

News & views



Figure 1 | Lake Junin, located between the eastern and western mountain chains of the Peruvian Andes.

JONATHAN CHANCASANA/ALAMY

Climate science

Sediment study finds the pulse of tropical glaciers

Aaron E. Putnam

In regions of the globe at middle and high latitudes, glacial periods have waxed and waned for hundreds of millennia. Glacier-derived sediment in a Peruvian lake suggests that tropical glaciers have moved to a similar beat. **See p.301**

At the peak of the last ice age, about 20,000 years ago, vast ice sheets covered northern portions of continents in Earth's Northern Hemisphere, and glaciers extended from mid-latitude mountain chains in both hemispheres¹. These regions were simultaneously locked into a climate marked by cold temperatures and advancing glaciers, yet Earth's orbital history suggests that summers should have been warm in the

Southern Hemisphere and cool in the Northern Hemisphere¹. Since this conundrum emerged several decades ago, scientists have grappled with its implications, and its relationship with the origins of glacial cycles, which had varied regularly for hundreds of thousands of years. What caused synchronized bipolar ice-age cooling? And did glaciers in the tropics vary with the same rhythm as did those at higher latitudes? On page 301, Rodbell and

colleagues² show that the timing of glacial variations in the tropical Andes is strikingly similar to that at higher latitudes over a period of nearly 700,000 years.

Mountain glaciers are highly sensitive, purely physical monitors of climatic conditions. The worldwide retreat of mountain glaciers that has occurred over the past century or so in response to industrial-age warming is an iconic demonstration of ongoing climate change³. Likewise, glaciers have sensitively monitored climate changes in the past. Evidence for ancient glacier fluctuations is imprinted on the landscape and preserved in sediments. One means of reconstructing past glacier variations involves the mapping and dating of glacial landforms, such as moraine ridges, which form from the material dumped at the edge of a stabilized glacier and delineate former ice boundaries. These landforms provide direct, physical evidence of the extent of previous glaciers.

However, older landforms tend to be overriden and destroyed by more recent glacier advances, leading to an incomplete archive⁴. Rodbell and colleagues showcase another approach to reconstructing glacier activity. This involves examining accumulations of

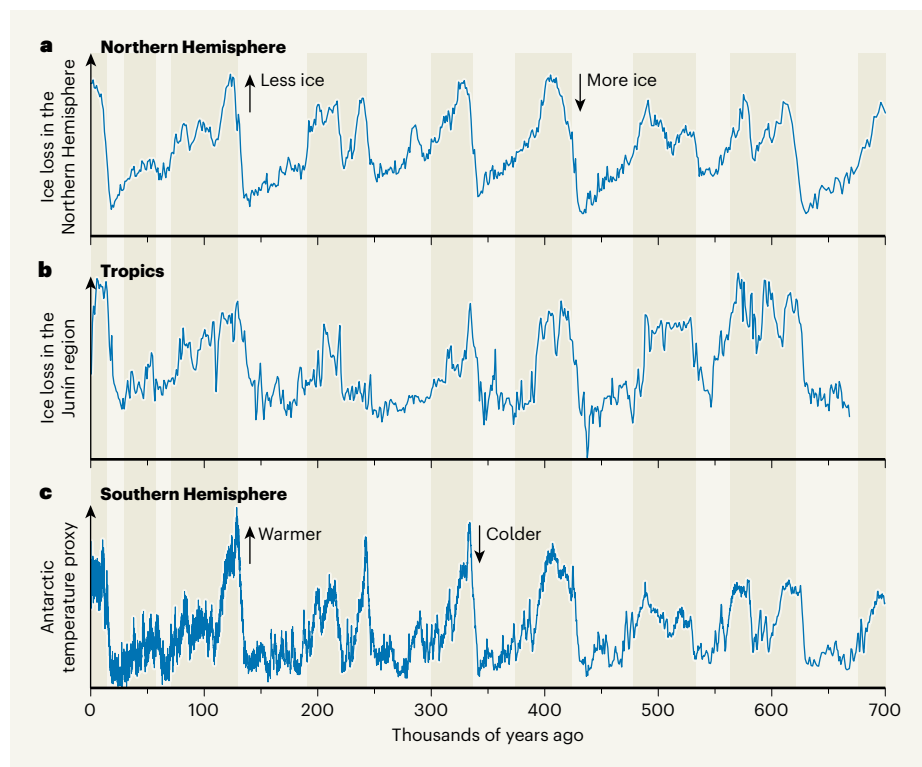


Figure 2 | Glacial periods in the tropical Andes correspond to global ice-age climate cycles. Earth's Northern and Southern hemispheres are both known to have experienced oscillations in glacial periods in the past, but it remains unclear whether tropical glaciers also underwent such changes. Rodbell *et al.*² used glacier-derived sediment from Lake Junín in the Peruvian Andes to reconstruct a 680,000-year record of glacial variation in the region. **a**, The authors compared their results with proxy measurements of global ice volume from another study¹². **b**, From their measurements of the material properties of the sediment, Rodbell *et al.* computed a proxy for the extent of ice loss in the Lake Junín region. **c**, The authors also compared their findings with proxy temperature measurements inferred from cores drilled from Antarctic ice¹³. Together, the results suggest that tropical regions have undergone the same climatic variations as those attributed to the polar regions. (Adapted from Figs 3 and 4 of ref. 2.)

glacier-derived sediments that have been transported by meltwater and deposited in downstream lake basins. Although not as direct as moraine-based reconstructions, the approach has the advantage of accessing potentially longer and more-continuous records of glacier activity than can be obtained by studying landforms.

