

1 **Heterochrony in the evolution of the planktonic foraminifera *Trilobatus sacculifer* plexus**

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4 RRH: HETEROCHRONY IN THE *TRILOBATUS SACCULIFER* PLEXUS

5 LRH: ANIEKE BROMBACHER ET AL.

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7

8 *Abstract.*—Planktonic foraminifera are extremely well-suited to study evolutionary change in the
9 fossil record due to their high-resolution deposits and global distribution. Species are typically
10 conservative in their shell morphology with the same geometric shapes appearing repeatedly
11 through iterative evolution, but the mechanisms behind the architectural limits on foraminiferal
12 shell shape are still not well understood. To understand when and how these developmental
13 constraints evolve, we study morphological change leading up to the origination of the unusually
14 ornate species *Globigerinoidesella fistulosa*. We measured the size and circularity of over 900
15 specimens of *G. fistulosa*, its ancestor *Trilobatus sacculifer* and intermediate forms from a site in
16 the Western Equatorial Pacific. Our results show that the origination of *G. fistulosa* from the
17 *Trilobatus sacculifer* plexus involved a combination of two heterochronic expressions: earlier
18 onset of protuberances (pre-displacement) and steeper allometric slope (acceleration) as compared
19 to its ancestor. Our work provides a case study of the complex morphological and developmental
20 changes required to produce unusual shell shapes and highlights the importance of developmental
21 changes in evolutionary origination.

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Introduction

31
32 Trait variation amongst individuals provides the constituents for evolution through natural
33 selection. Since the seminal works of Gould (1977) and Alberch et al. (1979), the importance of
34 heterochrony in facilitating trait variation, and the resultant link between ontogeny and
35 phylogeny, has become increasingly appreciated in the field of evolutionary developmental
36 (palaeo)biology (Dobrevá et al. 2022; Keyte and Smith 2014). Heterochrony may be broadly
37 defined as a change to the timing or rate of developmental events, relative to the same events in
38 the ancestor (e.g., McNamara (2012); see comparable definitions in Alberch et al. (1979); Gould
39 (1977); McKinney and McNamara (1991); McNamara (1986)) and is widely regarded as having
40 a central role in morphological evolution following the formalisations of Gould (1977) and
41 Alberch et al. (1979).

42
43 There are two expressions of heterochrony, termed paedomorphosis and peramorphosis (Alberch
44 et al. 1979; McNamara 1986). These are not processes, as is often erroneously assumed (see
45 discussion in McNamara (1986)), but resultant expressions of trait morphology. Paedomorphosis
46 results from a descendant morphospecies passing through fewer ontogenetic stages than its
47 ancestor so that the descendant exhibits adult characters that were juvenile characters in the
48 ancestor (Alberch et al. 1979; McNamara 1986). Conversely, peramorphosis results from the
49 descendant passing through more ontogenetic stages than its ancestor, with the descendant
50 exhibiting adult characters beyond that of the ancestor (Alberch et al. 1979; McNamara 1986).

51
52 Paedomorphosis and peramorphosis each result from three different (and opposing)
53 heterochronic expressions. Peramorphosis includes hypermorphosis (continued development past

54 the ancestor stage, Fig. 1A), pre-displacement (earlier onset of trait development in the
55 descendant, Fig. 1B) and acceleration (faster development in the same amount of ontogenetic
56 time as the ancestor, Fig. 1C). Paedomorphosis can result from hypomorphosis (reduced duration
57 of development, Fig. 1D), post-displacement (later onset of trait development, Fig. 1E) or
58 deceleration (slower trait development in the same amount of ontogenetic time as the ancestor,
59 Fig. 1F). Note that following Reilly et al. (1997), two of the terms, hypomorphosis and
60 deceleration, have been chosen to replace progenesis and neoteny of Alberch et al. (1979).

61
62 The fossil record is integral in studies assessing the role of heterochrony in the evolution of novel
63 forms as the traits of interest are often morphological. However, a long-acknowledged problem
64 for palaeontologists is determining the ontogenetic age of fossils. Although it is possible to infer
65 age in some groups, such as fossil bivalves (Jones and Gould 1999), trilobites (Whittington
66 1957), fish (Trueman et al. 2016), trees (Falcon-Lang 2015) and dinosaurs (Sanchez et al. 2010;
67 Sander and Klein 2005), age is a poorly constrained parameter in most fossil organisms. To this
68 end, size is often used as a proxy for age, and assessments of heterochrony are often identified
69 under the framework of “allometric heterochrony” (McKinney and McNamara 1991; McKinney
70 1986; Wei 1994). Allometry describes trait covariation with body size according to a power
71 relationship (Huxley 1932) and is therefore ideally suited to studies of heterochrony in the fossil
72 record.

