separately from all of the varied ptychopariids 432 included in the analysis, representing a unique order within the subclass Librostoma. 433 Entomaspidid Polyphyly. In the retrieved phylogenies, harpidids are nested within the 434 polyphyletic entomaspidids. The harpidid clade includes all three of the harpidid taxa 435 present in the data matrix and is defined by several morphological characters, such as a 436 genal ridge running posterolaterally from the eye; concave genae; radiating, 437 anastomosing genal cacae; an expanded L3; and the lack of genal spines. In addition, 438 some (though not all) harpidids are distinguished by marginal sutures. Importantly, this 439 suggests that the so-called "hypoparian" suture condition, where the cephalic sutures skirt 440 the margin of the cephalon (Raw 1949), emerged at least twice within the harpetids: once 441 in the harpidids and once again in the harpetidids. Given the number of morphological

characters uniting the recognized harpidids, it seems desirable to retain the familyHarpididae, though the group currently falls within the entomaspidid grade.

444 Three taxa previously assigned to the harpetidids —*Conococheaguea ovata*, 445 Bowmania lassieae, and Heterocaryon vargum-also form a small clade within the 446 entomaspidid grade. That these three should resolve here, rather than among the 447 harpetidids, is perhaps unsurprising given their unusual morphology. For example, none 448 of these taxa displays the usual "harpetid brim" (Fig. 2). Bowmania instead sports a wide 449 fringe of radiating spines (Ludvigsen 1982; Adrain and Westrop 2004) that may have 450 performed a similar ecological function, making it perhaps the most morphologically 451 unusual of all harpetids. Meanwhile Conococheaguea and Heterocaryon have no brim-452 equivalent structure, only a narrow trough (Rasetti 1959; Adrain and Westrop 2004). 453 Moreover, these taxa lack other key harpetidid synapomorphies, such as a tuberculate eye 454 structure, alae, marginal sutures, and broad, flattened genal prolongations. 455 The genera Conococheaguea, Bowmania, and Heterocaryon should be removed 456 from the harpetidids and assigned to a separate family. Heterocaryon was once the type 457 for the trilobite family Heterocaryonidae, proposed by Hupé (1953). The family is no 458 longer recognized, due to the supposed similarity between the genera *Heterocaryon* and 459 *Bowmania* and the genus *Entomaspis* in both cephalic and pygidial structure (Ludvigsen 460 1982). However, these findings indicate that the name could be resurrected to describe

this new clade of harpetids, which until this point have remained largely in a taxonomic

462 limbo (Hupé 1953; Rasetti 1959; Jell and Adrain 2002). This new incarnation of the

463 family Heterocaryonidae is defined by a few key synapomorphies, including high

464 cephalon convexity and equilateral glabellar lateral margins.

465 Harpetidid Genera. With Conococheaguea, Bowmania, and Heterocaryon recognized as 466 heterocaryonidids, the harpetidids resolve as a clade. They are the largest harpetid family 467 and include many currently recognized genera. However, the monophyly of several of 468 these genera now appears dubious.

469 The genus Scotoharpes is clearly polyphyletic. Most species of the putative genus 470 form a loose grouping, with a clade of three taxa ("Scotoharpes" spasski, "Scotoharpes" 471 tatouyangensis, and "Scotoharpes" raaschi) forming a polytomy with two other 472 Scotoharpes species, as well as a substantial clade of other harpetidids. Yet even if these 473 two Scotoharpes ("Scotoharpes" loma and Scotoharpes domina, the type species for the 474 genus) group with the others, this grouping would be paraphyletic. There are also two 475 other supposed Scotoharpes ("Scotoharpes" latior and "Scotoharpes" consuetus) that fall 476 much more basally within the harpetidids and do not appear closely related to each other. 477 Therefore, Scotoharpes monophyly is rejected. 478 Some characters that were supposedly diagnostic for *Scotoharpes*, such as a 479 glabella that is longer than it is wide, deep posterior glabellar furrows, the absence of a 480 large anterior boss, and the anterior-posterior position of the eyes (Ebach and McNamara 481 2002), now appear plesiomorphic for harpetidids. Others, such as low alae, deep pits

demarcating the outer margin of the genal roll, and a flat preglabellar field, appear in only some species of the genus. This finding supports the assessment of Ebach and McNamara (2002), who noted in passing that *Scotoharpes* might very well be non-monophyletic and consist of several clades, describing the genus as a "dumping ground".

