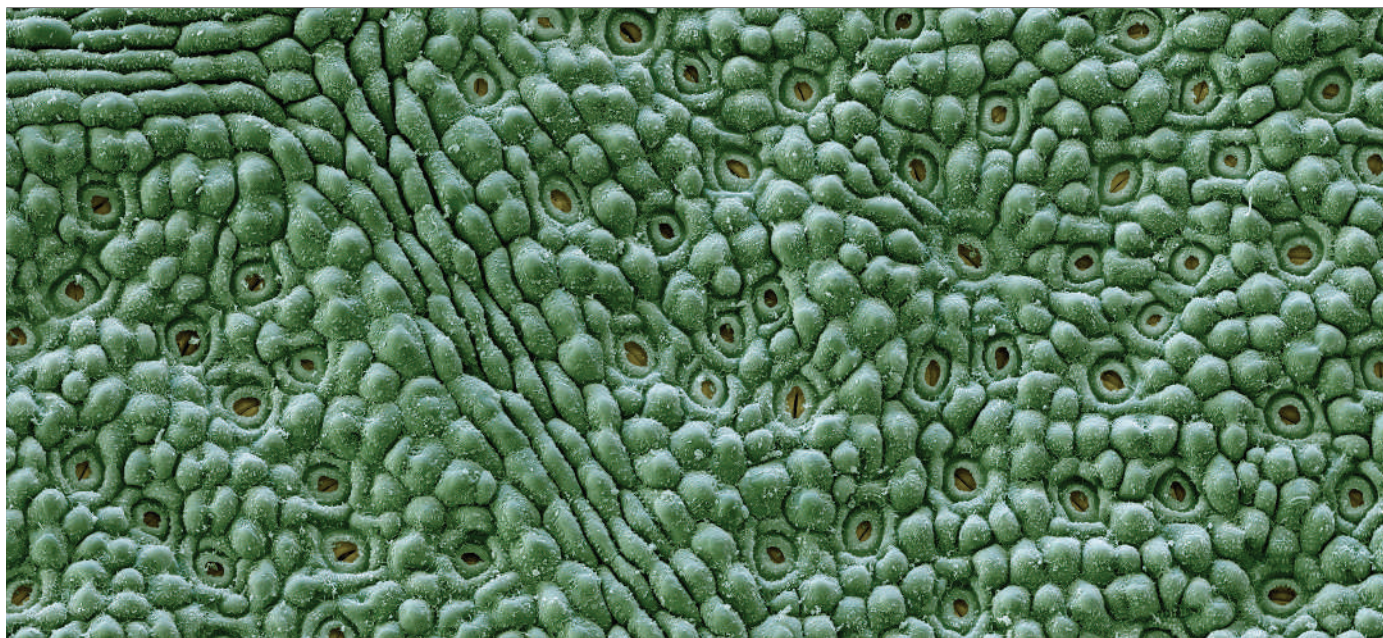


NEWS & VIEWS



EYE OF SCIENCE/SPL

GLOBAL CHANGE

The water cycle freshens up

Damon Matthews

Rivers are delivering increasing amounts of fresh water to the ocean. The cause seems to be the influence that higher concentrations of atmospheric carbon dioxide are having on water use by plants.

Measurements of stream flow around the world have documented an increase in the amount of water that runs off the continents and returns to the ocean¹. This trend has been occurring since the beginning of the century, yet changes in precipitation over land do not sufficiently account for this increase. On page 835 of this issue, Gedney *et al.*² identify an important contributor to increasing global runoff — decreased evaporation resulting from the influence of elevated atmospheric carbon dioxide on plant physiology (Fig. 1, overleaf).

Carbon dioxide is the currency of plant photosynthesis: plants take up CO₂ from the atmosphere and incorporate it into their tissues in the form of organic carbon compounds. This uptake of CO₂ is accomplished through plant stomata — small openings in the surface of leaves (pictured above) that open and close to allow the exchange of CO₂ and other gases with the atmosphere. During gas exchange, water is inevitably lost to the atmosphere, again through stomatal openings. This is the process of plant transpiration, which, on a global scale, mediates the transfer of water from the soil into plant tissues, and out through stomata to the atmosphere. On vegetated land, plant

transpiration can make a substantial contribution to total surface evapotranspiration, which represents the sum of plant transpiration and other surface evaporation.