73
74 Planktonic foraminifera are a perfect target group for investigations into heterochrony. They
75 have one of the best and most complete fossil records of any group (e.g., Lazarus 2011; Norris
76 2000), phylogenetic relationships between taxa are well resolved (Aze et al. 2011; Kennett and

77 Srinivasan 1983; Olsson et al. 1999; Pearson et al. 2006a; Wade et al. 2018) and every chamber
78 from the first (proloculus) to the last is retained through growth. Brummer et al. (1986) and
79 Brummer et al. (1987) proposed five ontogenetic stages (prolocular, juvenile, neanic, adult, and
80 terminal stages) in most morphospecies of planktonic foraminifera. Transitions from one
81 ontogenetic stage to the next are determined by a size threshold, rather than chamber number
82 (Brummer et al. 1986, 1987; Caromel et al. 2016; Caromel et al. 2017; Schmidt et al. 2013; Wei
83 et al. 1992) so size is a good approximation for ontogenetic age in planktonic foraminifera.
84 Finally, the concept of heterochrony could explain the apparent lack of functional morphology in
85 some foraminifera traits. Heterochrony could potentially explain the evolution of traits without
86 known functions if a particular ontogenetic stage, rather than morphology, is selected for.
87 Therefore, heterochrony presents an additional framework to study planktonic foraminifera
88 evolution.

89
90 Here we investigate if heterochrony took place during the origination of the planktonic
91 foraminifer *Globigerinoidesella fistulosa*, a species characterised by an unusually ornate, digitate
92 morphology with numerous protuberances on its final chamber(s) (Fig. 2). *Globigerinoidesella*
93 *fistulosa* evolved from the *Trilobatus sacculifer* plexus when a small subset of the *T. sacculifer*
94 population (which includes morphospecies *T. trilobus*, *T. immaturus* and *T. quadrilobatus*, see
95 Poole and Wade (2019) for taxonomic discussion) increased in size, developed more extreme
96 protuberances and gradually diverged into *G. fistulosa* (Chaisson and Leckie 1993; Parker 1967;
97 Poole and Wade 2019) (Fig. 2). The complex shell shape of *G. fistulosa* stands out among
98 planktonic foraminifera, which are typically limited in morphological variation to the same basic
99 shapes (Norris 1991). To understand the drivers of morphological innovation in foraminifera we

100 quantify test size and shape in *T. sacculifer* and *G. fistulosa* before and after the origination of *G.*
101 *fistulosa*. We compare our results to previously published cases of heterochrony in planktonic
102 foraminifera to assess if developmental expressions can be rewired to overcome developmental
103 constraints.

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Methods

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Study species.—*Globigerinoidesella fistulosa* is a short-ranging morphospecies with a distinct stratigraphic range. Both its origination and extinction have been used as markers in Neogene planktonic foraminiferal biostratigraphy (Wade et al. 2011). *Globigerinoidesella fistulosa* evolved from the *Trilobatus sacculifer* plexus in the late Pliocene (King et al. 2020; Raffi et al. 2020) and went extinct in the early Pleistocene, marking the Base of Subzone PT1a (Raffi et al. 2020). It is assigned to the genus *Globigerinoidesella* (El-Naggar 1971) as the radially elongated protuberances on the final chambers are considered a genus-level characteristic (Spezzaferri et al. 2015). The phylogenetic relationships are well-constrained and the morphospecies *T. sacculifer* and *G. fistulosa* are morphologically disparate (Poole and Wade 2019), but intermediate specimens bridge the morphological evolution (**Error! Reference source not found.**) and remain as common as *G. fistulosa* s.s. throughout the stratigraphic range of *G. fistulosa* (Poole and Wade 2019). *Trilobatus sacculifer* has a much longer stratigraphic range. It evolved in the early Miocene (Kennett and Srinivasan, 1983) and persists throughout the stratigraphic range of *G. fistulosa*. It is still alive today (Wade et al. 2011), occupying the mixed-layer (Rebotim et al. 2017) in warm tropical oceans and harbouring some of the highest concentrations of algal photosymbionts in modern planktonic foraminifera (Kucera 2007; Takagi

122 et al. 2019). Geochemical data indicates that *G. fistulosa* had the same habitat as *Trilobatus*
123 (Poole 2017).

