





**Fig. 1.** Illustrations of Milankovitch grand cycles over the past 1–11 My generated from the astronomical solution in ref. 9. (A) Amplitude modulation of precession by eccentricity. The black line is the climatic precession [= eccentricity  $\times$  sin(precession angle)]; the red line is the amplitude modulation and reveals cycles at  $\sim 100,000$  and  $\sim 405,000$  y and grand cycle nodes at  $\sim 2.4$  My. (B) Amplitude modulation of obliquity. The black line is the obliquity solution; the red line is the amplitude modulation of the dominant 41,000-y obliquity cycle, with a conspicuous  $\sim 1.2$ -My grand cycle.

Graptoloid colony size generally ranged from a few millimeters up to  $\sim 200$  mm in maximum dimension, although the individual zooids measured less than 2 mm in length (20). The colonies lived suspended in the ocean waters at a range of depth zones and are inferred to have filtered out microphytoplankton, bacterioplankton, and other particulate organic matter as their principal food source (21–23). The graptoloids are, therefore, inferred to have been primary consumers in the food chain and consequently, would have been sensitive to environmental parameters that controlled their main trophic resource, namely nutrient flux, ocean stratification and chemistry, redox profile, local and global ocean circulation systems, and therefore, global marine climate (16, 21, 24, 25). In support of this environmental sensitivity, positive excursions in the global  $\delta^{13}\text{C}_{\text{carb}}$  isotope curve—interpreted as reflecting carbon burial and associated global cooling (26–28)—coincide with falling or minimal values in the graptoloid raw species richness curve, although the causal linkage was complex and is not fully understood (16). Furthermore, the transition in global climate from greenhouse to icehouse in the Late Ordovician is marked by a step change in the graptoloid species extinction rate (16, 17), a change from background to episodic extinction, and a change in the dependence of extinction risk on species age (17).

To evaluate periodic environmental pacing in the graptoloid macroevolutionary record, it is necessary to have a long time series of speciation and extinction observations and to minimize aliasing of frequencies. These data should, therefore, be as highly resolved as possible. Here, we use the high-resolution time series of graptoloid speciation and extinction probabilities derived from the global composite that was developed using constrained optimization (CONOP) (29) from 518 stratigraphic sections. The complete composite spans the entire history of the clade from 491 to 411 Ma, contains 2,041 species, has been calibrated directly by 23 integrated radioisotopic dates, and is the basis of the Ordovician and Silurian global geological timescales (14, 15). To reduce stochastic noise in the signal while retaining maximum resolution, we fit discrete time hidden Markov models (HMMs) (30) to the raw time series of speciation and extinction probabilities at a temporal resolution of 0.05 My (*Materials and Methods*).

## Results

The time series of graptolite HMM species turnover (speciation plus extinction HMM probabilities) reveals a strong 2.6-My rhythm expressed in both the time frequency result (Figs. 2 C and D and 3 and Figs. S3 and S5) and power spectrum for the entire study interval (Fig. S2); this rhythm is close to that of the modern day orbital eccentricity grand cycle. In contrast, a  $\sim 1.3$ -My rhythm that is weak in the total spectrum is dominant in the early portion of the record, with a transition between the two in the interval from 460 to 453 Ma (Figs. 2 C and D and 3 and Fig. S4). This signal is close to that of the modern day obliquity grand cycle. Together, these two cycles explain between 9 and 16% of the total variance in the turnover signal (Fig. 3A). Both rhythms are statistically significant. The testing of statistical significance in time series analysis is a complex issue that is addressed in detail in *Materials and Methods* and *Supporting Information*.

Although the grand cycles are expected to have influenced Paleozoic climate, the tempo of the Milankovitch cycles for this distant time interval cannot be predicted reliably from theory (9). This study suggests the existence of a 2:1 resonance of the grand cycles as is observed in the Late Cenozoic. These 2.6- and 1.3-My cycles emerge from time series derived from a single HMM (our key result) (Figs. 2 C and D and 3 A and B and Fig. S5A) and from averaging of many HMMs (*Supporting Information* and Fig. S5B). They are evident in time series based on raw probabilities (*Supporting Information* and Fig. S5C), and our conclusions are, therefore, not dependent on the fitting of HMMs, although the signal is weakened somewhat by noise in comparison with the HMM time series. Furthermore, these cycles are also observed in the time series of HMM speciation and extinction analyzed separately (Fig. S5 D and E), although the 1.3-My cycle is weak in the result for speciation. Finally, our conclusions are not affected if we allow for phyletic gradualism in the graptoloid clade, even when modeled with unrealistically high levels of pseudospeciation and pseudoextinction (*Supporting Information* and Fig. S5F).

## Discussion

The inferred transition from obliquity-dominated to eccentricity-dominated grand cycles (Figs. 2 C and D and 3) in the Late Darriwilian coincided with the peak of the Great Ordovician Biodiversification Event—the greatest expansion of global biodiversity





It seems, therefore, that Darrivilian reorganization of the graptoloids might well have been adaptive and related directly or indirectly to progressively changing global climatic conditions that were themselves related in some way to the transition from obliquity- to eccentricity-dominated grand cycles. In contrast, graptoloid reorganization that accompanied the HME resulted from a mass extinction associated with rapid environmental change, although the role of Milankovitch cycles in forcing this rapid change remains unclear. In addition to these major transitions, this analysis shows that, throughout the entire lifespan of the graptoloid clade, species turnover was driven in part by fluctuations in climatic volatility related to the Milankovitch grand cycles.