486 *Lioharpes* also appears to be polyphyletic. The two species in this analysis resolve
487 in a polytomy in the parsimony consensus tree and resolve as polyphyletic in the

488	Bayesian tree. As with Scotoharpes, the members of Lioharpes seem to share a
489	generalized harpetid morphology, with little to unite them in particular. For example, the
490	radiating ridges found at the genal roll-brim boundary, thought by Fortey and Owens
491	(1997) to be diagnostic for <i>Lioharpes</i> , are also seen in other harpetidid genera such as
492	Bohemoharpes and Scotoharpes (Norford 1973; Ebach and McNamara 2002). Likewise,
493	the narrow alae seen in Lioharpes are also seen in some Scotoharpes, Dubhglasina, and
494	Brachyhipposiderus, suggesting this character is plesiomorphic for harpetidids (Norford
495	1973; Ebach and McNamara 2002).
496	The genus Helioharpes has already been identified as a subjective synonym of
497	Harpes by Jell and Adrain (2002). This study supports this conclusion; both
498	'Helioharpes' included in our analysis independently appear as sister taxa to separate
499	clades of Harpes. In fact, recognizing the synonymy of Harpes and Helioharpes almost
500	reveals a monophyletic Harpes, as all 'Helioharpes' and Harpes in this analysis form a
501	single clade. However, this clade also contains the genus Dolichoharpes.
502	Several potential solutions exist. One is simply to synonymize Dolichoharpes
503	with Harpes. This would create a monophyletic Harpes, but may seem unsatisfactory, as
504	many Dolichoharpes have a distinctive appearance that is different from other harpetidids
505	(Whittington 1949). In particular, the genal prolongations of <i>Dolichoharpes</i> often appear
506	narrower than those of Harpes, sometimes dramatically so as in the case of
507	Dolichoharpes dentoni (the representative of the genus included in this analysis; see Fig.
508	1). However, this striking change in appearance is achieved by a relatively small angular
509	rotation of the genal spines, and Harpes and Dolichoharpes are united by many other,
510	subtler morphological similarities. For example, anterolaterally directed eye ridges

511 appear to be a synapomorphy of *Dolichoharpes* and *Harpes* (including 'Helioharpes') 512 (Ebach and McNamara 2002). Therefore, it may be best to treat Dolichoharpes in 513 synonymy with *Harpes*, or to acknowledge that *Harpes* may comprise multiple 514 recognizable genera. Complicating the issue is that fact that Harpes is another 515 phylogenetic "dumping ground" (Ebach and McNamara 2002) for ambiguous harpetid 516 taxa. As such, Harpes (as presently conceived) may well be genuinely polyphyletic, 517 consisting of two related but distinct clades, each also closely related to *Dolichoharpes*. 518 In this case, the clade containing the type species, *Harpes macrocephalus*, would be the 519 genuine *Harpes*, while the other may represent a novel genus. 520 Another possible instance of paraphyly is seen in Hibbertia. The two Hibbertia 521 included in this study appear in the parsimony consensus tree as a grade leading to the 522 problematic Harpes and/or Dolichoharpes clade discussed above. However, in the 523 Bayesian tree *Hibbertia* resolves as a clade. Further research is needed to fully assess the 524 monophyly of this genus. 525 All other harpetidid genera included in this analysis appear to form monophyletic groups. Some of these are represented by only one species, and so their monophyly has 526 527 yet to be genuinely tested; such is the case for Kielania, Brachyhipposiderus, and 528 Dubhglasina. Other genera, such as Globoharpes and Eskoharpes, appear well supported. 529 *Eskoharpes* is particularly notable, as its clade includes "*Harpes*" neogracilis, supporting 530 its transfer to Eskoharpes by McNamara et al. (2009).

531 Disparity in Harpetida

532 Disparity Through Time. In the disparity corrected analysis, the sum of ranges and sum of

variance (Fig. 4; Fig. 5) both show only a muted peak in harpetid disparity during the

Ordovician. If genuine, this early peak may represent the initial diversification of
harpetids, which would be consistent with the work of previous researchers (Foote 1997;
Hughes *et al.* 2013) who found that clades generally morphologically diversify early in
their history.

538 No abrupt Late Ordovician decline is seen in harpetid disparity (Fig. 4; Fig. 5). 539 Instead, disparity appears to decrease slowly and steadily from the Late Ordovician 540 onward. The rate of decrease does not significantly increase during the Late Ordovician 541 mass extinction. This finding closely resembles that of Ruta et al. (2013), which showed 542 that amonodont therapsid disparity decreased steadily over time, relatively unaffected by 543 the end-Permian mass extinction. More broadly, these findings might be said to agree 544 with those of Lupia et al. (1999), which showed that the rate and character of change in 545 the disparity of Late Cretaceous angiosperms was not altered by the end-Cretaceous mass 546 extinction, and with Zelditch et al. (2003), whose work with piranha suggested that 547 disparity tends naturally to decay over time. This scenario also shows that disparity and 548 diversity were significantly decoupled in harpetids, which supports the idea that disparity 549 and diversity are frequently decoupled (Foote 1993; Lupia 1999; Thorne et al. 2011; 550 Hopkins 2013; Ruta et al. 2013).

The fact that harpetids in particular were relatively unaffected by the Late Ordovician mass extinction may perhaps be explained by their life history strategy. Harpetid larvae are thought to have been benthic rather than planktonic (Chatterton and Speyer 1989). In this they resemble sphaerexochine trilobites, which also had benthic larvae and were largely unaffected by the Late Ordovician mass extinction. Both of these examples agree with the general findings of Chatterton and Speyer (1989), who

concluded that trilobites with benthic larvae were generally far more resilient to the LateOrdovician mass extinction.

