Morphological bottlenecks and phylogenetic restructuring following the end-Cretaceous mass extinction

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Motivation

Mass extinctions disrupt the balance of clade richness across the tree of life. Certain modes of life are permanently lost, others persist through the survival of lineages or by independent re-evolution. Do priority effects impact the rebound from the extinction, where the taxonomically richest clade in an adaptive zone diversifies to the greatest extent? Or does this pattern arise because surviving genera in either scenario have high morphological disparity, which increases the probability of taxonomic and morphologic evolution?

Methods

Morphological data

- 1 image of shell across 330 genera from 70 families from the latest Cretaceous (Maastrichtian 72.2-66 Ma); collected from monograph or museum specimen

Quantifying shell shape

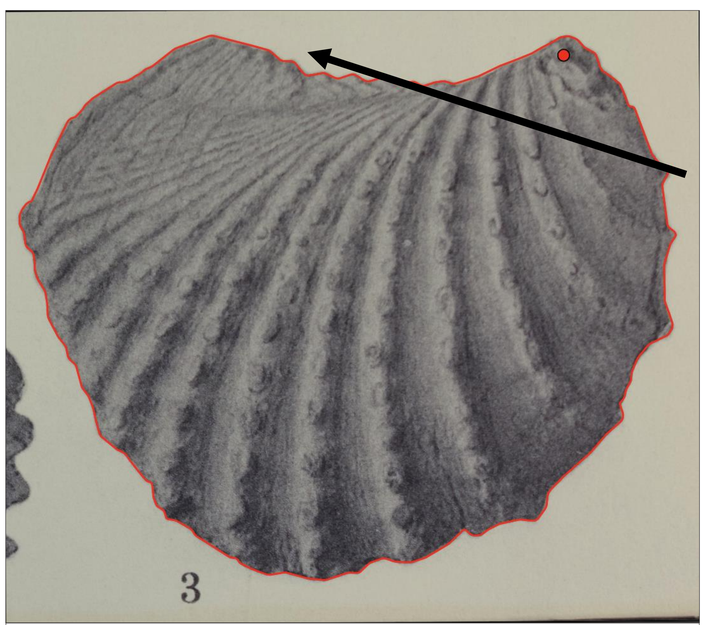
- Landmarked beak, hinge axis, commissural profile (data figure below)

Shell shape analysis

- Scaled landmarks to unit size, aligned to hinge axis, translated to shell centroid, mirrored right valves to left valves. Shell profile semi-landmarks slid to minimize bending energy between specimens.
- Made morphospace using principal components analysis (PCA) of landmarked data - retained PC1-PC8 (=95% of total shape variation)

Morphospace analysis

- Analyzed changes in morphospace as similarity in:
- Position of centroid: PDPOC = 100 – (100 x $\Delta POC/SOR_{pre\text{-}extinction}$)
- Sum of ranges: PSOR = 100 x $SOR_{survivors}/SOR_{pre\text{-}extinction}$
- Sum of variance: PSOV = 100 x $SOV_{survivors}/SOV_{pre\text{-}extinction}$



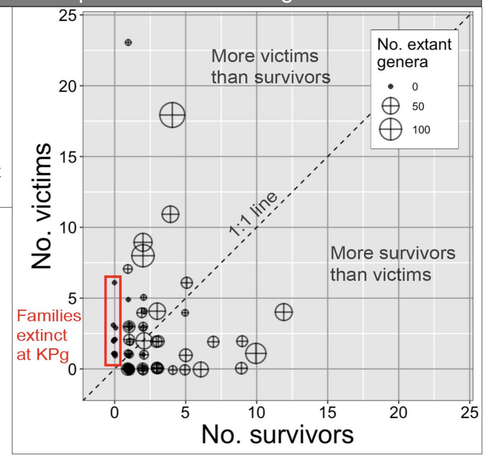
Data Figure. Ext. view, right valve of *Trigonia castrovillensis.* Stephenson 1941, plate 19 fig. 3

Results

Result 1: Taxonomic survivorship not tied to extant genus richness

Figure 1. Impacts of taxonomic bottlenecks and survivorship on extant genus richness. Dashed line shows the 1:1 relationship. Number of surviving genera per family vs. number of genera lost per family across the KPg with points sized by number of extant genera.

GRAPHICAL HYPOTHESES



Result 2: Morphologic disparity not tied to extant genus richness

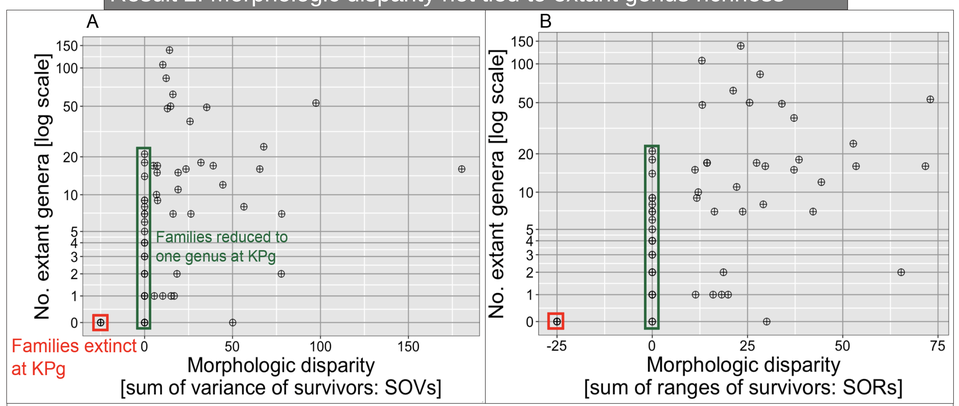


Figure 2. Impacts of surviving morphologic disparity across the KPg on extant genus richness among families. (a) Number of extant genera in family vs. morphologic disparity measured as sum of variance of principal component scores 1-8 for shell profile shape. (b) Number of extant genera vs. morphologic disparity measured as a sum of ranges of principle component scores 1-8 for shell profile shape.

