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Supplementary Materials for

Algal plankton turn to hunting to survive and recover from end-Cretaceous impact darkness

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A Matrix Community Model Figs. S1 to S7 Tables S1 to S4 References

Other Supplementary Material for this manuscript includes the following:

(available at advances.sciencemag.org/cgi/content/full/6/44/eabc9123/DC1)

Data file S1

A Matrix Community Model

The evolutionary ecosystem model represents a fixed-volume homogenous culture containing an arbitrary number of potential plankton phenotypes. The model environment is broadly analogous to a well-mixed ocean surface layer. Subsurface waters containing a fixed concentration of the limiting nutrient (N) are entrained into the surface layer at a constant rate (κ) , with surface waters containing nutrients and plankton populations mixed out at an equivalent rate. Nutrients within the surface layer are taken up by the plankton community.

$$
\frac{dN}{dt} = \kappa (N_0 - N) - \sum_{j=1}^{J} \mu_j B_j \tag{1}
$$

Here μ_j and B_j are the gross biomass specific growth rate and nitrogen biomass of population j.

Plankton growth model

For a single plankton population, B (mmol N m⁻³), the net biomass-specific population growth rate is represented by a generic growth equation that includes the potential for both autotrophic and heterotrophic growth, alongside losses to predation and a mortality term that includes a baseline value (δ) and density-dependent term $(B\delta)$.

$$
\frac{1}{B}\frac{dB}{dt} = \mu + \lambda \cdot G^+ - G^- - (1+B)\delta
$$
 (2)

Here, μ is the biomass-specific light and nutrient-limited growth from autotrophic metabolism, λ is the grazing assimilation efficiency, and G^+ and G^- are the biomass-specific gains from prey and losses to predators, respectively.

Phototrophic growth: Autotrophic plankton growth is represented by the Monod (*74*) model, such that

$$
\mu = \frac{\mu_{max} \cdot \alpha \cdot N}{\mu_{max} + \alpha \cdot N} \cdot \gamma \tag{3}
$$

Here μ_{max} is the maximum autotrophic growth rate (d⁻¹), N is the environmental concentration of dissolved nitrate (mmol N m-3), and α is the biomass-specific nitrate affinity (m3 (mmol N)⁻¹ d⁻¹). The dimensionless light-limitation factor, γ , is simply a prescribed scalar that is set to a constant value.

Heterotrophic growth: The biomass-specific rate of predation approximates a linear "Holling type I" function (75) of prey biomass (B_{prey}), modified by the 'availability' of the prey to the predator, ϕ , and the grazing attack rate g . The attack rate is down-regulated at low total prey concentrations, providing a 'refuge' for prey that serves to dampen population instabilities (*76*).

$$
g' = g \cdot (1 - e^{\Lambda \cdot \phi \cdot B_{prey}})
$$
 (4)

Gains from predation (modified by λ in equation [1\)](#page-1-0) are thus described by

$$
G^{+} = g' \cdot \phi \cdot B_{prey} \tag{5}
$$

Losses to predators are given by

$$
G^{-} = g'_{pred} \cdot \phi \cdot B_{pred} \tag{6}
$$

Phenotypic traits in the plankton community

We consider a community of J potential phenotypes. These are distributed across a two-dimensional trait space. The first trait dimension is made up of $\frac{1}{s}$ geometrically-spaced plankton size classes between 0.6 μ m and 6 mm ESD (equivalent spherical diameter). The second trait dimension is made up of J_t linearly-spaced trophic classes, defined by a dimensionless 'trophic index' (τ) . This specifies a position along a 'trophic spectrum' spanning phytoplankton $(\tau=1)$, a range of mixotrophs $(0<\tau<1)$ and zooplankton $(\tau=0)$. These two 'master traits' govern a wider range of other important traits within the model, including those related to population growth and predator-prey interactions.

Size-dependent physiology: The size-dependent parameters of the growth model are assigned according to empirically- constrained allometric scaling laws (*64, 77*), as defined in table S4a. While biomassspecific nitrate affinity and grazing clearance rates are reasonably well-described as power-law functions of cell volume (fig. S7), μ_{max} has been shown to follow a more complex monomodal relationship with cell volume (77, 78). Here we approximate μ_{max} as a size-dependent function, governed by three empirically-constrained physiological parameters: the theoretical growth rate at infinite quota (μ^{∞}), the maximum cellular N uptake rate (ρ_{max}) and the minimum cellular N quota (Q_{min}). While these parameters are not resolved by the Monod model given in equation [2,](#page-1-1) they fully constrain μ_{max} under an assumption of cellular equilibrium (*79, 80*), such that

$$
\mu_{max} = \frac{\mu^{\infty} \cdot \rho_{max}}{\mu^{\infty} \cdot Q_{min} + \rho_{max}} \tag{7}
$$