559 Despite their resilience, harpetid disparity remained low or continued to fall from 560 the Late Ordovician onward, until the group went extinct at the end of the Devonian; no 561 long-term recovery of disparity could be discerned (Fig. 4; Fig. 5). This finding is again 562 consistent with Ruta et al. (2013) and also with Thorne et al. (2011), which found that 563 ichthyosaurs failed to fully recover their former disparity following the end-Triassic mass 564 extinction. These cases are analogous to that of a "Dead Clade Walking" or DCW 565 (Jablonski 2002), where a clade that fails to recover in terms of taxonomic diversity 566 following a mass extinction. However, the failure of a clade to recover in terms of 567 disparity (rather than diversity) in the aftermath of an extinction event lacks a widely 568 accepted name. The authors submit the term "Fixed Clade Walking" or FCW as a 569 possible designation for such cases that would mirror the cadence of the term "Dead 570 Clade Walking" while emphasizing a loss of morphological variability. 571 The concept of an FCW is related to, but not synonymous with, the concept of 572 stabilomorphy (Kin and Błażejowski 2014). On its surface, an assessment of 573 stabilomorphy simply observes that a group of organisms—like harpetids—remains 574 relatively morphologically stable over time and space. However, Kin and Błażejowski 575 (2014) also explicitly links stabilomorphy to successful adaptation, writing of 576 stabilomorphs "...their level of adaptation, the quality of their adaptive strategy is so high 577 (so effective), that small changes which had to continually occur over several millions 578 years...did not result in any significant morphology variations."

579 In contrast, the term "Fixed Clade Walking" claims no relationship between a loss 580 of morphological variability and successful adaptation. Instead, an FCW implies a form 581 of "survival without recovery" (Jablonski 2001). Following a major perturbation, an 582 FCW is unable to generate new morphologies, not because their adaptive strategy is 583 beyond improvement, but because changed conditions suppress further morphological 584 innovation.

585 Morphospace Through Time. Studying harpetid morphospace provides additional insights 586 (Fig. 6). Early in their history, harpetids' morphospace occupation expands considerably 587 (Fig. 6). PERMANOVA testing confirms that Cambrian and Ordovician harpetid 588 morphospace were statistically significantly different (Table 2). These changes support 589 an assessment of early diversification and moreover show that harpetids were very 590 morphologically dynamic during their early history. However, this dynamicity seems to 591 wane somewhat as the order enters the Silurian. Although Silurian and Ordovician 592 harpetid morphospace remain statistically different, the significance of this difference has 593 declined (Table 2). In particular, the area of morphospace occupied during the Late 594 Ordovician is quite similar to that occupied throughout the Silurian. Yet the sum of 595 variance does gradually decline (Fig. 4; Fig. 5), even while overall morphospace 596 occupation changes little (Fig. 6). From this it seems clear that morphologies were being 597 removed in a random, non-selective fashion (Korn et al. 2013). These losses were 598 gradual, rather than occurring suddenly at the end of the Ordovician, indicating that 599 harpetid morphospace was generally agnostic to the Late Ordovician mass extinction. 600 During the Devonian the centroid harpetid morphospace shifts once more, and the 601 emergence of morphologically distinctive genera (*Eskoharpes* and *Globoharpes*) during

602	this time suggests that the order retained some ability to innovate. (Fig. 6). However, the
603	scale of these shifts in morphospace is relatively small (Fig. 6) and overall measures of
604	disparity continue their slow decline (Fig. 4; Fig. 5). Harpetids lose access to large areas
605	of morphospace and never regain any of regions they held prior to the end of the
606	Ordovician (Fig. 6). From this, it seems evident that harpetids became less
607	morphologically dynamic over their history. Other researchers have observed that groups
608	emerge from mass extinction events lacking the ability morphologically or ecologically
609	diversify (Jablonski 2002; Thorne et al. 2011; Ruta et al. 2013). It is possible that,
610	although the Late Ordovician mass extinction had little immediate impact on harpetid
611	disparity, the biotic crisis nevertheless permanently damaged harpetids' ability to
612	generate new morphologies, supporting our description of the order as a "Fixed Clade
613	Walking". These findings emphasize that the impacts of a mass extinction event can be
614	complex and may take many millions of years to fully unfold.
615	Patterns of Morphospace Occupation. The phylogenetic signal within harpetid
616	morphospace appears strong. Statistically significant differences are found between the
617	areas of morphospace occupied by all four putative harpetid families (Table 3). Of these,
618	three families also group well along PCO 1 and PCO 2 (Fig. 7). The polyphyletic
619	entomaspidids (perhaps unsurprisingly) do not group well (Fig. 7). This group also shows
620	the least statistically significant difference with another harpetid family, in this case the
621	harpidids (Table 3).
622	Harpetids associated with deep water habitats occupy significantly different areas

