Supporting Online Material for

Fossil Plant Relative Abundances Indicate Sudden Loss of Late Triassic Biodiversity in East Greenland

Jennifer C. McElwain,[*] Peter J. Wagner, Stephen P. Hesselbo

*To whom correspondence should be addressed. E-mail: jennifer.mcelwain@ucd.ie

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Methods

Assessing whether two assemblages share the same diversity.

We assess the likelihoods of particular RAD hypotheses using established protocol that both contrast different RAD models and accommodate sample size (*S1*). Of course, in addition to the most likely RAD for any one bed, there exist a range of other hypotheses that cannot be rejected (*S2, 3*). For example, the best-fit RADs for beds 1 and 2 are well within the range of RADs within 1-unit support of the best hypothesis for bed 1.5 (see, e.g., Fig. S1).

If all the beds had fit the same RAD model, then we could simply have examined hypotheses of static vs. shifting parameters. However, Bed 3 fits a lognormal significantly better than it fits a geometric whereas all of the other beds fit the geometric model best (Table 1). We therefore assessed one aspect of diversity: i.e., the richness (number) of taxa of some minimum abundance (here, $S_{f>10\text{-}6}$; note that the same results are achieved with other values of *f*). We modified the test to find RADs with $S_{f>10\text{-}6}$ in increments of 0.1 and assessed the likelihood of each for each bed. We restricted this to the model producing the most-likely RAD. In the case of beds best fitting geometric RADs, only the slope needs to be varied, and a particular set of slopes could be used for all beds. However, for Bed 3, two variables (the true richness and an "evenness" parameter of the log-normal) needed to be assessed. For any combination of richness and evenness, there was a different number of taxa with $S_{f>10—6}$. Therefore, for each $S_{f>10\text{-}6}$, we used the lognormal parameters maximizing the likelihood of that $S_{f>10\text{-}6}$ given Bed 3's data.

We then examined the likelihood of the predicted $S_{f>10\text{-}6}$ for each hypothesis of changing diversity given the distribution of each bed. We could use log-likelihood ratio tests because the simpler

hypotheses all are special cases of the more complicated ones. The null hypothesis, a single diversity, is the special case of decreasing diversity over time in which the slope of decrease is 0. The continuously decreasing diversity hypothesis is a special case of the 4-parameter hypothesis in which the exponential component of decrease is invariant and at 0 (thus making it linear) and in which the onset of decrease is invariant and always in the first bed.

Note that the Signor-Lipps effect (*S4*) cannot affect inferences made using this approach. The Signor-Lipps effect is important only when using "range-through" inferences of richness: that is, counting taxa not found in a bed but assumed to be present because they are observed in lower (earlier) and higher (later) beds. Here, such taxa are ignored in the analyses. The analyses infer some number of unsampled-but -present taxa, which no doubt includes some unspecified range-through taxa. However, the range-through taxa might be locally extinct at this time; conversely, the unsampled-but-inferred taxa might also include taxa with last appearances preceding the bed or first appearances after the bed.

Testing whether two portions of the same bed represent the same fauna.

Bed 5, at 46 meters in the section, marks the TJB in East Greenland (*S5, 6*). There is a marked shift in generic composition within that bed itself (Fig S2), with an apparent "turnover" around 46.6 meters. We modify the techniques used above with existing techniques (e.g., *S2*) to assess whether the floral composition of the first 30 cm (Bed 5A) is appreciably different from that of the last 30 cm (Bed 5B).

Although the "lumped" assemblage of Bed 5 best fits a Zero Sum RAD, the Zero Sum does a poor job of predicting either Bed 5A or Bed 5B: in fact, that model can be rejected for both 5A and 5B individually (Table S1). Moreover, whereas a geometric RAD fits Bed 5A significantly better than any other RAD, both the Zipf and Lognormal fit bed 5B significantly better than does the

geometric. Thus, we can reject the hypothesis that Beds 5A and 5B reflect the same constructional rules. In the absence of any compelling evidence of taphonomic changes (each part of Beds 5A and 5B contains taxa that are sampled elsewhere in Bed 5), this suggests a marked ecologic turnover.

