CLIMATE SCIENCE

Oddities in ocean record resolved

An analysis of the record of sea surface temperature reveals that some climate variations that are thought to have occurred in the North Atlantic and the North Pacific oceans are an artefact of changes in measurement approaches. SEE LETTER P.393

ZEKE HAUSFATHER

Reducing uncertainties in the historical record of Earth's surface temperature can improve scientists' ability to understand and explain changes in the climate over the past 150 years. This is particularly important for the early part of the twentieth century, because the cause of observed warming at that time remains fiercely debated[1]. On page 393, Chan *et al.*[2] demonstrate an innovative approach to account for differences in how sea surface temperature was measured in the early twentieth century. Their results suggest modestly less warming in the North Atlantic Ocean and substantially greater warming in the North Pacific Ocean during the period from 1908 to 1941, relative to previous estimates. Such findings indicate that intrinsic climate variability has a smaller impact on regional warming rates than was thought.

Improving historical temperature estimates has long been a key focus for climate researchers. Until the past few decades, most temperature measurements on both land and ocean were not aimed at detecting long-term climate changes. Rather, they were mainly intended to document average climate conditions or were for shorter-term meteorological purposes[3]. Adjustments to measurement methods that introduced biases of a few tenths of a degree Celsius were common. Although these biases were of little concern at the time, they become substantially more relevant when trying to detect long-term changes in global temperature of about 1 °C over the past 150 years.

The record of global surface temperature is produced by combining measurements of sea surface temperature (SST) with measurements of air temperature over land and ice. The largest remaining uncertainties in the global temperature record are associated with the SST estimates. Specifically, changes in observational instrumentation and techniques over time, coupled with patchy metadata (information about data) and sparse sampling in some regions complicate the interpretation of the historical record[4].

"The method offers an innovative solution to the lack of good ship metadata during the early twentieth century."

Initially, SST estimates were made using wooden buckets that were thrown over the sides of ships, filled with water and hauled up. The temperature of the water in the buckets was then measured using a thermometer. While the buckets were being hoisted up, evaporative cooling and exposure to ambient conditions would often reduce the temperature of the water by a few tenths of a degree Celsius.

This bias was exacerbated by a transition to poorly insulated canvas buckets in the late nineteenth century, and these buckets continued to be the main means of SST measurement until the period of the Second World War. Accounting for the cold bias in bucket measurements is the single largest adjustment to the ocean (and global) temperature record. Without the adjustment, the estimated rate of ocean warming from 1850 to the present would be about 30% higher[5].

A bucket measurement can be affected by a wide range of factors. These include the height of the ship, the composition and size of the bucket, how long it remains in the sea, whether the water is stirred before measurement and how long the thermometer is left in the water. Little of this information was recorded in a form that has survived to the present day. As a result, researchers have often had to inaccurately treat many bucket measurements as having the same magnitude of bias.

Chan and colleagues found a clever way to tackle this problem. They looked at the difference between SST measurements that were made within 300 kilometres and 2 days of one another, producing a data set of 6 million measurement pairs between 1908 and 1941. Ships were grouped by national origin, on the assumption that ships from the same country would tend to have similar measurement practices at any given time. The authors found sizeable offsets in SST estimates between ship