624 is consistent with the work of Hopkins (2014), which revealed strong environmental

of morphospace than those associated with shallow water habitats (Table 4). This finding

623

625 influence on patterns of disparity in trilobites, and emphasizes the way in which studies 626 of disparity can bridge the gap between ecological and phylogenetic understandings of 627 evolutionary history. One interesting detail of this analysis is that *Bowmania* emerges as a 628 generalist harpetid, despite its unusual morphology. This places Bowmania into the same 629 ecological category as taxa with a more generalized harpetid morphotype like Harpes and 630 Bohemoharpes, which appear quite distantly from Bowmaina (Fig. 8). This may support 631 the idea that *Bowmania* evolved a different solution to a recurring ecological problem, 632 using a fringe of radiating spines in place of the familiar harpetid brim.

633

634 SYSTEMATIC PALAEONTOLOGY

635 Class TRILOBITA Walch, 1771

636 Subclass LIBROSTOMA Fortey, 1990

637 Order HARPETIDA Whittington, 1959

638 *Diagnosis.* Cephalon subsemicircular to ovate in outline, with long genal prolongations

639 (broad, flat) or spines (narrow, rounded). Glabella convex, narrowing forward, with up to

640 three pairs of lateral glabellar furrows, preoccipital pair isolating triangular lateral lobes;

occipital ring convex; preglabellar field sloping outward and downward to flat or

642 upwardly concave fringe or bilamellar border; alae may be present; prominent eye lobes

or tubercles centrally located on genae, with strong eye ridges and in some forms with

644 genal ridges also; sutures commonly marginal except on dorsal side at genal angles, and

645 (in genera with eye lobes) where sections of sutures run inward close together. Thorax

646 with 12 or more segments; axis convex; pleurae flat, with broad pleural furrows.

647 Pygidium short, subtriangular or elongate, with convex axis. Radiating, anastomosing

- 648 genal caecae may be present on genae and preglabellar field, and extending onto fringe;
- 649 external surface of cephalon may be tuberculate or granulose (modified from Fortey and
- 650 Owens 1997).
- 651 *Range*. Upper Cambrian to Upper Devonian.
- 652
- 653 Family 'ENTOMASPIDIDAE' Ulrich in Bridge, 1931
- 654 *Type genus. Entomaspis* Ulrich in Bridge, 1931.
- 655 Included genera. Baikadamaspis Ergaliev, 1980; Entomaspis Ulrich, 1931; Notchpeakia
- 656 Adrain and Westrop, 2006.
- 657 Diagnosis. Exoskeleton small. Cephalon semicircular, characterized by anterior and
- posterior sections of facial sutures close to each other, both directed outward-backward;
- 659 librigenae fused together through doublure, consisting of narrow dorsal strips connecting
- 660 eyes to margin and genal spines (modified from Fortey and Owens 1997).
- 661 *Remarks*. The family Entomaspididae is resolved in the present analyses as polyphyletic
- and needs to be redefined so as to be monophyletic. The family is here used to denote
- various basal harpetids, with the quote marks denoting polyphyly.
- 664 Range. Upper Cambrian to Lower Ordovician.
- 665
- 666 Family HETEROCARYONIDAE Hupé, 1953
- 667 *Type genus. Heterocaryon* Raymond, 1937.
- 668 Included genera. Bowmania Walcott, 1925; Conococheaguea Rasetti, 1959;
- 669 Heterocaryon Raymond, 1937.

670 Diagnosis. Angle of cephalic curvature greater than 90 degrees. Yoked librigenae, but 671 lacking true bilamellar fringe. Facial sutures directed outward and forward. Small eye 672 lobes, diverging posteriorly, with eye ridges anterolaterally directed. High cephalon 673 convexity and equilateral glabellar lateral margins. Highly convex genae. Lacking alae. 674 Narrow, rounded genal prolongations (i.e. spines). Pygidium of four to eight segments. 675 *Remarks.* This family level name has been resurrected to describe a clade including the 676 genus *Heterocaryon* and two other taxa previously assigned to Harpetidae but whose 677 unusual morphology otherwise placed them within the entomaspidid grade in these 678 phylogenetic analyses. 679 Range. Upper Cambrian. 680 681 Family HARPIDIDAE Whittington, 1950 682 Type genus. Harpides Beyrich, 1846. 683 Included genera. Chencunia Qiu, 1984; Dictyocephalites Bergeron, 1895; Harpides

- Beyrich, 1846; *Kitatella* Petrunia in Khalfin, 1960; *Loganopeltis* Rasetti, 1943;
- 685 Loganopeltoides Rasetti, 1945; Metaharpides Pillet and Courtessole, 1980; Paraharpides
- 686 Pillet and Courtessole, 1980; *Pscemiaspis* Abdullaev, 1970.
- 687 *Diagnosis*. Cephalic border not sharply set off from convex genae and preglabellar field;
- alae small, semicircular; facial sutures marginal, or with parallel anterior and posterior
- 689 sections running close to each other and directed anterolaterally from eye tubercles to
- 690 margin; genal caeca radiating over cheek lobes and in some extending onto cephalic
- 691 border. Hypostome subrectangular, length (sag.) equal to that of glabella. Thorax with 20
- or more segments; axis narrow; long (tr.) pleurae curving back at outer part may be