To derive a long-term record of tropical glaciation, Rodbell and colleagues extracted an impressive 95-metre-long sediment core from Lake Junín (Fig. 1), which lies between the eastern and western mountain chains of the Peruvian Andes. Although the nearby mountains are too low to support present-day glaciers, impressive moraine structures situated upstream of Lake Junín mark the limits of former ice-age glaciers⁵.

The team used extensive radiocarbon dating, uranium–thorium dating and geomagnetic measurements to establish that material in the core spans a time period of 680,000 years. Among a host of analyses, the authors measured the titanium-to-calcium ratio, which reflects the proportion of the sediments that have been eroded from nearby continental rocks. They also determined the

magnetic susceptibility of the sediments – a measure of how readily they can be magnetized. Together, these data suggest that glacier-derived sediment found its way into the lake basin. This interpretation is bolstered by the fact that an increase in the flux of glacial sediment, as estimated by Rodbell and colleagues, coincided with the time of construction of moraine ridges in the Lake Junín catchment (see, for example, ref. 5).

The 680,000-year record of Lake Junín sedimentation shows a striking correspondence to the rhythm of high-latitude glacial cycles inferred from sediment records obtained in deep-sea investigations. Increases in the amount of glacial sediment delivered to the lake coincided with ice-age expansions of the large Northern Hemisphere ice sheets. Furthermore, glacial periods for Junín correspond to cold intervals registered in Antarctic ice cores – although it should be noted that the Antarctic temperature reconstruction was used to help build the timeline of the Junín record. These observations suggest that the rhythm of ice ages for most of the past million years encompassed the entire globe (Fig. 2).

Rodbell and colleagues² attribute the general similarities between high- and low-latitude glacier expansions to a combination of factors related to the growth of the large northern ice sheets and the global impacts of reduced greenhouse-gas concentrations. They suggest that certain characteristics of the Lake Junín record arose from expansions of large northern ice sheets that were related to the redistribution of sunlight on Earth's surface, driven by slow variations in the tilt and wobble of Earth's axis. The authors also point to climate-induced changes in precipitation patterns to explain differences between signatures of tropical Andean glaciers and Northern Hemisphere ice volume, and to account for millennial-scale fluctuations in the Lake Junín record.

However, mysteries remain with regard to the global picture. For example, tropical Andean glaciers seem to have achieved and then sustained their maximal extent before the ice sheets hit their maximum volumes during the most recent glacial cycle^{2,5–7} – and in the case of glaciers in the Lake Junín catchment, perhaps earlier cycles as well. This also seems to be true of mid-latitude mountain glaciers in both hemispheres (see, for example, refs 8, 9). Tropical and mid-latitude glacier systems also receded rapidly at the end of the last ice age – outpacing the demise of the ice sheets and the rise in atmospheric carbon dioxide to concentrations expected in an interglacial period (see, for example, refs 7–10).

Perhaps local factors account for this. But another possibility is that a third factor was involved in driving temperature changes of similar timing and severity around the planet, influencing both large ice sheets and small mountain glaciers. The polar regions have conventionally been emphasized as drivers and pacemakers of ice-age climate variability. However, the tropics include the Indo-Pacific Warm Pool, Earth's 'heat engine', which can produce rapid global temperature shifts^{8,11}. The tropics might also be sensitive to changes in Earth's orbit and climate dynamics occurring at higher latitudes^{8,11}. Given the correspondence between signatures of tropical glacial periods and higher-latitude ice-age climate changes, it is perhaps worth considering the role of the tropical regions themselves in facilitating a nearly synchronous rhythm of global ice ages⁸.

It is clear from Rodbell and colleagues' innovative record that any hypothesis to explain what drove ice-age climate cycles must account for the near-simultaneity of glacial periods in the tropical Andes, and glacier and climate changes at higher latitudes in both polar hemispheres. The authors have demonstrated an exciting strategy for approaching this problem through detailed sediment-based reconstructions of glacier melt paired with precise moraine chronologies.

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Neuroscience

A gene-expression axis defines neuron behaviour

Hongkui Zeng & Saskia E. J. de Vries

A combination of functional imaging and gene-expression profiling in brain tissue has been used to unravel the properties of 35 subtypes of neuron in mice, revealing a gene-expression axis that governs each subtype's activity. **See p.330**

An essential step towards understanding how the brain works is to create a catalogue of brain-cell types. Cell-type classification has been transformed by single-cell transcriptomics, which reveals the entire repertoire of expressed genes (the transcriptome) in each of thousands or millions of single cells isolated from a brain region of interest¹. But what do these cell types do, and what parts do they play in neuronal circuits? On page 330, Bugeon *et al.*² attempt to address these questions by developing an approach to measuring the *in vivo* activities of transcriptomically defined cell types in the mouse visual cortex.