Result 3.1: Shifts in morphospace today is not strictly tied to genus richness

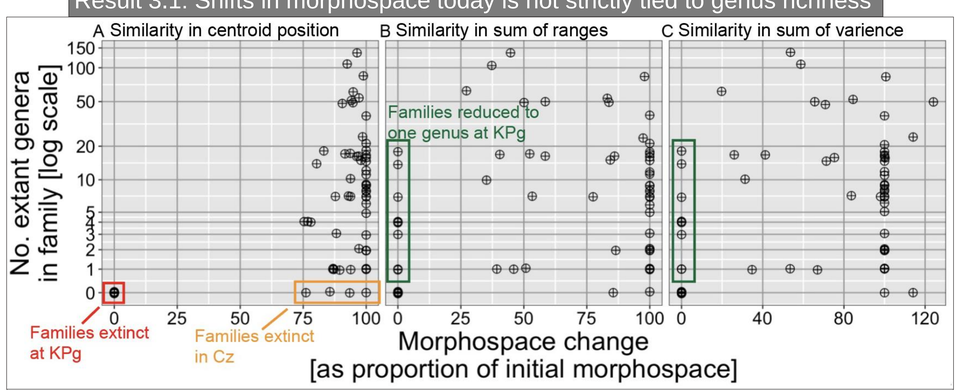


Figure 3. Impacts of changes to a family's morphospace across the KPg on its extant genus richness today. (a) Change in the centroid position. (b) Change in the range of the morphospace. (c) Change in the variance of the morphospace.

Result 3.2: Total reduction in morphospace range and variance *and* lateral shifts morphospace restrict genus richness today.

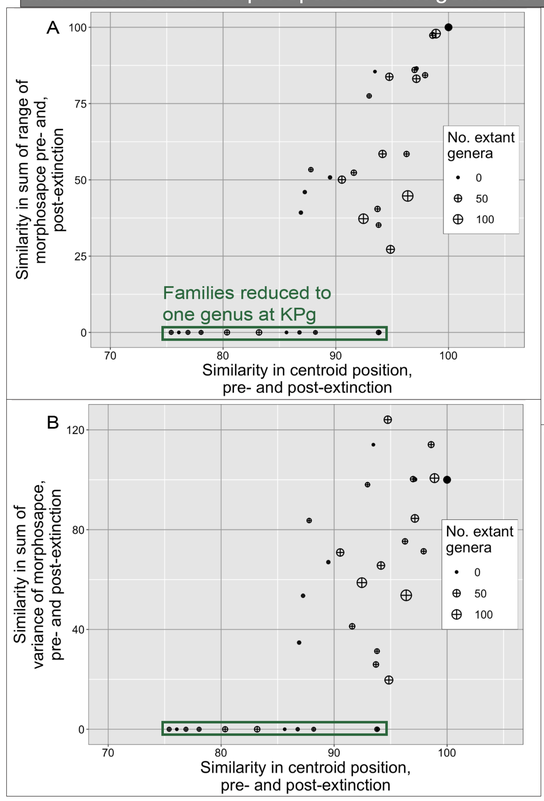


Figure 4. Changes to the position and extent of a family's morphospace across the end-Cretaceous mass extinction. **(a)** Similarity in the position of the morphospace centroid on the x-axis vs. the similarity in the range of morphospace on the y-axis. **(b)** Similarity in the position of the morphospace centroid on the x-axis vs. the similarity in the variance of morphospace on the y-axis.

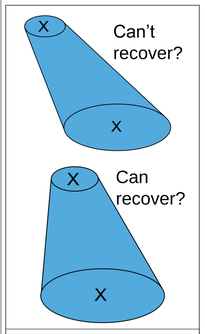


Figure 5. Illustration of thinning with or without significant shift in centroid.

Discussion

1. **Taxonomic richness in families today not tied to survivorship.**
   - Families with relatively low survivorship and high proportional extinction have reached similar levels of genus richness today as those with high survivorship and low proportional extinction.
2. **Taxonomic richness today not tied to high morphological disparity of shell shapes in surviving genera.**
   - Eight of the top-10 families in extant genus richness had low disparity of survivors (only 6-20% of the maximum measured disparity for families); thus, the accumulation of high taxonomic diversity today is not strictly tied to high initial disparity in the Cenozoic.
3. **Change in a family's morphospace occupancy across the KPg appears to have a many-to-one mapping with its extant genus richness.**
   - 5 of the top-10 families experienced some of the greatest range reductions across the KPg. Further, 2 of 4 "dead-clade-walking" families survived the KPg with full morphological range.
4. **Being reduced to one genus at the margins of the family's morphospace appears to limit taxonomic recovery: strong effects of contingency?**
   - Families bottlenecked to one genus—virtually total reduction in morphospace range and variance—*and* had lateral shifts in their morphospace position are restricted to low genus richness today.

References/Acknowledgments

Thank you to the Smithsonian National Museum of Natural History for providing me with the opportunity to conduct summer research and thank you to the NSF for funding this REU experience.

REU Site, OCE-1560088

REFERENCES