Sudden Productivity Collapse Associated with the Triassic-Jurassic Boundary Mass Extinction

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The end-Triassic mass extinction is one of the five most catastrophic in Phanerozoic Earth history. Here we report carbon isotope evidence of a pronounced productivity collapse at the boundary, coincident with a sudden extinction among marine plankton, from stratigraphic sections on the Queen Charlotte Islands, British Columbia, Canada. This signal is similar to (though smaller than) the carbon isotope excursions associated with the Permian-Triassic and Cretaceous-Tertiary events.

The Triassic-Jurassic (T-J) boundary mass extinction, one of the five most severe in Phanerozoic history, led to the demise of as many as 80% of all living species (1–3). Unanswered questions about the extinction concern its duration, its severity, and whether it affected global productivity. The extinction in marine strata has recently been dated at 199.6 ± 0.3 million years ago (Ma) by means of high-resolution U-Pb zircon geochronometry (4), but it is unknown whether the extinctions were synchronous on land and in the sea, because this date seems slightly later than the extinction dated on land (5). It has been suggested that the T-J extinction, unlike the Permian-Triassic (P-T) and Cretaceous-Tertiary (K-T) events, did not affect the carbon cycle long enough to cause a clear perturbation in δ13Corg (5),
leading to the conclusion that this mass extinction did not significantly affect bioproductivity on a global basis or the long-term burial of organic carbon. We present here a record of a rapid and negative excursion in carbon isotopes at the top of the uppermost stage of the Triassic and including the T-J boundary, from a stratigraphic section that appears relatively unaffected by diagenesis. This isotopic anomaly is coincident with a sudden extinction of marine plankton (Radiolaria) at the paleontologically defined T-J boundary.

We studied the uppermost Peril (Triassic: Upper Norian) and Sandilands (Triassic-Jurassic: Rhaetian to Pliensbachian) formations at two sites on the Queen Charlotte Islands, British Columbia, Canada: Kennecott Point (Fig. 1) (latitude 53°54'48.4"N, longitude 133°09'17.8"W) and Kunga Island [a proposed candidate for the type section of the T-J boundary (7)] (latitude 52°45'31.4"N, longitude 131°33'36.6"W), located approximately 165 km southeast of Kennecott Point. The uppermost Peril Formation consists of black calcareous shale and siltstone, whereas the overlying Sandilands Formation consists of laminated, thinly bedded, organic-rich siltstone and black shale interbedded with thicker turbiditic sandstone and tuff (8). At both sections, the T-J boundary is placed, on stratigraphic grounds, at the base of the Lower Hettangian Canopus merum radiolarian zone, which is equivalent to the North American Psiloceras assemblage of the ammonoid standard zonal sequence (9). Stratigraphic sections at both localities have been correlated palaeontologically (10), and the boundary at Kunga Island (Fig. 2) lies 6.3 m above a tuff dated to 199.6 Ma (4).

Bulk samples of black shale were collected stratigraphically from both sections and analyzed for organic carbon with mass spectrometry (11). Total organic carbon (TOC) at both sections varies from 1 to 6% for the samples. At Kennecott Point (Fig. 1), there is no significant correlation between TOC and $\delta^{13}$C$_{org}$ ($R^2 = 0.006$). At Kunga Island, however, there is a significant correlation ($R^2 = 0.64$), which suggests that extensive diagenetic alteration of these strata may have occurred.

At both Kennecott Point and Kunga Island, a significant turnover of radiolarian fossils occurs at the level of the palaeontologically defined T-J boundary. In neither section is there any discernible lithological change across this interval. At Kunga Island, more than 60 species of radiolarians disappear across the boundary interval (12), whereas more than 50 species disappear in the Kennecott Point section (13). The disappearance of the Kennecott Point radiolarians is less precisely located, because there is a lack of radiolarian-bearing concretions over a 6-m-thick stratigraphic interval in which the extinction level must lie. The highest Rhaetian (Triassic) ammonoid recovered at Kennecott Point, Choristoceras rhaeticum, was found 16 m below the boundary, and the lowest Hettangian ammonite, Psiloceras pacificum, was found 6 m above the boundary. No ammonites are present at either section.
have been recovered near the boundary interval at Kunga Island.

Bulk samples collected across the boundary interval at Kennecott Point yielded a stratigraphically restricted (~5 m), ~2 per mil (%) change in $\delta^{13}$C$_{org}$, followed by a return to values that were slightly more negative than those beneath this excursion. Although the magnitude of the excursion is not as great as that seen at most P-T or K-T boundary sites, what stands out about the isotope record that we have recovered from the Kennecott Point boundary interval is that the absolute values are well below the background variation in the rest of the section (which spans all of the Rhaetian Stage and the upper part of the Norian and lower part of the Hettangian stages) and are defined by multiple samples.

Samples collected from the Kunga Island section also show a significant deviation from background $\delta^{13}$C$_{org}$ values across the T-J boundary. Unlike the Kennecott Point results, however, the deviation in $\delta^{13}$C$_{org}$ is positive rather than negative and is defined by a single sample. In its positive trend, the Kunga Island excursion thus resembles the isotopic record from the T-J section at Kendelbach, Austria, which has been ascribed to diagenesis (6). Although the positive correlation of percent TOC and $\delta^{13}$C$_{org}$ at Kunga Island suggests that the observed isotopic values obtained from there may have been compromised by diagenesis, the Kennecott Point samples show no such evidence either from isotopes or lithology (14).

