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CLIMATE SCIENCE

Global warming and tropical carbon

An innovative use of measurements of atmospheric carbon dioxide constrains the possible range of carbon-cycle responses to climate change during the twenty-first century, lowering expectations of tropical-forest dieback. [SEE LETTER P.341](#)

JAMES T. RANDERSON

Tropical forests and savannahs are responsible for most of the annual exchange of carbon dioxide between the atmosphere and the land surface. Long growing seasons and high rainfall create extremely productive tropical ecosystems¹ that store a considerable amount of the world's above-ground biomass². The fate of this carbon pool could influence future atmospheric carbon levels and thus our ability to stabilize greenhouse gases at levels that do not dangerously interfere with the climate system³. On page 341 of this issue, Cox *et al.*⁴ report findings that will enable the development of more realistic future scenarios of climate-carbon interactions in tropical ecosystems*.

Over the past decade, tremendous progress has been made towards integrating the carbon cycle into global climate models known as Earth-system models. Simulations using such models have shown that carbon stocks in tropical forests will become increasingly vulnerable to climate change during the twenty-first century, given future 'business as usual' scenarios of fossil-fuel emissions. In one model, for example, climate warming and elevated levels of CO₂ reduced precipitation across the Amazon, which led to a die-off of forests and thus further warming⁵. In several other models, increases in drought stress in forests across the tropics decreased plant growth (net primary production), and so accelerated carbon losses from these ecosystems⁶.

These interactions, in which climate change induces a carbon-cycle change that contributes to additional warming, are called positive climate-carbon feedbacks. The strength of these feedbacks varied by more than a factor of seven for models analysed⁶ as part of the Intergovernmental Panel on Climate Change's Fourth Assessment Report. In most models, the response of tropical ecosystems dominates the strength of the global-scale climate-carbon feedbacks, although losses from high-latitude carbon pools are also important in models that incorporate the best current representation of permafrost-soil physics⁷.

Cox *et al.* have developed an approach for

*This article and the paper under discussion⁴ were published online on 6 February 2013.

reducing the considerable uncertainty that is associated with the size of tropical climate-carbon feedbacks. They used an 'emergent model constraint'⁸ to refine the probable range of sensitivities of tropical-land carbon fluxes to climate change during the twenty-first century. This approach has previously been used to constrain projections of climate change, and involves two steps. First, a statistically significant relationship must be found between contemporary and future model predictions for an ensemble of Earth-system models from different research centres. Second, observations must be used to limit the possible range of contemporary behaviours described by those models.

The authors show that this approach can be applied to the carbon cycle, and demonstrate that models that show higher levels of year-to-year (interannual) variability of atmospheric CO₂ levels in response to variations in climate

modes, such as the El Niño–Southern Oscillation, tend to predict larger losses of carbon from the tropics in response to twenty-first-century climate change. Cox *et al.* combined the obtained linear relationship with high-quality measurements of atmospheric CO₂ and temperatures from global observing networks, and narrowed the range of probable future outcomes. Their analysis led to a striking conclusion: many Earth-system models probably overestimate the magnitude of the tropical carbon losses that would occur in response to climate warming. As a result, the authors argue, the likelihood of a tropical dieback event is considerably lower than might be inferred from earlier work.

Does this mean that we no longer need to worry that climate change will bring about the loss of tropical-forest ecosystems? Not necessarily. Obtaining the correct magnitude of year-to-year atmospheric CO₂ responses to climate modes is necessary, but not sufficient, for accurate, longer-term carbon-cycle predictions over decades to centuries. For example, temperature changes and drought events that drive much of the interannual variability in contemporary atmospheric CO₂ concentrations have a fairly short duration because of the physical processes that regulate the El Niño–Southern Oscillation. These climate anomalies therefore have considerable immediate effects on 'fast' tropical-ecosystem processes, such as gross primary production, ecosystem respiration and fires. But they probably have



Figure 1 | Fire fighting in an Indonesian tropical forest. Cox *et al.*⁴ report that the likelihood of tropical forests dying off in response to global warming is much lower than previous studies have suggested. However, the effects of events such as tropical-forest fires must be integrated into climate models to assess more accurately the risk of dieback.

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only moderate effects on tree recruitment, competition and mortality, which are likely to shape ecosystem responses to climate change on longer timescales. New observations of forest dynamics are needed for further advances, along with improved representation in Earth-system models of climate feedbacks that are associated with human activity, such as fires⁹ (Fig. 1) and land-use change¹⁰.