During the Late Cenozoic, long-period mammalian turnover pulses coincided with 1.2-My obliquity and 2.4-My eccentricity nodes in the theoretical astronomical solution (6, 9) during times of minimum variability in insolation that were associated with global cooling and ice sheet expansion. We cannot determine the phase relationship between the Paleozoic grand cycles in graptolite turnover and astronomical forcing, since accurate astronomical solutions are not available for the Ordovician and Silurian. Integration of the graptolite species turnover results with climate proxy time series, however, would allow phase relationships between climate volatility at the scale of the grand cycles and graptoloid turnover to be determined.

We cannot say with certainty whether the observed cyclicity in graptoloid species turnover is driven more by speciation or extinction. Correlations between both processes and turnover are about the same, suggesting that they are equally important in driving turnover, and speciation and extinction are themselves significantly cross-correlated (Pearson correlation coefficients: HMM speciation vs. turnover 0.854,  $P < 0.001$ ; HMM extinction vs. turnover 0.873,  $P < 0.001$ ; HMM speciation vs. extinction 0.492,  $P < 0.001$ ). That said, however, separate spectral analyses of HMM speciation and extinction time series show that the grand cycles consistently explain a higher proportion of the spectral variance for extinction than origination (Fig. 3C and Fig. S5 D and E). This may suggest that extinction in the graptoloids was influenced more strongly by these astronomical cycles than speciation, although further testing is required.

## Materials and Methods

Because graptoloid diversity is low at each end of the CONOP composite and stochastic errors are, therefore, large, we restrict our analyses to the interval 481–419 Ma and ignore the intervals between 491–481 and 419–411 Ma. We also remove 247 species that have been assigned a zero range in the composite—those that have first appearance age equal to the last appearance age. These species are removed because we assume that they are most likely to be rare and undersampled taxa; indeed, of the 247 zero-range species, 210 are known from a single section only, and nearly all of the rest are known from just two sections, where a section is an outcrop or core from which species have been identified from one or more rock layers. In contrast, the remaining species are found in an average of 5.5 sections each. Our final composite contains 1,794 species with range ends that are resolved to 1,902 distinct levels (time horizons). The average spacing of CONOP levels in time is 0.033 My, and the median is 0.012 My. Because uneven spacing of levels hampers interpretation of extinction and speciation probabilities used here, we move speciation and extinction events at each of the CONOP-derived levels onto a series of 0.05-My-spaced “pseudolevels.”

To extract high-resolution macroevolutionary time series, we have used discrete time HMMs (30) to identify a parsimonious set of discrete speciation and extinction probability states in the data and to predict time series of those

states given the observations. “Raw” speciation and extinction probabilities are calculated as the number of speciations or species extinctions at each pseudolevel, respectively, divided by the number of species extant at each level ([Supporting Information](#)). The use of HMMs reduces stochastic noise in the signal and avoids loss of resolution that would result from use of coarser time bins as required by standard macroevolutionary rate metrics or use of moving window metrics and the resultant imposed autocorrelation. In particular, because of the limited numbers of speciations and/or extinctions at each pseudolevel, the raw probabilities are expected to be noisy; HMMs are an effective tool for change point analysis and can be used to determine whether abrupt changes in the time series exceed the noise and should be considered meaningful or not. As implemented here, the HMMs assume that the observed process obeys a binomial distribution, where the number of “successes” at each pseudolevel is the number of speciations or extinctions and the number of Bernoulli trials is the total number of species crossing that level. For the results presented here, we have calculated species turnover as the sum of HMM speciation-state probability and extinction-state probability at each pseudolevel. Relationships between different rate and probability metrics, for a short segment of our time series, are illustrated in Fig. 4, which shows the smoothed per lineage million years rates (18), the raw speciation and extinction probabilities at each pseudolevel, the HMM speciation and extinction probability states at each pseudolevel, and the resulting turnover time series.

We test for candidate grand cycles in the resultant graptoloid HMM turnover record using multitaper method (36) spectral techniques, which permit a robust assessment of the variance in turnover that is associated with the grand cycles. In addition, temporal evolution of potential grand cycles is evaluated using Evolutive Power Spectral Analysis (EPSA) (37), Evolutive Harmonic Analysis (EHA) (38), and Taner bandpass filtering (19). EPSA and EHA utilize three  $2\pi$  prolate tapers with a 20-My moving window, and a linear trend is removed from each window before analysis. During spectral analysis, we use Monte Carlo simulation of stochastic surrogates, which have the same sampling characteristics and noise model parameters as observed in the data, to assess the suitability of particular background noise models (autoregressive lag-1 and power law models) in the estimation of statistical significance. These tests use a range of standard spectral methods and identify particular background estimation approaches that are optimal for our data. At the same time, we apply several multiple statistical test corrections to protect against inflated false-positive rates that result from the simultaneous testing of many null hypotheses at different spectral frequencies. Again, given dependence of false-positive rates on the noise model used, the multiple test corrections are evaluated using surrogate simulations. During estimation of statistical significance, we investigate specific frequency bands of interest that are relevant to the grand cycles but also present “global” confidence limits. Results of these tests will be specific to any given dataset: for example, we use the age-scaled CONOP time series; in contrast, the use of more normal depth-scaled data may require the investigator to prospect across a wider range of frequencies than tested here. To facilitate broader application of these approaches, we provide a series of functions in the open source software used here for time series analysis (see below).

Significance levels of correlation coefficients between different time series are evaluated using the phase randomized surrogate approach (39) for serially correlated data.

All of these analyses were undertaken in the R language for statistical computing (40). Details of data manipulation, HMM-fitting procedures, time series analyses, and sensitivity analyses are presented in [Supporting Information](#) along with the data and R code used to generate the analyses.

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