Of additional potential interest is the fact that the implied diversity of Bed 5B is appreciably greater than that of Bed 5A (Fig. S3). This is consistent with an idea of rapid ecological rebound, with the rebound supporting a much larger number of relatively rare ($10^{-2}>f>10^{-3}$) genera. It also is consistent with the idea that the community assemblage rules were more complicated in the rebound than afterwards. Alternatively, because mixing of exponential distributions also creates lognormal distributions, it is possible that the assembly rules were inconsistent and that Bed 5B essentially mixes communities. However, as this is based on only 44 specimens, this inference is very tentative.
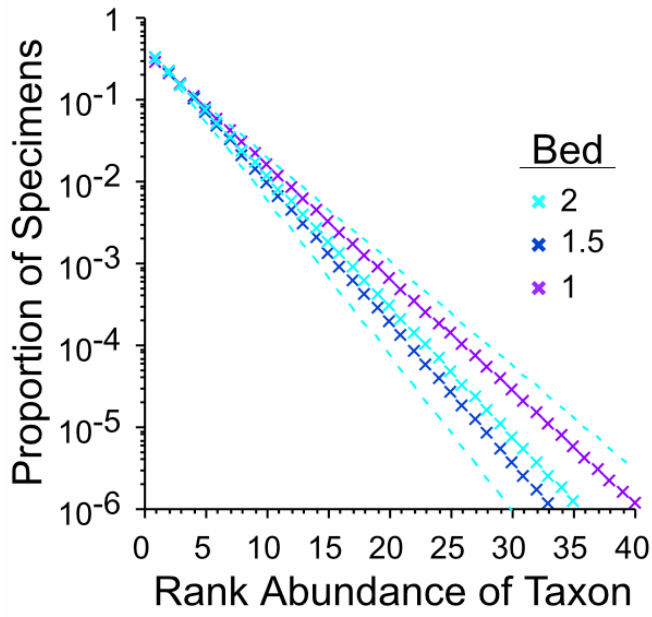
Fig. S1. Best model RADs for beds 1, 1.5 and 2, plus RADs within one unit support of the ML RAD for bed 1.5. We clearly cannot reject the idea that all three beds had the same RAD and that the differences in best model RADs are simply due to sampling error.