Plants can regulate the opening and closing of stomata in response to changing environmental conditions; in a high-CO₂ atmosphere they are more efficient in their use of soil moisture. The stomata do not open as much or for as long, and less water is lost from leaves to the atmosphere³. As a consequence, plants acquire enough carbon through their stomata with less water uptake from the soil. The result is that continental evapotranspiration is reduced, more moisture is left in the soil, and this additional surface water can lead to increased continental runoff⁴.

Using a technique known as 'optimal fingerprinting' (also known as 'detection and attribution'), Gedney *et al.*² show that this direct effect of elevated CO₂ on plant transpiration is the dominant contributor to observed increases in continental runoff. Optimal fingerprinting is simply a statistical regression in which a model simulation is compared with observations to isolate which processes in the model are consistent with the observed data. If

a model simulation is consistent with observations, the process that drives the model trend is said to be 'detected' in the observations; if the observed trend is also inconsistent with other plausible explanations, then the trend can be 'attributed' to a specific cause.

Gedney *et al.* investigated four plausible contributors to observed increases in runoff: climate change leading to changes in temperature and precipitation; land-use change and consequent changes in vegetation cover; so-called 'solar dimming', resulting from an increasingly hazy atmosphere; and the direct effect of CO₂ on plant transpiration. The effects of each of these on surface runoff were simulated using a sophisticated land-surface and vegetation model, and the results of the model were compared with historical observations of continental runoff. The authors' analysis shows that model-simulated runoff trends are consistent with the observed trend only when the direct effect of CO₂ on transpiration is included in the simulation. So they attribute increases in continental runoff over the past century to the physiological effect of elevated atmospheric CO₂.

Detection and attribution has been widely

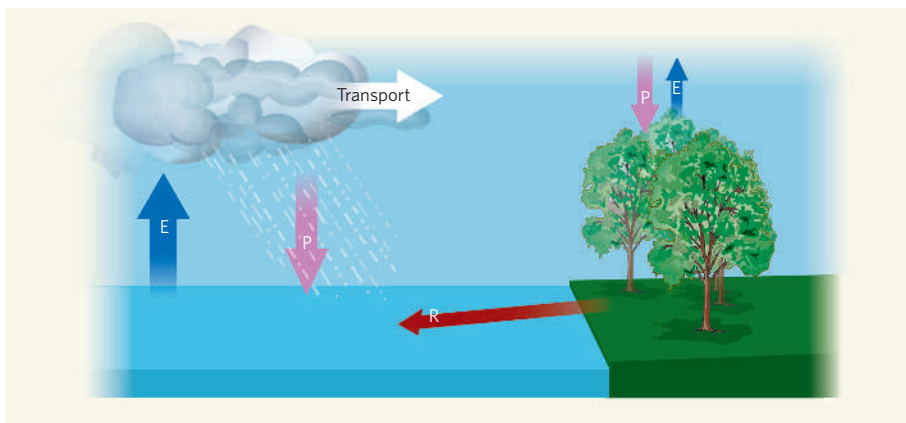


Figure 1 | Plants, CO₂ and the global water cycle. The balance between precipitation (P) and evaporation (E) over land determines the surface runoff (R), which returns water from the continents to the oceans. Plant photosynthesis plays an integral role in the global water cycle, by mediating the transfer of water from the land surface to the atmosphere. Elevated CO₂ can lead to closure of leaf stomata, which reduces leaf water loss and thereby decreases overall continental evaporation. Gedney *et al.*² show that this process, initiated by increased atmospheric CO₂, can account for the increases in surface runoff observed over the past century.

used in climate science to attribute observed climate trends to both natural and anthropogenic causes⁵. Recent increases in surface temperature have been successfully attributed to increases in CO₂ and other greenhouse gases⁶, as have changes in other climate variables such as ocean heat content⁷ and sea-level pressure⁸. Gedney and colleagues' research represents the first time that detection-and-attribution techniques have been used to

successfully link changes in the functioning of terrestrial ecosystems to human influences on the atmosphere.

As with any statistical analysis, these results are only as sound as the model used, the experimental design and the quality of observations. As our understanding of the terrestrial biosphere and our ability to model and monitor it improves, contributors to observed runoff trends that were not considered in this

study may well be identified. Gedney and colleagues' findings are nonetheless an important step forward in our understanding of the diverse and complex ways in which human activities are affecting the global climate system. The findings have implications for future surface warming and freshwater availability, both of which could increase if CO₂ continues to affect surface-water fluxes as demonstrated here. This research also opens some fascinating avenues of investigation — such as the possibility of using records of river runoff to monitor the functioning of terrestrial ecosystems in response to climate change, or of studying how changes in runoff induced by elevated CO₂ might affect ocean circulation.