With μ^{∞} , ρ_{max} and Q_{min} constrained by observations (77, 80), equatio[n 7](#page-2-0) yields a reasonable fit to measurements of μ_{max} (fig. S7a), with a monomodal size-dependence peaking at ~6 μ m (80). Figure S7b and c are the assumed size-dependences of the biomass-specific nitrate affinity, α (64), and the grazing clearance rate, $g(62)$.

Size-dependent interactions: Organism size also determines the availability of prey to predators, ϕ . This is an approximately log-normal function of the predator-prey volume ratio (θ) , such that $\phi = 1$ when $\vartheta = \vartheta_{opt}$ (81), as shown in figure S7d.

$$
\phi = \exp\left(-\left[\ln\left(\frac{\vartheta}{\vartheta_{opt}}\right)\right]^2 \cdot \frac{1}{2\phi_{\sigma}^2}\right) \tag{8}
$$

Trade-off between autotrophy and heterotrophy: Organisms are positioned along a trophic spectrum between autotrophy and heterotrophy according to a trophic index, τ . Strictly autotrophic phytoplankton are assigned $\tau = 1$, while strictly heterotrophic zooplankton are assigned $\tau = 0$. If μ_{max} and g are the size-dependent maximum growth rates and grazing clearance rates of these phytoplankton and zooplankton specialists, the corresponding rates for all populations are given by

$$
\mu_{max}(\tau) = \tau \cdot \mu_{max} \tag{9}
$$

$$
g(\tau) = \tau \cdot g \tag{10}
$$

Size-independent parameters are defined in table S4b.

Matrix notation

For mathematical and computational convenience, each phenotype in the two-dimensional trait space is assigned a single phenotypic index, $j = \{1, 2, ..., J\}$, where $J = J_s \cdot J_t$. This indexing scheme allows all populations in the local community to be represented as a column vector,

$$
\vec{B} = \begin{bmatrix} B_1 \\ B_2 \\ \vdots \\ B_J \end{bmatrix}
$$

In a similar fashion, traits that vary among the community can also be written as vectors. For example, the nitrate affinities of every population in the community can now be written as

$$
\vec{\alpha} = \begin{bmatrix} \alpha_1 \\ \alpha_2 \\ \vdots \\ \alpha_J \end{bmatrix}
$$

Note that parameters remain as scalars if they are assumed to be equal for all phenotypes. Throughout the text, every vector is written underneath an arrow (e.g. \vec{x}) and every matrix is written in bold text (e.g. x). Element-wise multiplication will always be denoted with a '·' symbol. If no symbol is used between vectors or matrices, then the matrix product is used.

Ecological dynamics

Using the above notation, equation [2](#page-1-1) can now be rewritten for the entire community as follows

$$
\frac{1}{\vec{B}}\frac{d\vec{B}}{dt} = \vec{\mu} + \lambda \cdot \vec{G}^+ - \vec{G}^- - (1+B)\delta
$$
\n(11)

The gross autotrophic growth rate of the community is given by

$$
\vec{\mu} = \frac{\vec{\mu}_{max} \cdot \vec{\alpha} \cdot P}{\vec{\mu}_{max} + \vec{\alpha} \cdot P} \cdot \gamma \tag{12}
$$

and the community grazing terms are

$$
\vec{G}^+ = \vec{g}' \cdot \left(\phi^{\mathrm{T}} \vec{B}\right) \tag{13}
$$

$$
\vec{G}^- = \boldsymbol{\phi}(\vec{B} \cdot \vec{g}') \tag{14}
$$

Here ϕ is the $[J_{prey} \times J_{pred}]$ 'grazing kernel' describing the availability of each population (as prey) to each population (as a predator), as shown in figure S7d. In equation [13,](#page-4-0) $\phi^T \vec{B}$ describes the sum of all prey biomass available to each predator (where ϕ^T is the transpose of the grazing kernel). When multiplied by \vec{g}' , this gives the pre-assimilation grazing by each population on all available prey. The matrix product $\phi(\vec{B} \cdot \vec{g}')$ in equation [14](#page-4-1) describes the total rate of predatory losses suffered by each prey. The grazing refuge is calculated according to the prey available to each predator, such that

$$
\vec{g}' = \vec{g} \cdot (1 - e^{\Lambda \left[\phi^T \vec{B}\right]}) \tag{15}
$$