124

125 *Material.* —Ocean Drilling Program (ODP) Site 1115 is located in the western Woodlark
126 Basin, western Pacific (9°11.382' S, 151°34.437' E) at a water depth of 1149 m (Fig. 3) (Shipboard
127 Scientific Party, 1999). Hole 1115B was chosen primarily because the *G. fistulosa* specimens are
128 abundant and well-developed. Our sampling method was to examine end-members i.e., before the
129 first occurrence of *G. fistulosa sensu stricto* (s.s.), and samples towards the end of the *G. fistulosa*
130 range. The evolution of *G. fistulosa* occurred rather gradually, to ensure maximum morphological
131 differentiation with its ancestor we chose to analyse *G. fistulosa* and contemporary specimens of
132 the *T. sacculifer* plexus from a time slice close to the top of the stratigraphic range of *G. fistulosa*.
133 Eleven pre-speciation late Pliocene samples containing solely *T. sacculifer* plexus (*T. trilobus*, *T.*
134 *immaturus* and *T. quadrilobatus*), were examined from 24X (216.82-224.02 mbsf). Two closely
135 spaced samples were analysed from core 10H (mean depth 88 mbsf) following the speciation (i.e.,
136 post-speciation samples) where *T. sacculifer*, *G. fistulosa* and intermediate specimens are all
137 present in each sample. Samples from 10H were pooled in order to increase the sample size and
138 statistical power. Samples were dry sieved at the 250- μ m size fraction to avoid inclusion of
139 juvenile specimens. Adult specimens of both study species are much larger than 250 μ m across
140 and there was no abrupt cutoff in the size data (see Results section and figures) so there was
141 minimal risk of missing smaller adult specimens. All samples were picked for all *T. sacculifer*
142 plexus and *G. fistulosa* tests, resulting in over 900 specimens. Specimens were positioned in
143 umbilical view and imaged using a camera mounted on a light microscope. Images were analysed
144 using the Image Pro Premier software (version 9.3).

145
146 *Stratigraphy*. —Chuang et al. (2018) provide an integrated stratigraphy for Site 1115,
147 incorporating paleomagnetic reversal events with planktonic foraminifer and calcareous
148 nannofossil bioevents and high-resolution oxygen isotope analysis tied to the benthic foraminifer
149 oxygen isotope reference curve (LR04 stack of). Unfortunately the Chuang et al. (2018)
150 integrated stratigraphy ends slightly younger than our studied interval. We used biostratigraphy
151 (Poole 2017; Chuang et al. 2018) and magnetostratigraphy (Takahashi et al. (2001), to determine
152 the age of the samples studied, extrapolating back in time from the tuned record of Chuang et al.
153 (2018) (Fig. 4, Table 1). Chuang et al. (2018) used the magnetostratigraphy of Cande and Kent
154 (1995), we have refrained from updating the Site 1115 record to more recently published
155 magnetostratigraphies to keep our time scales consistent. Note, the biostratigraphy of the Bottom
156 of the *Pulleniatina* L5 coiling shift in Chuang et al. (2018) is significantly older (~127 kyr) than
157 calibrations from other Indo-Pacific sites (Pearson et al. 2023), thus we have removed this event
158 from Figure 3. However, the Top of the *Pulleniatina* L5 coiling shift at 1.777 ± 0.003 Ma is
159 extremely consistent with the global calibration of 1.78 ± 0.01 Ma from multiple Indo-Pacific sites
160 (Pearson et al. 2023). We follow Poole and Wade (2019) and limit *G. fistulosa* s.s. to specimens
161 typically possessing four broad, flattened final chambers, that increase rapidly in size, with one
162 or more finger-like protuberances, multiple supplementary apertures and a distinct lip on the
163 primary aperture. Our lowest occurrence of *G. fistulosa* s.s. is thus higher than indicated by
164 Shipboard Scientific Party (1999) for Hole 1115B. Furthermore, we find the highest occurrence
165 of *G. fistulosa* at 88 mbsf (Poole 2017), which is a slightly higher level than in the Shipboard
166 Scientific Party (1999) and Chuang et al. (2018).
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168 *Analysis.*—All specimens were analysed for total test area and curvature as measured from
169 two-dimensional images (Fig. 5). Test curvature is calculated as follows:

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$$171 \qquad C = \frac{P^2}{4\pi A} \qquad (1)$$

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173 Here P is test perimeter (μm) and A is test area (μm^2). The equation divides specimen perimeter
174 length by surface area, as measured from the umbilical side. Lengthier perimeters score higher
175 curvature values, and thus specimens that are lobate with high numbers of protuberances such as
176 *G. fistulosa* s.s. will have higher curvature values than specimens with a more rounded test
177 periphery like *T. sacculifer* s.s.