693 extended into spines, with deep pleural furrows and convex posterior bands (Fortey and

694 Owens 1997).

695 Range. Upper Cambrian to Lower Ordovician.

- 696
- 697 Family HARPETIDAE Hawle and Corda, 1847
- 698 *Type genus. Harpes* Goldfuss, 1839.
- 699 Included genera. Bohemoharpes Vanek, 1963; Brachyhipposiderus Jell, 1985;
- 700 Dolichoharpes Whittington, 1949; Dubhglasina Lamont, 1948; Eoharpes Raymond,
- 1905; Eskoharpes McNamara et al., 2009; Globoharpes McNamara et al., 2009; Harpes
- Goldfuss, 1939; *Hibbertia* Jones and Woodward, 1898; *Kathrynia* Westrop, 1986;
- 703 Kielania Vanek, 1963; Lioharpes Whittington, 1950; Palaeoharpes Lu and Qian in Zhou
- *et al.*, 1977; *Scotoharpes* Lamont, 1948.
- 705 Diagnosis. Eye tubercles each with two lenses; semicircular alae adjacent to posterior
- 706 glabellar lobes; bilamellar fringe with opposed pits in outer surfaces, genal rolls steeply
- sloping, brim gently sloping, with stout girder on lower lamella separating these two
- parts, flattened prolongations of fringe varying in length; cephalic suture skirts marginal
- band of fringe. Hypostome pear-shaped in outline, with ovate middle body, large anterior,
- small posterior, and wings. Thorax with 12 to 29 segments, pleurae bent down ventrally
- 711 at tips. Pygidium small, short (sag.), triangular, with few segments. External surface of
- glabella and genae with raised ridges in reticulate pattern, tuberculate, or smooth; minute
- tubercles on fringe between pits and marginal band, on internal rim, and elsewhere
- 714 (modified from Fortey and Owens 1997).
- 715 *Range.* Lower Ordovician to Upper Devonian.

717 CONCLUSIONS

718	The present study evaluates the morphology and evolution of harpetid trilobites, a
719	group that had long been easily recognized but often incompletely understood. This study
720	provides strong support for harpetid monophyly. Two of the three existing harpetid
721	families have also been found to be monophyletic, while the third, Entomaspididae, has
722	been found to be non-monophyletic. In addition, support has been found for the
723	monophyly of a fourth harpetid family, the Heterocaryonidae, which unites several
724	previously problematic taxa. At a finer taxonomic scale, several harpetid genera are
725	found to be poorly supported (e.g. Scotoharpes, Lioharpes), while several others are
726	found to be well supported (e.g. Eskoharpes, Globoharpes). Importantly, marginal
727	sutures, a key innovation within Harpetida (Rasetti 1945; Ebach and McNamara 2002),
728	are found to have arisen on at least two separate occasions within the order.
729	Harpetid disparity proves remarkably stable over geological time. A modest peak
730	in the Ordovician is followed by a slow decline throughout the Silurian and Devonian.
731	After the Ordovician, harpetids demonstrate little or no ability to colonize new areas of
732	morphospace. This may represent a fundamental loss of morphological variability in the
733	wake of the Late Ordovician mass extinction, a condition we here term "Fixed Clade
734	Walking." These findings demonstrate that mass extinction events may have complex
735	impacts that play out over many millions of years, affecting not only species diversity but
736	the range of living forms.

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- and analyzing harpetid trilobite fossils.
- 747

748 SUPPORTING INFORMATION

- 749 Appendix S1: Characters for Phylogenetic Analysis
- 750 Character 1. Angle of cephalic curvature. >90 degrees (0); \leq 90 degrees (1).
- 751 Character 2. Cephalon convexity. Low (0); high (1).
- 752 Character 3. Widest point of cephalon. Posterior one-third (0); anterior one-third (1).
- 753 Character 4. Marginal rim demarcated along its inner margin by enlarged pits. Inner
- margin of rim not demarcated by enlarged pits (0); row of enlarged pits
 demarcates inner margin of rim (1).
- 756 Character 5. Bilamellar brim. Absent (0); present (1).
- 757 Character 6. Bilamellar brim profile. Flat (0); concave (1); convex (2).
- 758 Character 7. Brim width. < glabellar length (0); \geq glabellar length (1).