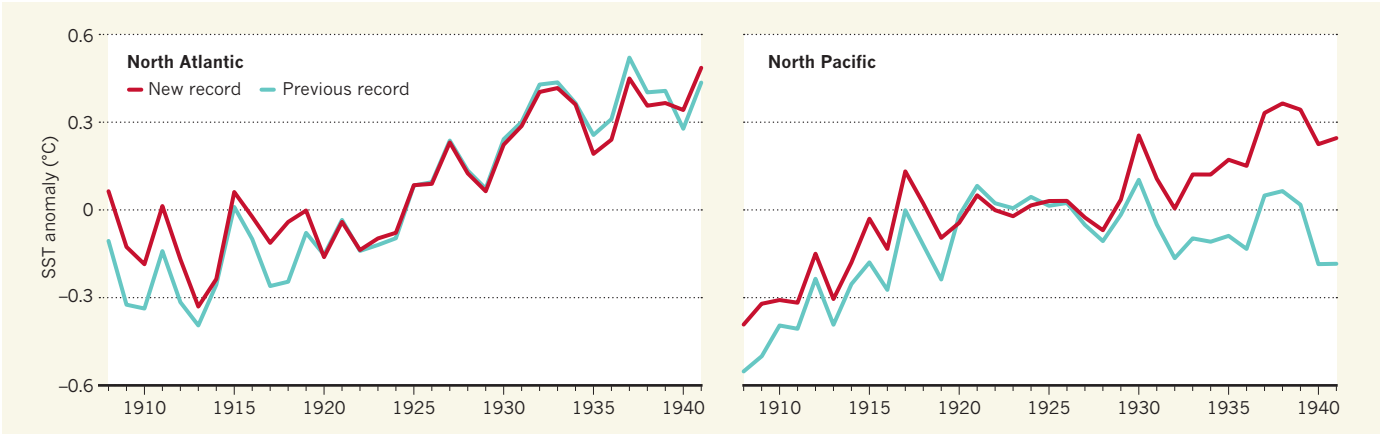

Figure 1 | Adjustments to sea surface temperature (SST) data. Chan *et al.*[2] propose corrections to the SST record of the North Atlantic and the North Pacific oceans from 1908 to 1941. The new record suggests slightly less warming in the North Atlantic and much greater warming in the North Pacific, compared with the previous record. The SST data are expressed as a departure (anomaly) from the average value during the period 1920–29. (Adapted from Fig. 4 of the paper[2].)

groups, ranging from −0.3 °C to +0.6 °C.

Digging further into these differences, Chan *et al.* realized that measurements from Japanese ships in the North Pacific suddenly became about 0.35 °C cooler after 1930 when compared with measurements from other countries. This change was caused by the Japanese switching from recording temperatures in whole-degrees Fahrenheit to taking readings in degrees Celsius and then dropping any numbers after the decimal point. The authors identified a similarly large change in the North Atlantic that is associated with German readings, but the cause of this change is less clear.

Chan and colleagues' results suggest that scientists have been overestimating warming in the North Atlantic and substantially underestimating warming in the North Pacific during the early twentieth century because of not fully accounting for biases in bucket measurements (Fig. 1). These findings bring the difference in estimated warming between the two regions in line with projections from climate models. However, there are still large differences between models and observations in the overall rate of global ocean warming during this period.

The authors' approach of comparing groups of proximate-ship measurements is conceptually similar to that used in identifying problems in the land temperature record, whereby each weather station is compared with its neighbours to find and remove localized biases[6]. The method offers an innovative solution to the lack of good ship metadata during the early twentieth century and provides a major advance in our understanding of historical ocean measurements.

This study, and recent major updates to the SST record at the UK Met Office's Hadley Centre[7], provide a useful reminder that large systematic biases might remain in our observational temperature records. Improved quantification of these biases is still a key technical challenge for researchers, and will help to address questions about the performance of climate-model simulations of the past and the role of intrinsic climate variability in historical temperature change. ■

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1. Haustein, K. & Otto, F. E. L. *J. Clim.* https://doi.org/10.1175/JCLI-D-18-0555.1 (2019).
2. Chan, D., Kent, E. C., Berry, D. I. & Huybers, P. *Nature* **571**, 393–397 (2019).
3. Kent, E. C. *Bull. Am. Meteorol. Soc.* **98**, 1601–1616 (2017).
4. Lenssen, N. J. L. *et al. J. Geophys. Res. Atmos.* https://doi.org/10.1029/2018JD029522 (2019).
5. Kennedy, J. J., Rayner, N. A., Smith, R. O., Parker, D. E. & Saunby, M. *J. Geophys. Res. Atmos.* **116**, D14103 (2011).
6. Menne, M. J. & Williams, C. N. Jr. *J. Clim.* **22**, 1700–1717 (2009).
7. Kennedy, J. J., Rayner, N. A., Atkinson, C. P. & Killick, R. E. *J. Geophys. Res. Atmos.* https://doi.org/10.1029/2018JD029867 (2019).