178

179 We study allometric relationships between test size and curvature to detect the presence of
180 heterochrony during speciation. Allometry can be expressed in the classic power law equation of
181 Huxley (1932):

182

$$183 \qquad y = bx^\alpha \qquad (2)$$

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185 Here, α and b are constants (α is the scaling exponent coefficient), x is size, and y is the response
186 trait. When expressed in logarithmic transformed notation, the scaling relationship becomes
187 linear:

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$$189 \qquad \log y = \log b + \alpha \log x \qquad (3)$$

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191 Here, α is the slope of the relationship and $\log(b)$ is the intercept. Both determine the type of
192 heterochrony quantitatively: unchanged slopes and intercepts indicate hyper- or hypomorphosis
193 (Fig. 1A, D), whereas a change in intercept points to pre-/post-displacement (Fig. 1B, E) and a
194 change in slope shows acceleration or deceleration (Fig. 1C, F).

195

196 Differences in slopes and intercepts among species and time slices were quantified with Linear
197 Mixed Effect models using the R package “nlme” (version 3.1.152) (Pinheiro et al. 2021; R Core
198 Team 2021). The models looks for linear trends among subsets of the data (here: species or time
199 slices) by comparing support for four different scenarios:

200

- 201 1) No overall trend between curvature and area with a consistent slope across species;
- 202 2) No overall trend between curvature and area, but varying species-specific slopes;
- 203 3) A relationship between curvature and area with a consistent slope across species;
- 204 4) A relationship between curvature and area with species-specific slopes.

205

206 Variance differences among species or time slices were assessed using the varIdent function in
207 nlme (Pinheiro and Bates 2000). The model with the lowest Akaike Information Criterion (AIC)
208 value (a measure for model parsimony) and the highest Akaike weight (a measure for relative
209 model likelihood) has the most statistical support among those models fitted.

210

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Results

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213

Preceding speciation, *T. sacculifer* alternates between intervals of low and high curvature,
whereas average size remains unchanged (Fig. 6) resulting in parallel allometric slopes with

214 different intercepts. The linear mixed effect models confirm that the size-curvature slopes remain
215 parallel throughout the pre-speciation interval (Table 2). After speciation, the intermediate
216 specimens also show comparable curves to *T. sacculifer*, but with intermediate specimens
217 showing both larger size and higher curvature than the ancestral forms (Fig. 7).
218 *Globigerinoidesella fistulosa* is larger on average than both *T. sacculifer* and intermediate forms,
219 although it should be noted that maximum size varies very little among species. Rather, the range
220 in size of both *G. fistulosa* and intermediate specimens is narrower and concentrated at the larger
221 end of the size range of *T. sacculifer*. In contrast, the range of curvature values for *G. fistulosa* is
222 much higher than both ancestral forms and increases strongly with size. This results in an
223 allometric slope significantly different from its ancestors (Table 3, Fig. 7). A visual inspection of
224 the residuals shows that they are approximately Normally distributed, satisfying the model
225 prerequisites (Supplementary figures S1 and S2).

226

227

Discussion

228 We study allometric relationships between test size and curvature to detect the presence of
229 heterochrony during speciation. The allometric slopes in *T. sacculifer* immediately prior to the
230 origination of *G. fistulosa* show shifts between high and low curvature (Fig. 6). The parallel
231 slopes, and similar size throughout the pre-speciation interval suggest a pattern of alternating
232 pre- and post-displacement (Fig. 1B, E). Changes in *T. sacculifer* outline shape are primarily
233 driven by variation in the shape of the sac-like final chamber (Poole and Wade 2019), suggesting
234 that in the pre-speciation interval, the *T. sacculifer* plexus alternated between more and less
235 “*fistulosa*-like” final chambers. These phases could be a plastic response to local environmental
236 change. Schmidt et al. (2016) showed that *T. sacculifer* size and shape is partly controlled by

237 temperature. The pre-speciation interval includes Marine Isotope Stage M2, an unusually
238 pronounced glacial stage by Pliocene standards (Lisiecki and Raymo 2005), which likely
239 contributed to local environmental fluctuations that may have fed through to morphological
240 changes.