- Character 8. Narrowing of brim along prolongations. Brim constant in width for the
 majority of prolongation (0); brim narrowing almost from the level of the
 occipital ring (1).
- 762 Character 9. Pitting present on outer field of cephalon/brim. Absent (0); present (1).
- 763 Character 10. Brim pitting extent. <50% of the brim surface visibly pitted (0); >50% of
 764 the brim surface visibly pitted (1).
- 765 Character 11. Radiating ridges at the genal roll-brim boundary. Absent (0); present (1).
- 766 Character 12. Girder separating genal rolls from brim. Absent (0); present (1).
- 767 Character 13. Girder kink. Absent (0); present (1).
- 768 Character 14. Deep pits along outer margin of genal roll. Absent (0); present (1).
- 769 Character 15. Position of hypostome constriction. Anterior one-fourth of hypostome (0);
 770 midpoint of hypostome (1).
- 771 Character 16. Median tubercule on frontal lobe. Absent (0); present (1).
- 772 Character 17. Preglabellar transverse ridge. Absent (0); present (1).
- 773 Character 18. Anterior preglabellar depression. Absent (0); present (1).
- 774 Character 19. Anterior boss. Absent (0); present (1).
- Character 20. Anterior boss inflation. Slight inflation (0); bulbous, rising above the
 surrounding surface (1).
- 777 Character 21. Vaulted inner genal roll. Absent (0); present (1).
- 778 Character 22. Genal roll profile. Convex (0); concave (1).
- 779 Character 23. Glabellar morphology. Narrowing anteriorly (0); widening anteriorly (1).
- 780 Character 24. Depth of 1st pair of lateral glabellar furrows (S1). Deep, well defined (0);
 781 shallow, poorly defined (1).

- 782 Character 25. Morphology of S1. Posterolaterally directed furrows (0); J-shaped furrows
 783 not continuous with S0 (1).
- 784 Character 26. Second pair of lateral glabellar furrows (S2). Absent (0); present (1).
- 785 Character 27. Third pair of lateral glabellar furrows (S3). Absent (0); present (1).
- 786 Character 28. Length of 1st pair of lateral glabellar furrows (S1). <50% of glabellar
 787 width (0); >50% of glabellar width (1).
- 788 Character 29. Maximum length of S2 or S3. Long, c. 50% of glabella width (0); short, c.
 789 25% of glabella width (1).
- Character 30. Positioning of S2 and S3. Well-spaced (0); S2 and S3 close together, third
 pair of glabellar lobes (L3) expanded (1).
- 792 Character 31. Cross-sectional morphology of glabellar furrows. Rounded (0); incised793 (1).
- Character 32. Curvature of glabellar furrows S2–S3. Straight (0); incurving (curve posteriorly) (1); outcurving (curve anteriorly) (2).
- 796 Character 33. Glabellar lateral margins. Converging anteriorly (0); parallel (1).
- 797 Character 34. Relative volume of first pair of glabellar lobes (L1). L1 <10% of glabellar
- 798 volume (0); L1 > 10% of glabellar volume (1).
- 799 Character 35. Glabellar and genal primary surface ornament/sculpture. Tuberculate (0);
- 800 reticulation of pits (1); fine granulations (2).
- 801 Character 36. Sagittal crest. Absent (0); present (1).
- 802 Character 37. Yoked librigenae. Absent (0); present (1).
- 803 Character 38. Facial suture position. Cuts through outer margin of cephalon (0); skirts
 804 margin (1).

805	Character 39.	Angle of anterior facial suture and transverse line passing through both
806		compound eyes. 30–45 degrees (0); \geq 60 degrees (1); \leq 0 degrees (2).
807	Character 40.	Cephalic sutures with marked inward curve just posterior to cephalic
808		margin. Absent (0); present (1).
809	Character 41.	Eye structure. Eye lobes (0); tubercles (1).
810	Character 42.	Angle formed by axis of greater elongation of eye with longitudinal axis
811		of cephalon. Diverging posteriorly (0); equilateral (1).
812	Character 43.	Lateral position of eye. Closer to alar furrow (0); closer to axial furrow
813		(1).
814	Character 44.	Anterior-posterior position of eye. On posterior of cephalon $(0-45\%)(0)$;
815		on midline or anterior $(48\%+)$ (1); eye encompasses entire cephalon length
816		(2).
817	Character 45.	Genal ridge running postero-laterally from eye. Absent (0); present (1).
818	Character 46.	Eye area in dorsal view (as percentage of cephalon). 20–30% (0); <15%
819		(1).
820	Character 47.	Eye ridges. Absent (0); present (1).
821	Character 48.	Eye ridge direction. Anterolaterally directed (0); posterolaterally directed
822		(1); transversely directed (perpendicular to longitudinal axis of the body)
823		(2).
824	Character 49.	Ridge insertion on compound eye. Anterior point of eye (0); mid-point of
825		eye (1).
826	Character 50.	Genae curvature. Flattened/moderately convex (0); concave (1); extremely
827		convex (2).