GENETICS

How mutations express themselves

A method for detecting mutations and measuring gene-expression levels in the same cell has enabled an investigation into the effects of mutations in a specific gene on the emergence of a form of blood cancer. SEE ARTICLE P.355

SIDDHARTH RAJU & CHUN JIMMIE YE

The cells that circulate in the bloodstream perform various functions and, in adults, are derived from progenitor cells in the bone marrow. Mutations in the DNA sequences of progenitor cells can lead to changes in blood-cell development, sometimes resulting in cancer. Owing to technical constraints, elucidating the effects of progenitor mutations on blood-cell development has been challenging. On page 355, Nam *et al.*[1] report a method for detecting mutations and measuring gene expression in individual blood progenitor cells, and use it to analyse a mixture of progenitors with or without mutations in a cancer-linked gene. They show that progenitors that have the same mutation can give rise to cells with different gene-expression profiles.

Haematopoiesis — the process through which mature blood cells are formed from progenitors — is tightly regulated. The 'decision' that progenitor cells make as to which cell type to become is generally determined by the signals that they receive from their immediate surroundings. However, mutations that sometimes arise in these progenitor cells can result in the signals being blocked, overamplified or simply ignored, resulting in the enrichment or depletion of specific cell types and, in some cases, production of cancerous clones. Understanding how mutations in progenitor cells lead to changes in the production of different cell types is a key question.

Investigating how mutations in a progenitor cell affect its gene expression, and thus its identity and function, has been highly challenging, largely because mutant cells can be rare and often do not express molecular markers that can be used to separate them physically from non-mutant cells. Strategies to simultaneously detect genetic differences and measure gene expression in single cells have been used to assign cells from a mixture of immune blood cells to their human donor of origin[2], and to study changes in populations of host and

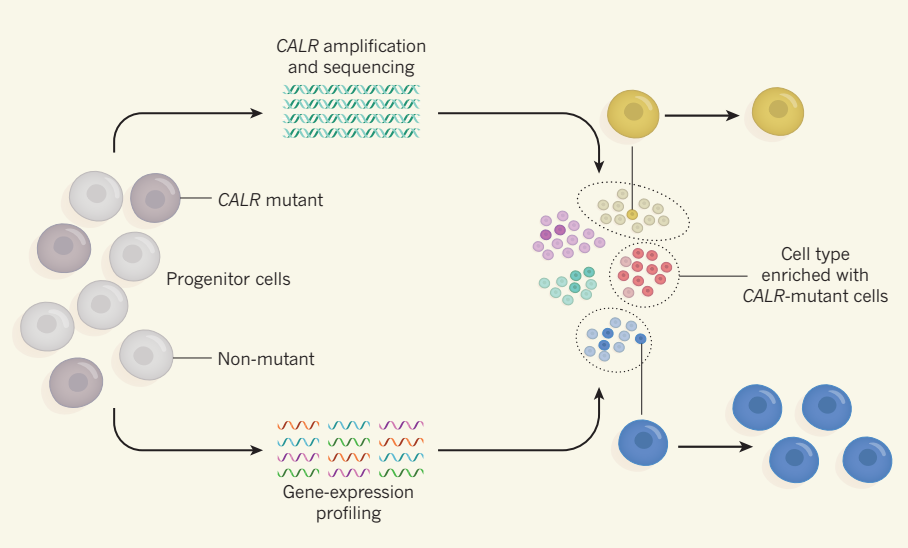

Figure 1 | An analysis of mutation status and gene expression in single cells. Nam *et al.*[1] sampled progenitor cells that give rise to blood cells from individuals who have a type of blood cancer that is caused by progenitor cells with mutations in the *CALR* gene. To distinguish mutant from non-mutant cells, the authors amplified and sequenced the *CALR* gene of individual cells. The authors also measured the levels of gene expression in each cell. They identified different cell types on the basis of a statistical analysis of the cells' gene-expression profiles (dotted circles represent statistical, rather than physical, cell groupings), and examined which of the cells in these different types had *CALR* mutations. Certain cell types were enriched in *CALR*-mutant cells, and *CALR* mutations had different effects (for example, on proliferation) in cells of different types.