241
242 Our morphometric analyses reveal an alternating pattern of low and intermediate curvature in the
243 *T. sacculifer* plexus (Fig. 6). This indicates that even before the origination of *G. fistulosa*, some
244 of the morphological variation necessary to produce the new species was already present in the
245 ancestor. However, pre-displacement was not enough to result in the unusual final morphology
246 of *G. fistulosa*. The increase in average size of intermediate specimens compared to *T. sacculifer*
247 (Fig. 7) points to hypermorphosis (Fig. 1A) on top of continued pre-displacement through higher
248 curvature at similar sizes in intermediate specimens. The final transition from intermediate
249 specimens to *G. fistulosa* is marked by a steeper allometric slope than both *T. sacculifer* and
250 intermediate specimens (Fig. 7). Additionally, *G. fistulosa* often develops protuberances on
251 multiple chambers in the final whorl (Poole and Wade 2019), which points to further pre-
252 displacement by earlier onset of protuberances and likely contributes to the observed high
253 curvature values. These results indicate that the origination of *G. fistulosa* involved a
254 combination of two peramorphic expressions: pre-displacement through earlier onset of more
255 pronounced protuberances and acceleration through a steeper allometric slope than its ancestor.

256
257 The steep allometric slope in *G. fistulosa* is likely directly related to the high number of
258 protuberances in the species. The area of the protuberances is very small compared to the total
259 test area, whereas a single protuberance can increase shell perimeter by as much as 50%. The

260 underfitting of the slope at the highest curvature values is likely the result of a handful of
261 specimens with multiple long protuberances which disproportionally affect the curvature values.
262

263 There are numerous described cases of heterochrony in the Cenozoic fossil record of planktonic
264 foraminifera, and both paedomorphic and peramorphic expressions have been observed in
265 quantitative and qualitative studies. For example, studies of the Paleocene-Eocene
266 *Globanomalina chapmani* - *Globanomalina luxorensis* - *Pseudohastigerina wilcoxensis* lineage
267 found evidence of pre-displacement (Speijer and Samir (1997) and hypermorphosis or
268 acceleration (Berggren et al. (1967). The Eocene transition from *G. australiformis* to
269 *Turborotalia frontosa* is interpreted as resulting from hypermorphosis (Olsson and Hemleben
270 2006; Pearson et al. 2006b). Interestingly, the subsequent *Turborotalia* lineage demonstrates a
271 regressive paedomorphic trend, which effectively reversed the former hypermorphosis
272 expression (Pearson et al. 2006b). Wei (1994) conducted a comprehensive study to calculate
273 allometric “trajectories” for assessing heterochronic modes over time in the morphological
274 evolution within species of the *Globorotalia (Globoconella) puncticulata-inflata* plexus.
275 Following the divergence of *G. (G.) puncticulata* and *G. (G.) inflata*, both morphospecies
276 underwent different modes of heterochrony (Wei 1994). In *G. (G.) puncticulata*, the change in
277 allometric trajectories suggested acceleration with later forms developing higher peripheral
278 roundness in comparison to same-sized ancestral forms (Wei 1994). In *G. (G.) inflata*, the initial
279 post-displacement trend is interpreted as a delay in the onset of the neanic ontogenetic stage and
280 probable cause of divergence between the morphospecies (Wei 1994). Interestingly, this is
281 followed by a reversing trend of pre-displacement (Wei 1994). Finally, Morard et al. (2019)
282 combined genetics and morphological measurements in modern species of the *Globigerinoides*

283 genus to explain the apparent mismatch between morphological disparity and a high degree of
284 genetic kinship. They found that relatively large morphological differences between closely
285 related species can be attained by small changes in the developmental sequence, highlighting the
286 importance of considering heterochronic expressions when studying planktonic foraminifera
287 evolution.