Evolutionary dynamics

Adaptive evolution is enabled by allowing a small fraction of each population's net growth rate to be diverted to neighbouring phenotypes in the trait space (*67, 82*). In practice, this is achieved by adding a small mutational flux, \vec{L}_e to equation [11,](#page-3-0) such that

$$
\frac{d\vec{B}}{dt} = (\vec{\mu} + \lambda \cdot \vec{G}^+ - \vec{G}^- - (1 + B)\delta) \cdot \vec{B} + \vec{L}_e
$$
\n(16)

Each element in \vec{L}_e describes the net flux of mutants in and out of each phenotypic class. We assume that mutants are produced as a fixed proportion of each population's gross growth rate, $\vec{\mu}_{ggr}$, where

$$
\vec{\mu}_{ggr} = (\vec{\mu} + \lambda \cdot \vec{G}^+) \cdot \vec{B} \tag{17}
$$

The mutational flux is calculated as the matrix product of $\vec{\mu}_{qgr}$ and the [$J \times J$] mutation matrix, **E**.

$$
\vec{L}_e = \vec{\mu}_{ggr} \mathbf{E} \tag{18}
$$

The mutation matrix itself is defined by the fraction of daughter cells in each population that, as mutants, are diverted to the neighbouring phenotypic class. This fraction could be a single value for both trait dimensions, but here we assume that the fractions σ_s and σ_t are diverted to adjoining phenotypes in the trophic and size dimensions, respectively. For a 51×51 trait space (J = 2061) the mutation matrix is extremely sparse, with a density of just under 0.2%. The mutation rate needs to be adjusted to account for the resolution of phenotypes (*67, 82*)

$$
\sigma_s = \sigma \cdot (J_s - 1)^2 \tag{19}
$$

$$
\sigma_t = \sigma \cdot (J_t - 1)^2 \tag{20}
$$

With adaptations represented as a diffusive flux, many populations with extremely low abundances can rapidly emerge across the trait space in just a few time steps. Aside from increasing the computational load of the model, the proliferation of traits by numerical diffusion may also lead to the emergence of populations with traits far removed from those already established in the system. As our goal is to model the emergence of phenotypes by descent from established populations, we prevent trait diffusion at low biomasses in two ways. First, we scale the growth and grazing rates by a function that decreases rapidly towards zero as a population's biomass falls below a functional extinction threshold, ϵ .

$$
\vec{\gamma}_{\epsilon} = 1 - e^{-\vec{B}/\epsilon} \tag{21}
$$

This factor is applied to growth and grazing as follows,

$$
\vec{\mu} = \frac{\vec{\mu}_{max} \cdot \vec{\alpha} \cdot P}{\vec{\mu}_{max} + \vec{\alpha} \cdot P} \cdot \gamma \cdot \vec{\gamma}_{\epsilon}
$$
\n(22)

and

$$
\vec{G}^+ = \vec{g}' \cdot \left(\boldsymbol{\phi}^{\mathrm{T}} \vec{B}\right) \cdot \vec{\gamma}_{\epsilon} \tag{23}
$$

$$
\vec{G}^{-} = \boldsymbol{\phi}(\vec{B} \cdot \vec{g}') \cdot \vec{\gamma}_{\epsilon} \tag{24}
$$

Secondly, we add an additional mortality term that becomes large as a population's biomass falls below ϵ .

$$
\vec{\delta}_{\epsilon} = 10 \cdot e^{-\vec{B}/\epsilon} \tag{25}
$$

This function is incorporated into equation [16,](#page-4-2) such that

$$
\frac{d\vec{B}}{dt} = (\vec{\mu} + \lambda \cdot \vec{G}^+ - \vec{G}^- - (1 + B)\delta - \vec{\delta}_\epsilon) \cdot \vec{B} + \vec{L}_e
$$
\n(26)

These modifications prevent the growth of populations at unrealistically low abundances. Functionally extinct populations can only recover when their biomass is raised back above ϵ by mutation from adjacent phenotypes in the trait space.