Single-cell transcriptomics has revealed many different groups of cortical neurons^{1,3,4} – about 95 in the mouse primary visual cortex, for instance³. These groups can be organized in a hierarchical manner on the basis of transcriptomic similarities and differences, forming a four-level structure of classes, subclasses, types and subtypes.

Unravelling the function of each of these groups requires the ability to distinguish them in living brains and measure their activities over time. This has become possible in the past few years thanks to spatial transcriptomics^{5–7}, in which gene expression is analysed in a brain slice, preserving the spatial location of each cell. Spatial transcriptomics can be conducted after *in vivo* functional studies in the same brain tissue, enabling researchers to assign transcriptomic identities to neurons for which other properties (such as activity or shape) have already been measured^{8,9}.

Bugeon and colleagues set out to increase

the scope of such post hoc spatial transcriptomic profiling, in terms of both the number of cells profiled and the number of genes probed in each cell. To do this, the authors developed a technique called coppaFISH, which determines the expression of 72 genes simultaneously in individual cells in thin brain sections. This expression profile can then be mapped to existing³ single-cell transcriptomes to decode fine-grained cell identities.

The researchers made use of this approach

to analyse one class of neuron, GABAergic inhibitory interneurons, in the mouse primary visual cortex. Inhibitory interneurons are neurons that send projections to local brain regions, and that typically suppress or shape the activity of excitatory neurons (the neurons that send long-range axon projections to other parts of the brain to convey sensory or behavioural information). There are dozens of inhibitory interneuron subtypes in the cortex, and their functional properties had not been studied in detail. The authors used a technique called calcium imaging (in which intracellular calcium levels act as a proxy for neuronal activity) to record the activity of large populations of these neurons as mice ran on a ball and responded to visual stimuli on a screen. The authors subsequently applied coppaFISH to the imaged tissue to identify cells in the superficial layers of the cortex (Fig. 1). They also performed a series of image-alignment tasks, to ensure that the correlations between the imaging and transcriptomic data for each cell were highly precise. In total, they obtained data for 1,090 interneurons.

The authors assigned these interneurons to 5 subclasses, 11 types and 35 subtypes, many of which had not previously been identified *in vivo* (such as a subclass named Sncg). They then used their data to analyse how each group responded to different visual stimuli and different brain states (that is, states characterized by patterns of activity that drive particular behaviours, such as running or being stationary). They found that the responses of the neurons to various features of the visual stimuli (such as orientation and direction selectivity) differed significantly across subclasses, but not types or subtypes. By contrast, responses to different brain states, as

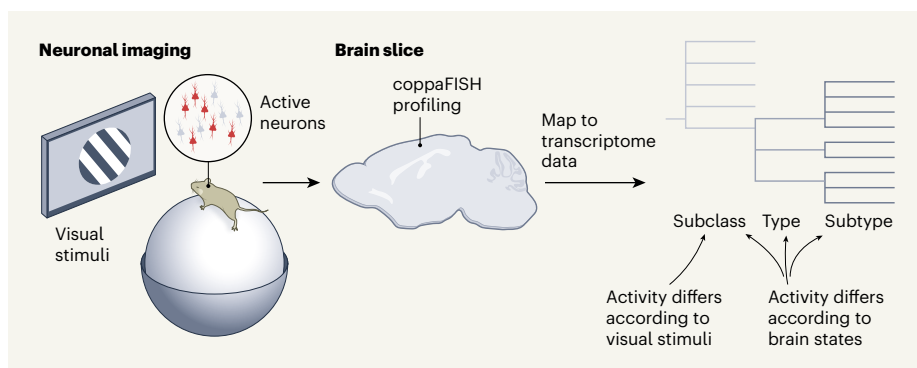


Figure 1 | Combining function with gene expression. Bugeon *et al.*² used imaging approaches to measure the activity of one class of neuron in the visual cortex of the mouse brain, while the animal ran on a ball and responded to visual stimuli on a screen. They subsequently analysed the expression of 72 genes in slices of brain containing the same neurons, using a technique called coppaFISH. The authors mapped the coppaFISH profile of each neuron onto existing gene-expression profiles (transcriptome data) for neurons of various identities – this enabled them to assign each of the neurons they had analysed to one of 5 subclasses, 11 types and 35 subtypes (for simplicity, only part of the tree is shown). Aligning the activity and coppaFISH data from each cell enabled the authors to determine how a cell's classification into a particular transcriptomic subclass, type and subtype related to its activity. Neurons exhibited different responses to visual stimuli at subclass level, whereas differences in brain-state-related activity (whether the mouse is running or stationary, for instance) were apparent at subclass, type and subtype levels.