



Figure 1 | Consequences of an intraplate earthquake. Yingxiu town, Wenchuan county, seen in the wake of the seismic events of 2008.

viscosity in the upper mantle, the result of an ancient, failed rift in the region.

Importantly, both models produce crustal deformation rates that are consistent with the rates observed by GPS measurements in the region; and both predict that the rate of large earthquakes seen over the past few thousand years is likely to continue for thousands of years into the future, because of the long time it takes for the triggered viscous flow in the lower crust and upper mantle to diminish. In other words, seismic hazard in the region remains high. The paper by Calais *et al.* is valuable both in reinforcing that point and in providing a plausible mechanism that merits further investigation.

It has been argued⁸ that, as in the New Madrid region, several intraplate fault zones in Australia have exhibited episodes of relatively frequent earthquakes separated by long periods of quiescence. Similar behaviour may characterize earthquakes in the southeastern United States near Charleston, South Carolina⁹. These

regions, as well as others that have been struck by intraplate earthquakes, deserve detailed study, with the aim of revealing what might have triggered the release of strain energy stored in Earth's crust for millions of years. ■

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OCEANOGRAPHY

Century of phytoplankton change

David A. Siegel and Bryan A. Franz

Phytoplankton biomass is a crucial measure of the health of ocean ecosystems. An impressive synthesis of the relevant data, stretching back to more than 100 years ago, provides a connection with climate change.

In 1865, Father Pietro Angelo Secchi was asked to map the clarity of the Mediterranean Sea for the Papal navy. He invented the simplest of oceanographic instruments: a 20-centimetre-wide white disk that is lowered until the observer loses sight of it, and for nearly 100 years determinations of Secchi depth were a routine part of oceanographic

observations^{1,2} (Fig. 1, overleaf). Secchi-depth determinations assess light penetration in the upper ocean, and can be related to phytoplankton abundance. Along with measurements of the upper-ocean concentration of chlorophyll, which is found in all phytoplankton, Secchi-disk depths provide the only data available for assessing changes in the global

ocean biosphere over the past century.

Boyce *et al.*³ (page 591 of this issue) have revisited those data, and have synthesized all available information to assess changes in phytoplankton biomass on decadal to centennial timescales, and over regional to global spatial scales. Taking great care, they created time series of phytoplankton biomass in the pelagic ocean, quantified as surface chlorophyll concentrations. They find a strong correspondence between this chlorophyll record and changes in both leading climate indices and ocean thermal conditions. They also show statistically significant long-term decreases in chlorophyll concentrations for eight of the ten ocean basins, and for the global aggregate.

Boyce and colleagues' findings are consistent with analyses of satellite observations of ocean colour, in which decreases in indices of phytoplankton productivity are mirrored by increases in ocean warming^{4–6}. Satellite ocean-colour observations sample the entire globe within two days. In fact, in less than 30 seconds, the Sea-viewing Wide Field-of-view Sensor (SeaWiFS) makes nearly half a million independent observations — equivalent to the entire historical record synthesized by Boyce and colleagues. But high-quality, global satellite observations of the ocean biosphere have been available for little more than a decade — too short a time to quantify and understand the causes of long-term trends⁷.

The analyses of Boyce *et al.* document the historical record. Looking into the future, however, satellite measurements will be the main source of data for assessing change in pelagic ecosystems. The principle is simple — the colour of the 'water-leaving' sunlight is used to determine chlorophyll concentrations. Turning that principle into practice is not simple.

First, satellites measure the reflected sunlight at the top of the atmosphere, and, typically, fewer than 10% of the photons detected relate to the oceans' water-leaving signal. Hence an atmospheric correction is required to quantify a much smaller ocean-colour signal⁸. Furthermore, the measurements must be accurate and stable enough to assess change over inter-annual timescales⁹. This requires both the on-orbit assessment of alterations in sensor characteristics over time, and a procedure to provide absolute sensor calibration^{8–10}. Finally, a bio-optical model is needed to convert the remote assessments of ocean colour to oceanographically relevant quantities¹¹, along with field observations to validate the satellite results. Thus, many interdependent components are required to create satellite observations of ocean colour that will be useful in assessing the response of ocean ecosystems to climate change.