- 828 Character 51. Radiating, anastomosing genal caeca. Absent (0); present (1).
- 829 Character 52. Axial furrow depth. Shallow (0); deep (1).
- 830 Character 53. Extension of axial furrows beyond glabella onto genal roll. Absent (0);
- 831 present (1).
- 832 Character 54. Alae. Absent (0); present (1).
- 833 Character 55. Alae strength as defined by alar furrow. Faint (shallow alar furrow) (0);
 834 strong (deep alar furrow) (1).
- Character 56. Alae morphology. Subdivided into two crescentic portions by presence of
 interalar furrow (0); continuous, interalar furrow absent (1).
- 837 Character 57. Relief of alae. Depressed or sunken (0); flattened/low relief (1); inflated838 (2).
- 839 Character 58. Vaulting of inflated alae. Inflated alae not exhibiting vaulting (0); inflated
 840 alae vaulted (1).
- 841 Character 59. Alae size. Small (<L1)(0); large $(\geq L1)(1)$.
- 842 Character 60. Alae direction. Transversely/laterally directed (0); anterolaterally directed843 (1).
- Character 61. Large pits on genal area opposite alae. Absent or not enlarged (0); present
 and enlarged (1).
- 846 Character 62. Anterior alar ridge. Absent (0); present (1).
- 847 Character 63. Median tubercule on occipital ring. Absent (0); present (1).
- 848 Character 64. Genal spines or prolongations. Postero-lateral margin of cephalon
- 849 extending into genal spines/prolongations (0); cephalon not extending into
 850 genal spines/prolongations (1).

851 Character 65. Cross-sectional morphology of genal spines or prolongations. Broad, 852 flattened (prolongations) (0); narrow, rounded (spines) (1). 853 Character 66. Genal spine or prolongation curvature. Interior/proximal margin straight 854 (0); interior/proximal margin incurving (1). 855 Character 67. Genal spine or prolongation angle of divergence. High (\geq 30 degrees) (0); 856 moderate (11 to 29 degrees) (1); reduced (≤ 10 degrees) (2). 857 Character 68. Curvature of genal spines or prolongations. Straight (rapidly flattens from 858 cephalon) (0); concave (twisted along length of prolongation) (1). 859 Character 69. Genal spine or prolongation length. Longer than cranidium (0); equal to or 860 shorter than cranidium length (1). 861 Character 70. Thoracic axis width (at broadest point). \leq glabellar width (0); = glabellar 862 width (1); > glabellar width (2). 863 Character 71. Free thoracic tergite count. $\leq 15(0)$; $\geq 16(1)$. 864 Character 72. Form of pleural spine terminations on thoracic tergites. Acute, spinous (0); 865 blunt (1). 866 Character 73. Pygidium with medial posterior indentation. Absent (0); present (1). 867 Character 74. Number of axial rings in pygidium. 4-5(0); 3(1); 2(2); 7-8(3). 868 Character 75. Pleural field margin. Downturned (0); upturned (1); flat (2). 869 Character 76. Terminal lappets. Absent (0); present (1). 870

871 DATA ARCHIVING STATEMENT

- 872 Data for this study, including a full set of character state illustrations are available in
- 873 MorphoBank: <u>http://morphobank.org/permalink/?P2804</u> [login with user name 2804;

- 874 password "papersINpalaeontology"] [please note that the data for this paper are not yet
- published and this temporary link should not be shared without the express permission of
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885 AUTHOR CONTRIBUTIONS

- <u>JCL conceived of the initial study; JDB and JCL developed the study; JDB gathered the</u>
- 887 <u>study data; JDB performed analyses with input from JCL; JDB and JCL interpreted the</u>
- 888 results of the analyses; JDB and JCL wrote the manuscript.

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1255 EXPLANATIONS OF FIGURES AND TABLES

- 1256 FIG. 1. Fossil trilobites of the order Harpetida. A: Lioharpes venulosus, B:
- 1257 Dolichoharpes dentoni (?), C: Kielania dorbignyana, D: Bohemoharpes ungula, E:
- 1258 Scotoharpes spasskii, F: Hibbertia wegelini. 1 cm scale bar included where available.
- 1259
- 1260 FIG. 2. Morphology of the harpetid cephalon.
- 1261

1262 FIG. 3. Revised harpetid phylogeny and harpetid families. A: Consensus of 18 most

1263 parsimonious trees from TNT. B: Bayesian tree from MrBayes. Green: Bremer support

- 1264 values, Red: Bootstrap values, Blue: Jackknife values, Black: posterior probabilities
- 1265 values.

1266

1267 FIG. 4. The disparity of the order Harpetida (including reconstructed ancestors) through

1268 time, with stage level temporal resolution. Red: Sum of variances. Blue: Sum of ranges.

- 1269 Minimum number of harpetid genera in relevant time bin. Dashed lines represent major
- 1270 mass extinction events.

1271

1272 FIG. 5. The disparity of the order Harpetida (including reconstructed ancestors) through

1273 time, with period level temporal resolution. Red: Sum of variances. Blue: Sum of ranges.