Damon Matthews is in the Department of Geography, University of Calgary, 2500 University Drive NW, Calgary, Alberta T2N 1N4, Canada.
e-mail: dmatthew@ucalgary.ca

1. Labat, D., Godderis, Y., Probst, J. L. & Guyot, J. L. *Adv. Wat. Res.* **27**, 631–642 (2004).
2. Gedney, N. *et al.* *Nature* **439**, 835–838 (2006).
3. Medlyn, B. E. *et al.* *New Phytol.* **149**, 247–264 (2001).
4. Field, C., Jackson, R. & Mooney, H. *Plant Cell Environ.* **18**, 1214–1255 (1995).
5. International Ad Hoc Detection and Attribution Group *J. Clim.* **18**, 1291–1314 (2005).
6. Tett, S. F. B. *et al.* *J. Geophys. Res.* **107**, 4306 (2002).
7. Reichert, K. B., Schnur, R. & Bengtsson, L. *Geophys. Res. Lett.* **29**, 1525 (2002).
8. Gillett, N., Zwiers, F. W., Weaver, A. J. & Stott, P. A. *Nature* **422**, 292–294 (2003).

DEVELOPMENTAL BIOLOGY

Two paths to silence merge

Panthea Taghavi and Maarten van Lohuizen

To maintain their identity across generations, specialized cells must heritably repress swathes of genes — keeping active only genes necessary for the cell's purpose. Now it seems two repressive pathways join forces.

Even though cells of all developmental stages carry the same DNA, they have their own identity, defined by the combination of proteins expressed in each cell. These expression patterns, although set early during development, are reproduced in each mature, specialized cell later in life, over many cell divisions. This phenomenon is referred to as 'cellular memory'. Any perturbation of this fine-tuned system is a hazard to proper development and health.

Cellular memory is thought to be regulated by two 'epigenetic' mechanisms, which heritably change the characteristics of the cell without altering its DNA sequence. These mechanisms do this by altering the chromatin (the DNA and its associated proteins), which changes the availability of the genes to be expressed. One mechanism involves a group of enzymes that attach methyl groups to the DNA, the DNA methyltransferases (DNMTs);

the other involves Polycomb group (PcG) proteins, which modify the histone proteins around which the DNA is wrapped. On page 871 of this issue, Viré *et al.*¹ show a direct interaction between DNMTs and the Polycomb protein EZH2 that hints at how these complex systems might collaborate to set up cellular memory.

DNA methylation helps to reorganize chromatin into a 'silent' state in which genes are not expressed. In mammals, DNMT3A and -3B are mainly responsible for establishing methylation at previously unmethylated sites, whereas DNMT1 is the major maintenance methyltransferase, reproducing existing methylation patterns during cell division².

PcG proteins were originally identified for their role in maintaining the repressed state of certain developmental genes in the fruitfly *Drosophila*. EZH2 is a histone methyltransferase

that can methylate lysine 27 of the tail of histone H3 (H3-K27) or lysine 26 of histone H1 (H1-K26)³. This enzyme functions as part of the Polycomb repressive complexes 2 and 3 (PRC2/3), and whether it methylates H1 or H3 depends on which other proteins are in the complexes⁴. These histone modifications can attract other repressive complexes, such as Polycomb repressive complex 1 (PRC1), that then propagate the silenced state^{4,5}.

In their study, Viré *et al.* show convincingly that EZH2 interacts with all three DNMTs *in vitro* and *in vivo* (Fig. 1). DNMTs have not been found previously in purified PcG complexes from *Drosophila* or mammals, perhaps indicating that the interactions observed by Viré *et al.* are transient. How could these interactions affect the gene-expression programme of the cell? The authors find that proper repression of a few genes targeted by EZH2 requires both EZH2 and DNMTs. Moreover, EZH2 is needed to bring DNMTs to the regulatory regions ('promoters') of the EZH2 target-genes. Depletion of EZH2 disturbs this recruitment, derepressing the genes and allowing expression. At the same time, there is a decrease in the repressive histone H3-K27 methylation marks.

These results reveal that EZH2, as part of the PRC2/3 complexes, can physically recruit DNMTs to certain target-genes and that this process is essential for silencing the genes.