288

289 The peramorphic expressions of both pre-displacement and acceleration in the origination of *G.*
290 *fistulosa* bears close resemblance to the evolution of Eocene *Hantkenina*. Like *G. fistulosa*,
291 hantkeninids are bizarre-looking planktonic foraminifera characterised by tubulospines. The
292 tubulospines first developed on the final, adult chambers, before earlier trait onset in later
293 hantkeninid species (Pearson and Coxall 2014). Such a shift to earlier trait (tubulospine)
294 development in later morphospecies, such as *Hantkenina mexicana*, may therefore indicate pre-
295 displacement, although they are generally also larger than the transitional forms, pointing to
296 hypermorphosis (Pearson and Coxall 2014). To our knowledge, the hantkeninids and *G. fistulosa*
297 are the only species of planktonic foraminifera whose origination included multiple expressions
298 of heterochrony. Possibly, their extreme shapes could only be formed through multiple
299 developmental shifts, which might explain why unusual shapes such as protuberances and
300 tubulospines are so rare in planktonic foraminifera.

301

302 *Mechanisms.*—Although the aforementioned heterochronic changes explain how *G.*
303 *fistulosa* managed to reach a more extreme shape than most other planktonic foraminifera, the
304 drivers of these morphological adaptations are harder to interpret. The species' stratigraphic
305 range includes the onset of Northern Hemisphere glaciation (NHG, ~3.5 to 2.5 Ma) (Bailey et al.

306 2013; Westerhold et al. 2020). During this interval, Earth transitioned from a unipolar glacial
307 state, with large ice sheets only on Antarctica, to one that was sufficiently cool by ~2.5 Ma to
308 induce growth of large ice sheets in the Northern Hemisphere and associated rafting of icebergs
309 across the subpolar North Atlantic Ocean (Shackleton et al. 1984). The high-resolution oxygen
310 isotope record of *T. sacculifer* at Site 1115 does not indicate any dramatic change associated with
311 the extinction of *G. fistulosa* (Chuang et al. 2018). Furthermore, *G. fistulosa* was restricted to the
312 tropical oceans and its exposure to environmental change originating in the high northern
313 latitudes was therefore likely limited.

314
315 Both the *T. sacculifer* plexus and *G. fistulosa* are spinose, occupy the mixed-layer and harbour
316 algal photosymbionts. It has been shown that the acquisition of symbionts is necessary for *T.*
317 *sacculifer* to achieve maximum sizes (Bé et al. 1982). The large size of *G. fistulosa* compared to
318 *T. sacculifer* would have required even more symbionts than *T. sacculifer*, but the surface-area:
319 volume ratio in globular chambers of planktonic foraminifera, and thus space for symbionts,
320 decreases with increasing volume. The protuberances in *G. fistulosa* potentially counteract this
321 trend by increasing surface area to host more symbionts. Modern species with shells that have a
322 high surface area to volume ratio often show a higher increase in symbiont content with
323 increasing size than more spherical ones (Takagi et al. 2019), suggesting that irregular shapes are
324 beneficial to symbiont activity. This hypothesis could be tested in future studies by comparing
325 stable carbon isotopes between *G. fistulosa* and *T. sacculifer* to test for differences in symbiont
326 activity. The protuberances themselves are spinose (Poole and Wade 2019), further increasing
327 effective test size. Other digitate species such as the hantkeninids have been argued to evolve
328 elongated chambers to increase effective test size and food gathering efficiency (Coxall et al.

2007), which possibly further helped *G. fistulosa* to reach and maintain a large body size. Finally, it should be noted that there might not be any clear evolutionary advantage of the tubulospines. Much of the functional morphology of foraminifera shell shape remains unclear (Caromel et al. 2014; Renaud and Schmidt 2003), and the development of some morphological features may not have a specific functional response. An evolutionary advantage or fulfilment of a particular function does not need to be assumed by the development of a trait, such as protuberances in *G. fistulosa*.

Conclusions

The origination of the unusual test size and shape of *Globigerinoidesella fistulosa* was the result of a combination of pre-displacement and acceleration of ancestral traits found in *T. sacculifer*. These results imply that shifts in multiple developmental expressions are required for the origination of unusual morphologies. As both ancestor and descendant species continued to thrive following the origination of *G. fistulosa*, the drivers of morphological change are unlikely to be environmental changes that favoured one species over the other. Our work provides a case study of the complex developmental changes required to produce ornate shell shapes and highlights the importance of development in the origination of unusual forms.

Acknowledgements

We are grateful to R Morard, M R Petrizzo and an anonymous reviewer whose comments significantly improved the manuscript. This study was funded through a UK Natural Environment Research Council (NERC) studentship to C Poole and NERC grant NE/P019013/1 to BSW. A Brombacher and T Ezard were funded through NERC award NE/P019269/1.