Although the sudden extinction of radiolarians at the T-J boundary is the most important bioevent in our two studied sections, there is also a second event recorded lower in the Kennecott Point section, at the Norian/Rhaetian boundary, that is most prominently marked by the disappearance of monodit bivalves. The extinction of monodit bivalves in the section is associated with a gradual change in lithology, from massive and bioturbated black calcareous mudstone and siltstone with abundant bedding-plane concentrations of Monotis spp. in bituminous facies of the Peril Formation to thinly laminated black shale interbedded with more massive turbiditic siltstone and fine sandstone composing the Sandilands Formation. This lithological change extends over a few tens of meters. Ammonoid abundance also decreases significantly at this level, and their preservation changes from entire (but flattened) body fossils to impressions of shells with siphuncular structures preserved in three dimensions within the phragmococone outline. Trace fossil assemblages also change here, with an increase in Conodrutes on bedding planes in the dark shale facies, suggesting increasingly anaerobic bottom conditions (8). As shown in Fig. 1, this extinction interval is marked by an increase in $\delta^{13}$C$_{org}$ values in two samples, coincident with the disappearance of monoditids. Further sampling is needed to ascertain whether this isotopic change is significant and correlated with the extinction event.

The pattern of sudden extinction coincident with a $\delta^{13}$C$_{org}$ decrease at the Rhaetian/Hettangian (T-J) boundary at Kennecott Point is compatible with a sudden biological crisis affecting marine productivity. As yet there is no reliable means of dating the duration of this event in the Queen Charlotte Islands sections (although the presence of ashes will make such analyses feasible in the future). As a rough estimate, however, if the Hettangian Stage duration is taken as 6 million years in length (3), and assuming constant sedimentation rate at Kennecott Point during that time, then the duration of the isotopic excursion at the Kennecott Point section would be about 500,000 years in length, whereas the extinction event itself was likely on the order of 50,000 years or even less.

Other possibilities that could explain the observed pattern in carbon isotopes include a decrease in organic carbon burial coincident with the biodiversity decline of Radiolaria, and/or a rapid recycling of isotopically light bottom water caused by a shallowing of the water column pycnocline. However, it seems a more parsimonious interpretation that a single short-term event caused the observed isotopic pattern at the Kennecott Point T-J boundary. This pattern exhibits similarity with those seen at extinction boundaries such as the K-T and P-T, where extraterrestrial impact scenarios have been invoked.

**Fig. 2.** Measured stratigraphic section of the T-J boundary interval at Kunga Island, showing positive correlation of percent TOC and $\delta^{13}$C$_{org}$ suggesting diagenesis. The section is composed of massive thinly bedded siltstone. Data are presented as in Fig. 1.

**References and Notes**

11. Isotope analyses were performed in the University of Washington laboratory of P. Quay. Isotope analyses were done with two methods, both ultimately calibrated versus National Bureau of Standards–19 (NBS-19), for $^{13}$C = 1.95‰ versus the Vienna
African Origin of Modern Humans in East Asia: A Tale of 12,000 Y Chromosomes

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To test the hypotheses of modern human origin in East Asia, we sampled 12,127 male individuals from 163 populations and typed for three Y chromosome biallelic markers (YAP, M89, and M130). All the individuals carried a mutation at one of the three sites. These three mutations (YAP+, M89T, and M130T) coalesce to another mutation (M168T), which originated in Africa about 35,000 to 89,000 years ago. Therefore, the data do not support even a minimal in situ hominid contribution in the origin of anatomically modern humans in East Asia.

The "Out-of-Africa" hypothesis suggests that anatomically modern humans originated in Africa about 100,000 years ago and then spread outward and completely replaced local archaic populations outside Africa (1, 2). This proposition has been supported by genetic evidence and archaeological findings (3–9). The replacement in Europe was supported by recent ancient DNA analyses, which ruled out the contribution of Neanderthalans to modern Europeans (10, 11). However, it has been argued that the abundant hominid fossils found in China and other regions in East Asia (e.g., Peking man and Java man) demonstrate continuity, not only in morphological characters but also in spatial and temporal distributions (12–16). In this report, we test the competing hypotheses of modern Asian human origins using Y chromosome polymorphisms.

We sampled 12,127 male individuals from 163 populations across Southeast Asia, Oceania, East Asia, Siberia, and Central Asia and typed for three Y chromosome biallelic markers (YAP, M89, and M130) (17, 18) (Table 1). Being a single-locus multiple-site (i.e., haplotype) system, the Y chromosome is one of the most powerful molecular tools for tracing human evolutionary history (5, 9, 19–21). In previous Y chromosome studies, an extreme geographic structure was revealed in global populations in which the oldest clade represents Africans and the younger ones represent some Africans and all non-African populations (21). One Y chromosome polymorphism (C to T mutation) at the M168 locus is shared by all non-African populations and was originally derived from Africa on the basis of a study of 1062 globally representative male individuals (2). The age of M168 was estimated at 44,000 years (95% confidence interval: 35,000 to 89,000 years), marking the recent Out-of-Africa migrations (21). Under the M168T lineage, there are three major derived sublineages defined by polymorphisms at loci YAP (Alu insertion) (5), M89 (C to T mutation), and M130 (C to T mutation, also called RP54Y) (Fig. 1) (21, 22). Therefore, these three markers can be used to test the completeness of the replacement of modern humans of African origin in East Asia. An observation of a male individual not carrying one of the three polymorphisms would be indicative of a potential ancient origin and could possibly lead to the rejection of such completeness.

Each of the 12,127 samples typed carried one of the three polymorphisms (YAP+, M89T, or M130T) (Table 1). In other words, they all fall into the lineage of M168T that was originally derived from Africa. Hence, an ancient non-African Y chromosome was found in the extant East Asian populations (P = 5.4 × 10⁻⁶ assuming a frequency of 1/1000 of local contribution in the extant populations), suggesting an absence of either an independent origin or a 1,000,000-year shared global evolution. This result indicates that modern humans of African origin completely replaced earlier populations in East Asia.

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