Data from ODP Site 1209 (Shatsky Rise, equatorial Pacific), ODP Site 1262 (Walvis Ridge, South Atlantic) and IODP Site Data from ODP Site 1209 (Shatsky Rise, equatorial Pacific), ODP Site 1262 (Walvis Ridge, South Atlantic) and IODP Site Cretaceous survivor taxa comprise mostly *Zeugrhabdotus*, *Cyclagelosphaera*, *Markalius, Neocrepidolithus* (diploid phase Cretaceous survivor taxa comprise mostly Zeugrhabdotus, Cyclagelosphaera, Markalius, Neocrepidolithus (diploid phase post extinction event). Age models are detailed in Material and Methods (*24*). The genus *Cruciplacolithus* has been split **Figure S1. Relative abundance of key nannoplankton groups forming a succession of abundance peaks ('acmes').** post extinction event). Age models are detailed in Material and Methods (24). The genus Cruciplacolithus has been split Figure S1. Relative abundance of key nannoplankton groups forming a succession of abundance peaks ('acmes') into smaller and larger taxa (approximating to *Cr. primus* and *Cr. intermedius* + *Cr. asymmetricus*, respectively) using +2.5 M ainto smaller and larger taxa (approximating to Cr. primus and Cr. intermedius + Cr. asymmetricus, respectively) using 1403 and 1407 (Newfoundland Ridge, North Atlantic), and ordered by stratigraphic appearance in ODP Site 1209. 1403 and 1407 (Newfoundland Ridge, North Atlantic), and ordered by stratigraphic appearance in ODP Site 1209 coccoliths) and holococcoliths (haploid phase coccoliths). Data from ODP Site 1262 extends up to 63.2 Ma (~ coccolith length data (*24*).coccolith length data (24).

Figure S2a. Scanning electron microscope images of coccospheres with flagellar openings. The upper nine images are *Praeprinsius* specimens and the lower six are *Futyania,* which additionally display modified circum-flagellar coccoliths (i.e., coccoliths with a different morphology around the opening to those on the rest of the coccosphere, shaded in green for comparison with example noncircum-flagellar coccoliths highlighted in purple). For site and sample details see tables S1 and S2.

Figure S2b. Light microscope images of coccospheres with flagellar openings. The majority of the images are *Praeprinsius* specimens but the images in the lowermost row are *Futyania*. Full sample identifiers: 1407C 20-4, 125 cm; 1407A-23-2, 50 cm; 1049C-6-3, 1262B 21-7, 59 cm, 145 cm. For site and sample details see tables S1 and S2.

Figure S3. Location of sites used in this study. NR – Newfoundland Ridge (IODP Sites 1403 and 1407), BN – Blake Nose (ODP Site 1049), WR – Walvis Ridge (ODP Site 1262), MR – Maud Rise (ODP Site 690), SR – Shatsky Rise (ODP Site 1209 and 1210), Tu – Tunisia (El Kef outcrop) and NS – North Sea (proprietary well sample, see table S2). Sites marked as green are those from which we have coccospheres (see table S1), SR is marked in orange because we only have assemblage data and not coccosphere information from this site. In yellow are sites where published images of coccospheres show flagellar openings: 1. West Alabama (*37*), 2. Geulhemmerberg (Netherlands, ref. *38*), 3. DSDP Site 356, Sao Paulo Plateau (*39*) and 4. ODP Site 738, Kerguelen Plateau, Indian Ocean sector of the Southern Ocean (*40*). Location and dataset details in tables S1 and S2. The basemap is a 66 Ma reconstruction from the ODSN website (www.odsn.de).

Figure S4. Taxon-specific abundance data differentiated according to the presence of flagellar openings and degree of heterotrophy. (**A**) shows the abundances of different Danian taxa (from ODP Site 1209, sub-equatorial Pacific) color-coded according to whether their cells are flagellate (or considered mixotrophic) or not, blue and green, respectively. (**B**) shows modelled abundances of 'species' in the nannoplankton size range (2-20 microns) again color-coded according to whether the cells are flagellate. Note that mutation and evolution proceed much faster in the model because the model applies a simplified 'trait diffusion' approach to evolution (*24*).

Figure S5. Morphological variation across the early Danian taxon *Praeprinsius.* Data from ODP Site 1209 (Equatorial Pacific) and IODP Sites 1403 plus 1407 (North Atlantic). On the left is the percent abundance of *Praeprinsius* in cell numbers relative to total calcareous nannoplankton fossils, using highresolution coccolith abundance data (converted to cell numbers) (*24*) from ODP Site 1209 (original coccolith data from *9*). The vertical black lines indicate the time slices across which length measurements of individual coccoliths have been measured and integrated to produce the frequency plots (black histograms) of size on the right-hand side; these time slices are the same for the two sites. The black filled-in circle under each histogram indicates mean cell size and the red line shows one standard deviation either side of the mean. Number of liths measured per time slice per site is given as the n number for ODP Site 1209 and IODP Sites 1403 plus 1407, respectively. Coccolith length measurements have been converted to an estimate of the average cell size associated with coccoliths of this length via the conversion: cell size $= 1.447$ coccolith length $+ 1.14$. This conversion is based on measurements of 147 whole coccospheres and the coccoliths that form these coccospheres from samples that span the duration of the *Praeprinsius* acme from ODP Sites 1209, 1403 and 1407 (*25*). The similarity in means and trends in size across the two regions suggests global evolutionary size increases across *Praeprinsius*.