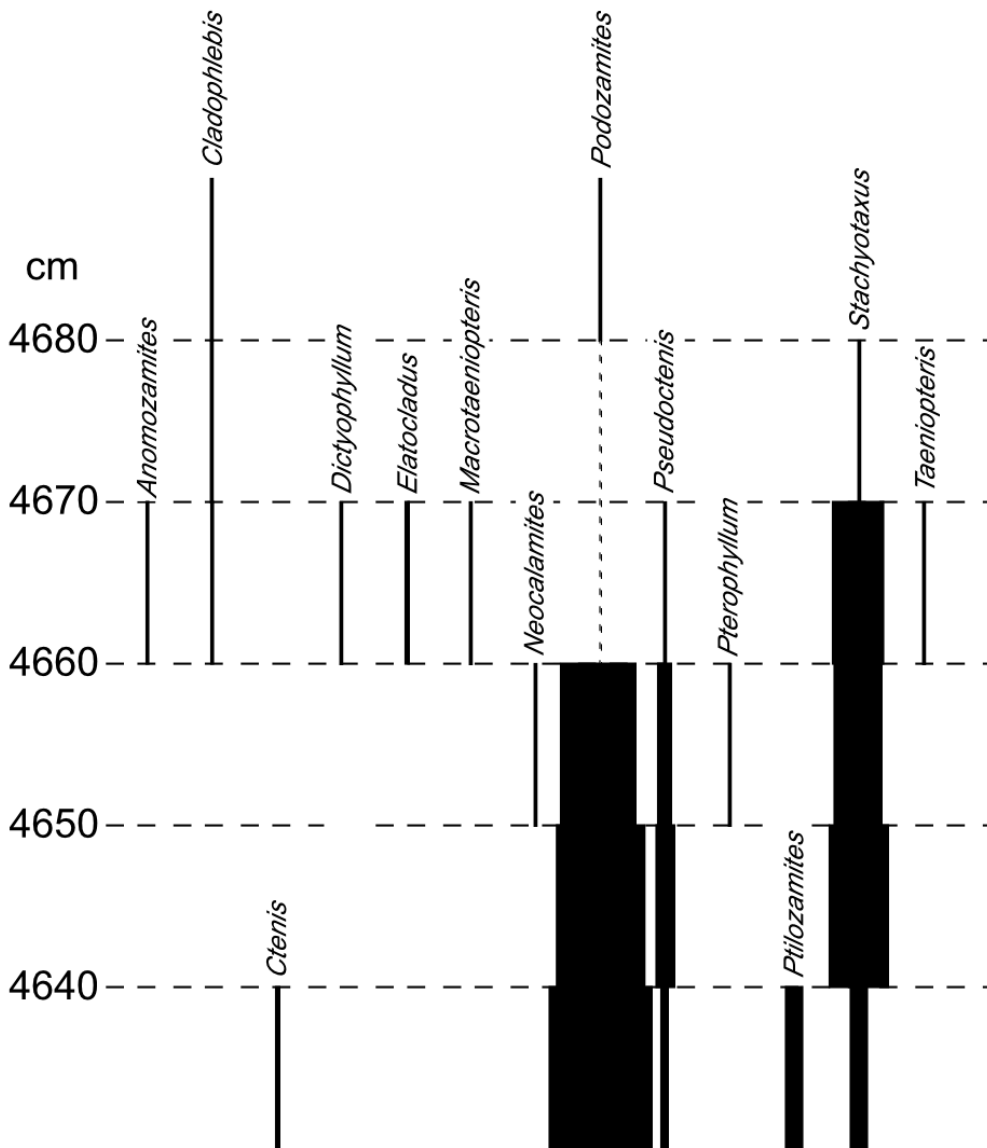
Fig. S2. Bed 5, divided into 10 cm units. Widths represent generic abundance, with narrowest lines representing one specimen. Bed 5A = 4630–4660 cm; Bed 5B = 4660–4690 cm.
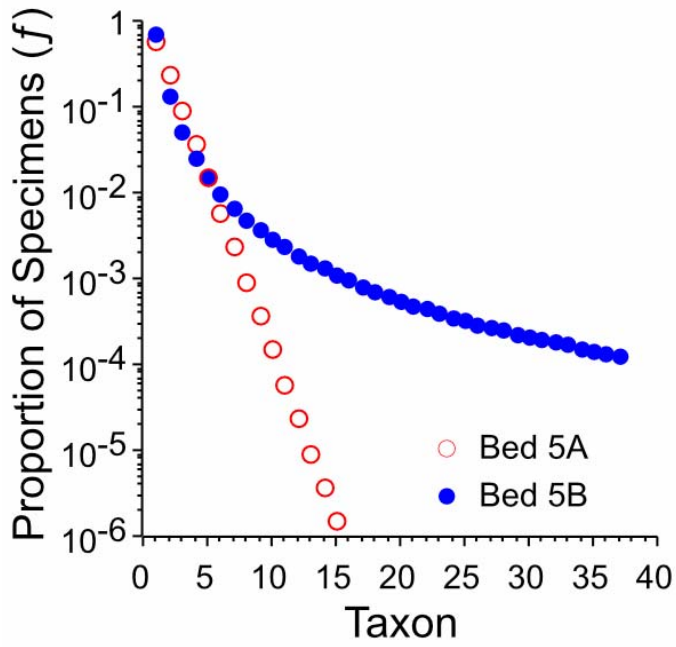
Fig. S3. Best RADs (geometric and Zipf, respectively) for Beds 5A and 5B. See Table S1.

Table S1. Modifed Akaike's Information Criteria (AICc) for best examples of each general RAD model. AICc = -2*lnL[H | data] * n/(n-k-1) where n is the number of specimens and k is the number of parameters (k=1 for geometric, k=2 for others.)

Bed	Genera	n	RAD Model AICc Geometric	Zero Sum	Lognormal	Zipf
5	13	318	90.5	**86.0**	97.9	94.7
5A	7	275	**52.4**	60.9	63.4	76.1
5B	9	43	36.9	40.1	32.8	**31.1**

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