1274	Minimum number of harpetid genera in relevant time bin. Dashed lines represent major
1275	mass extinction events.
1276	
1277	FIG. 6. Phylogenetically corrected harpetid morphospace occupation through time, with
1278	epoch level resolution.
1279	
1280	FIG. 7. Harpetid morphospace, partitioned by family. Yellow: Harpididae, Green:
1281	'Entomaspididae', Pink: Heterocaryonidae, Blue: Harpetidae.
1282	
1283	FIG. 8. Harpetid morphospace, partitioned by habitat affinity. Red: shallow water
1284	affinity. Blue: deep water affinity. Black: generalist. Yellow: Insufficient data.
1285	
1286	TABLE 1. Recognized harpetid genera included or excluded from these analyses.
1287	
1288	TABLE 2. PERMANOVA test results of Harpetida, including reconstructed ancestors,
1289	(Permutation N: 9999, Total sum of squares: 9731, F: 13.6, p (same): 0.0001) for
1290	statistical differences between taxa for each of the four period-level time bins based on
1291	PCO analyses. Values in regular font are for the Bonferroni corrected <i>p</i> -values, those in
1292	italics are the raw F values.
1293	
1294	TABLE 3. PERMANOVA test results of Harpetida (Permutation N: 9999, Total sum of
1295	squares: 9105, Within-group sum of squares: 7230, F: 7.521, p (same): 0.0001) for
1296	statistical differences between taxa for each of the four harpetid families based on PCO

- analyses. Values in regular font are for the Bonferroni corrected *p*-values, those in italicsare the raw F values.
- 1299
- 1300 TABLE 4. PERMANOVA test results of Harpetida (Permutation N: 9999, Total sum of
- 1301 squares: 3634, Within-group sum of squares: 3397, *F*: 1.603, *p* (same): .003) for
- 1302 statistical differences between taxa for each of the habitat affinities based on PCO
- 1303 analyses. Values in regular font are for the Bonferroni corrected *p*-values, those in italics
- 1304 are the raw F values.

TABLES

Genus	IncRud@d
Baikadamaspis	1308
Bohemoharpes	1200
Bowmania	1.309
Brachyhipposiderus	13/10
Chencunia	1311
Conococheaguea	1312
Dictyocephalites	$1 N^{12}$
Dolichoharpes	15413
Dubhglasina	13/14
Entomaspis	1315
Eoharpes	1716
Eskoharpes	1.210
Globoharpes	13/17
Harpes	13/18
Harpides	1319
Heterocaryon	1220
Hibbertia	13720
Kathrynia	1321
Kielania	13/22
Kitatella	122
Lioharpes	1.22.5
Loganopeltis	1 <i>\$</i> 24
Loganopeltoides	1325
Metaharpides	1 \$ 26
Notchpeakia	1727
Palaeoharpes	1 2/2 /
Paraharpides	13/28
Pscemiaspis	1.329
Scotoharpes	1 3 30

1306 Table 1: Recognized harpetid genera included or excluded from these analyses.

- 1332 Table 2: Statistical differences in harpetid morphologies across time.

	Cambrian	Ordovician	Silurian	Devonian
Cambrian	-	16.09	26.03	28.32
Ordovician	0.0006	-	3.613	8.482
Silurian	0.0006	0.0012	-	5.626
Devonian	0.0006	0.0006	0.0006	-

- 1334 Table 3: Statistical differences in harpetid morphologies across families.

	Entomaspididae	Heterocaryonidae	Harpididae	Harpetidae
Entomaspididae	-	5.195	5.877	4.383
Heterocaryonidae	0.0006	-	12.66	10.42
Harpididae	0.0054	0.0006	-	7.76
Harpetidae	0.0006	0.0006	0.0006	-

	Shallow	General	Deep ₁₃₃₇
Shallow	-	1.944	2.147
General	0.0222	-	1.599
Deep	0.0294	0.246	-

1336 Table 4: Statistical differences in harpetid morphologies across habitat affinities.



Figure 1: Fossil trilobites of the order Harpetida. A: Lioharpes venulosus, B: Dolichoharpes dentoni (?), C: Kielania dorbignyana, D: Bohemoharpes ungula, E: Scotoharpes spasskii, F: Hibbertia wegelini. 1 cm scale bar included where available.







Figure 3: Revised harpetid phylogeny and harpetid families. A: Consensus of 18 most parsimonious trees from TNT. B: Bayesian tree from MrBayes.



Figure 4: The disparity of the order Harpetida (including reconstructed ancestors) through time, with stage level temporal resolution. Red: Sum of variances. Blue: Sum of ranges. Minimum number of harpetid genera in relevant time bin. Dashed lines represent major mass extinction events.



Figure 5: The disparity of the order Harpetida (including reconstructed ancestors) through time, with period level temporal resolution. Red: Sum of variances. Blue: Sum of ranges. Minimum number of harpetid genera in relevant time bin. Dashed lines represent major mass extinction events.



Figure 6: Phylogenetically corrected harpetid morphospace occupation through time, with epoch level

resolution.



Figure 7: Harpetid morphospace, partitioned by family.



Figure 8: Harpetid morphospace, partitioned by

habitat affinity.