Figure S6. Illustration of spherical cap calculations. Under light microscope observation, the equatorial region of coccospheres is obscured and therefore only part of the area of the sphere can be observed clearly to assess for presence of coccosphere openings. We estimate that we can typically observe a part of the sphere corresponding to the pole of each coccosphere to about 65 degrees in the upper and lower hemispheres, correspond to 60% of the surface area.

Figure S7. Size-dependent ecophysiological parameters: (a) maximum growth rate,

 μ_{max} (64, 77, 80); (b) nitrate affinity, α (64); (c) grazing clearance rate, g (62); (d) predator-prey sizeratio-dependent capture efficiency, ϕ (63).

Table S1. Coccosphere observations by age and site. Underlined percentages are from SEM observations where only ~30-50% of the coccosphere surface can be seen clearly enough to assess presence of an opening. The rest are from LM observations where ~60% of the coccosphere surface can be seen clearly enough to assess presence of an opening (*24*) (see fig. S6). Taxa in bold indicate percent abundances of coccosphere openings which indicate that all individuals in the populations have openings. The thresholds are 30% in SEM and 60% under LM observation. The bottom four sites are ones for which images have been published that exhibit flagellar openings. *Neobisc. – Neobiscutum; Praepr. – Praeprinsius; Cruci. – Cruciplacolithus; Cocc. – Coccolithus; Erics. – Ericsonia*. Depths: mcd - meters composite depth; rmcd – revised meters composite depth; mbsf – meters below seafloor; El Kef m – meters above K/Pg boundary. Age models: *Biostratigraphy (shipboard, ref. *54*, and more recent revision herein); **ref *2*, based on cyclostratigraphy; †based on biostratigraphy (herein) and position of chron C29N/C29R boundary at 247.55 mbsf (*83*); ‡ref. *52* based on cyclostratigraphy. All ages use the Geological Timescale 2012 (GTS2012, *84*).

Table S2. Summary of main locations and datasets used in the study. *Diversity and taxon abundance data published in ref *9*. **Some coccosphere measurements utilized in ref *9* to produce their estimated average cell volume. †Based on our assessment herein (*24*). References for SR – *9, 19*; NR – *2, 54*; BN – *85*; Tu – *15, 18*; WR – *10, 12, 54*; MR – *18*. The single specimen of *Prinsius* imaged in Figure 2 from the North Sea is from Danian material from a proprietary well sample and therefore we are unable to provide additional information. See location map (fig. S3) for paleogeography.

Table S3. Paired-sample t-test results of flagellate communities through time. Comparison of percent flagellate cells (here using percent coccoliths) in the ealry Danian (acme phase up to 64.20 Ma) with the latest Cretaceous and the later Danian (post 64.20 Ma). Comparisons have only been made between populations at the same location. For Shatsky Rise (ODP Sites 1209 and 1210), we are able to directly compare coccolith abundance data from the early Danian with both the Late Cretaceous and the later Danian. For Walvis Ridge, we only have data allowing comparison of early Danian abundances with the Late Cretaceous, and for Newfoundland Ridge, only with the later Danian (*24*). For the mean, the first value given corresponds to the mean % flagellate abundance for the early Danian interval. The second value is the mean of the interval the early Danian is being compared with. The tests demonstrate that the interval up to approximately 64.2 Ma with unusually high levels of mixotrophic cells, is statistically distinct from either the preceding Late Cretaceous communities or the subsequent later Danian. SD – standard deviation, df – degrees of freedom, $t - t$ value, $p - p$ value.

Table S4a. Size-dependent parameters with allometric scaling coefficients reported in the

literature (64, 77, 62). The size-dependent value of each parameter, p, is given by $p = a \left(\frac{V}{V}\right)$ $\frac{v}{V_1}$ b , where V is the cell volume and V_1 is a normalisation constant of 1 μ m³. Note that μ^{∞} , ρ_{\max} and Q_{\min} are only used to constrain μ_{max} in equation [7.](#page-2-0)

Table S4b. Size-independent parameters.

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