Cox and colleagues' approach is exciting because it opens up fresh avenues for evaluating Earth-system models, and provides opportunities to reduce the uncertainties that are associated with future scenarios of global environmental change. Their study also provides clear motivation for scientists who study

the carbon cycle to develop more sophisticated approaches for parsing contributions to variability in contemporary atmospheric CO₂ that arise from changes in photosynthesis, fires, tree mortality, respiration from plants and microbes, and rates of ocean upwelling. The sensitivity of each of these processes to long-term climate change deserves further inquiry, both through mechanistic studies and through the discovery of additional emergent constraints, following Cox and co-workers' lead. ■

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MICROBIAL OCEANOGRAPHY

Killers of the winners

Viruses that infect the SAR11 group of oceanic bacteria have finally been found and sequenced. Because SAR11 is ubiquitous, these viruses may be the most abundant in the oceans — and perhaps in the entire biosphere. SEE LETTER P.357

DAVID L. KIRCHMAN

More than 20 years ago, the discovery of billions of viruses in the oceans was big news, worthy of articles in *Nature*¹ and on the front page of the *Washington Post*. A year later another *Nature* report was published², this time about the most abundant bacterial group in the oceans, cryptically called SAR11. The two stories now come together in a paper on page 357 of this issue. Zhao *et al.*³ describe DNA viruses that they call 'pelagiphages' and which infect laboratory-grown representatives of SAR11 bacteria

(Fig. 1). The authors use genomic-sequence data to argue that pelagiphages are among the most abundant viruses in the oceans and perhaps the entire biosphere. The report ends long-running speculation about SAR11, but prompts new questions about marine viruses and the control of microbes in the oceans*.

The general importance of bacteria in marine ecosystems was recognized long before the discovery of SAR11. Bacteria were known to be the most abundant organisms in the oceans — numbering nearly 10⁹ per

*This article and the paper under discussion³ were published online on 13 February 2013.

litre of surface sea water — and to be mediators of many biogeochemical processes in the cycling of carbon and other elements. However, until about 1990, microbiologists had identified only a few marine bacterial species because most could not be isolated and cultivated in the lab using the methods available at the time.

The development of cultivation-independent methods based on sequencing the 16S ribosomal RNA gene, which contains taxon-specific signatures, markedly enhanced our ability to distinguish between types of bacteria. These methods enabled the discovery of SAR11 bacteria in the Sargasso Sea² (hence the SAR moniker) and eventually their identification in every other marine system examined. There is even a relative of SAR11 in freshwater environments⁴. The bacteria's preferred habitat is the surface layer of the pelagic zone (water of oceans and lakes away from the shore and bottom), where the bacteria are so ubiquitous that when a SAR11 strain was finally isolated and cultivated in the lab it was dubbed *Pelagibacter ubique*⁵. This name was the inspiration for pelagiphage — the phages, or viruses of bacteria, found by Zhao and colleagues.

With the discovery of SAR11's abundance came the obvious question of why. What makes this bacterial clade so successful? Part of the answer is that the group is diverse, with different SAR11 types dominating different oceanic waters. But other bacterial groups are diverse, so why is SAR11 the clear winner in the oceans? One popular explanation, based on the small cell size and slow growth of *P. ubique*, is that SAR11 differs from other bacteria by being a defence specialist that fends off viruses and thereby achieves high abundance despite slow growth. This hypothesis was supported by the apparent lack of a SAR11-attacking virus, even though being perfectly impervious to viruses would make SAR11 unique in the biosphere.

In fact, the negative evidence was never very convincing, given the difficulties of identifying viruses in nature. The usual approach in virus characterization is to start by propagating the viruses in hosts grown on solid media,

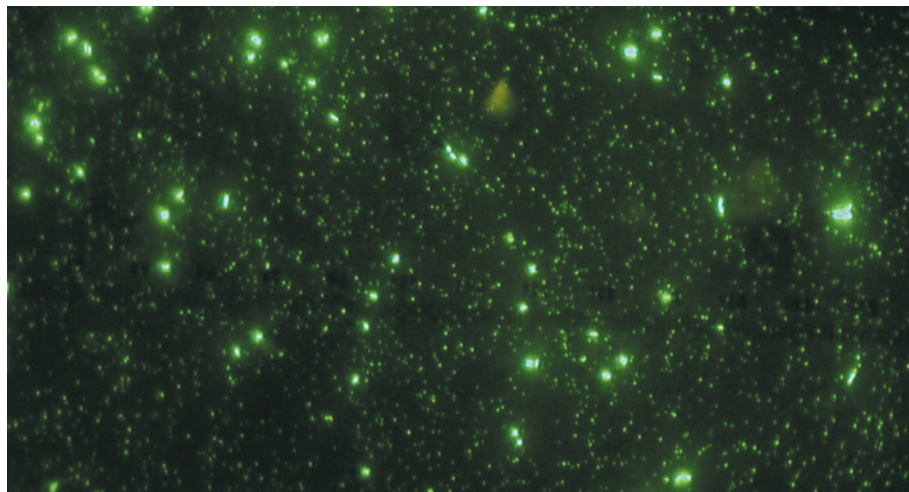


Figure 1 | Ocean inhabitants. A photomicrograph of a seawater sample taken off the coast of California. The larger dots are bacteria (about 0.5 micrometres in diameter) and the smaller ones are viruses; both are stained with the DNA-specific stain SYBR Green. The bacteria predominantly belong to the SAR11 group. Zhao and colleagues' results³ suggest that many of the viruses are pelagiphages that infect SAR11 bacteria.