Another consideration is that satellite missions planned at present have lifespans of only about five years, so establishing a multi-decadal time series of observations requires data from several missions. Unlike the Secchi disk,

the performance of spaceborne radiometers degrades with time, and the sensors often differ in design and performance from mission to mission. To ensure that geophysical changes are not confounded by instrumental changes and/or mission transitions, ocean-colour time series must be continuously monitored and periodically updated through reprocessing of the entire data record.

A prime example is the most recent reprocessing of the ocean-colour data sets provided by SeaWiFS and by the Moderate Resolution Imaging Spectroradiometer on Aqua (MODIS-Aqua). Advances in instrument calibration and improved atmospheric correction and bio-optical models, coupled with an unprecedented attention to processing consistency, reduced the discrepancy between the two missions for deep-water, global mean chlorophyll concentrations from 12% to less than 2% over their common mission times¹².

Characterization of the changes and functions of pelagic ecosystems, however, requires more than just a measurement of changes in the chlorophyll concentration. An advantage of multispectral satellite ocean-colour measurements is that distributions of other optically active constituents can all be determined^{9,13–16}. Examples are the concentrations of coloured dissolved and particulate organic matter, particle-size spectra, and phytoplankton physiological status based on remote sensing of ocean-fluorescence properties. A better understanding of the nature of climate-change impacts on the ocean biosphere will result from an assessment based on this broader suite of parameters.

Boyce *et al.*³ make a sorely needed contribution to our knowledge of historical changes in the ocean biosphere. Their identification of a



Figure 1 | The simplest of all oceanographic instruments. In this photograph, from 1949, a Secchi disk is being lowered into the sea to measure water transparency.

connection between long-term global declines in phytoplankton biomass and increasing ocean temperatures does not portend well for pelagic ecosystems in a world that is likely to be warmer — phytoplankton productivity is the base of the food web, and all life in the sea depends on it.

Unfortunately, owing to the costs and complexity of satellite ocean-colour systems and competing priorities for science funding, our

future ability to assess these changes is also in jeopardy. In the United States, a National Research Council study is under way to assess issues concerning sustained satellite ocean-colour observations¹⁷. Improving the long-term understanding of changes in pelagic ecosystems, initiated by Boyce *et al.*³, will depend on the resolution of these issues. ■

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METABOLISM

Tick, tock, a β -cell clock

Katja A. Lamia and Ronald M. Evans

The daily light–dark cycle affects many aspects of normal physiology through the activity of circadian clocks. It emerges that the pancreas has a clock of its own, which responds to energy fluctuations.

The pancreas is a mosaic organ: its different cell types regulate sugar and fat metabolism through controlled production of digestive enzymes and hormones in response to food and physiological demand. To maintain normal blood glucose levels after a meal, for instance, β -cells in pancreatic islets produce insulin, which then stimulates glucose uptake and storage by the muscle and fat cells, and stops glucose production and secretion by the liver. It is increasingly being appreciated that circadian clocks — sets of genes through which organisms keep track of time

— regulate these processes. But exactly how they function is not known. On page 627 of this issue, Marcheva *et al.*¹ report that pancreatic islets have a circadian clock that regulates insulin secretion, and that disruption of this clock causes greatly increased blood glucose due to impaired insulin secretion, a hallmark of diabetes.

Circadian biological phenomena — from the daily movements of plant leaves to human sleep–wake cycles — have been recognized for centuries, but their underlying physical and biochemical mechanisms have remained

mysterious. In 1972, a study² demonstrated that a brain region in the hypothalamus called the suprachiasmatic nucleus, which sits just above the optic nerves, is required for daily rhythms in animal behaviour. This established a physical location for the generation of rhythmic behaviour in mammals. The suprachiasmatic nucleus receives light signals through the optic nerves, and so uses daylight cues to set the clock time and to couple light–dark transitions to behavioural outputs.

Subsequent genetic studies identified several genes that mediate rhythmic behaviour. Biochemical investigation of the proteins expressed by these genes led to the current model of the mammalian circadian clock. This clock is a molecular oscillator based on a negative-feedback loop in which the transcription factors CLOCK (or the related protein NPAS2) and BMAL1 work together to drive the expression of many genes, including those encoding their own inhibitors — the period (PER1, PER2 and PER3) and the cryptochrome (CRY1 and CRY2) proteins³.