352 Samples were provided by the International Ocean Discovery Program (IODP) which is
353 sponsored by the U.S. National Science Foundation and participating countries. Thanks to Z
354 Tian, N Staikidou and D King for assistance with figures.

355

356 **Competing interests**

357 The authors declare no competing interests.

358

359 **Data availability statement**

360 Data is currently privately available from the Dryad repository:

361 <https://datadryad.org/stash/share/ixZXllt38iDtf5EyfN7J6jvVczOwPmaXM4gYTbWbuYc>. It will

362 be made publicly available upon publication of the manuscript.

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551

552 **Figure captions**

553 **Figure 1.** Schematic representations of trait development for the six types of heterochrony: a)
554 hypermorphosis, where traits develop longer in the descendent than the ancestor while the rate
555 and onset of trait development remain the same; b) pre-displacement, where the onset of
556 descendent trait development starts earlier while the rate of development remains the same; c)
557 acceleration, where the rate of trait development is higher in the descendent species while the
558 onset of development is the same as the ancestor; d) hypomorphosis, where traits stop
559 developing earlier in the descendant than the ancestor; e) post-displacement, where the onset of
560 descendant trait development starts later than in the ancestor; and f) deceleration, where the rate
561 of trait development is lower in the descendant than the ancestor.

562 **Figure 2.** (1) *Trilobatus sacculifer* (re-illustrated from Poole and Wade, 2019, Fig. 9D); (2) an
563 intermediate form between *T. sacculifer* and *Globigerinoidesella fistulosa* (re-illustrated from
564 Poole and Wade, 2019, Fig. 11L); (3) *Globigerinoidesella fistulosa* (re-illustrated from Poole
565 and Wade, 2019, Fig. 13J). All specimens from ODP Site 1115. All scale bars represent 100 μm .

566 **Figure 3.** Magneto- and bio-stratigraphy at ODP Hole 1115B. Gray shaded boxes indicate
567 intervals examined in this study for morphometric analysis. Magnetic chrons and bioevents from
568 Chuang et al. (2018), supplemented by planktonic foraminifera biostratigraphy in Poole (2017).

569 **Figure 4.** Location of ODP Site 1115 in the western Woodlark basin, equatorial Pacific.

570 **Figure 5.** Biometric and morphometric parameters measured on *Trilobatus sacculifer* and
571 *Globigerinoidesella fistulosa*.

572 **Figure 6.** *Trilobatus sacculifer* size and shape allometry in five time intervals from oldest (a) to
573 youngest (e) preceding the origination of *Globigerinoidesella fistulosa*. Blue and red arrows

574 indicate pre- and post-displacement respectively. Most stages include several samples: stage (a)
575 contains all samples from cores 24X-06 and 24X-05, stage (b) contains all samples from core
576 24X-04, stage (c) contains samples from core 24X-03, stage (d) contains all samples from core
577 24X-02 and stage (e) contains all samples from core 24X-01. See Table 1 for full sample IDs.

578 **Figure 7.** Log size and curvature for *Trilobatus sacculifer*, intermediate and *Globigerinoidesella*
579 *fistulosa* specimens. Straight lines show linear regressions for each species (*T. sacculifer*: $R^2 =$
580 0.17 , $p < 0.001$. Intermediate: $R^2 = 0.014$, $p < 0.001$. *G. fistulosa*: $R^2 = 0.29$, $p < 0.001$).

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589 **Table captions**

590 **Table 1.** Sample ID, depth and number of analysed specimens per sample. Abbreviations: mbsf =
591 metres below sea-floor; n = number of specimens. The pooled sample contains specimens from
592 sample IDs 1115B-10H-4 127-129 cm and 1115B-10H-3 104-106cm.

593

594 **Table 2.** Log likelihood, AIC and Akaike weights for all four analysed models of *Trilobatus*
595 *sacculifer* area and curvature preceding origination of *Globigerinoidesella fistulosa*. Δ AIC
596 represents the difference between AIC and the set's minimum AIC. The best performing model
597 based on AIC and Akaike weight is indicated in bold.

598

599 **Table 3.** Log likelihood, AIC and Akaike weights for all four analysed models comparing
600 *Trilobatus sacculifer* and intermediate specimen area and curvature. Δ AIC represents the
601 difference between AIC and the set's minimum AIC. The best performing model based on AIC
602 and Akaike weight is indicated in bold.

603